BEST AVAILABLE COPY

BA

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
24 October 2002 (24.10.2002)

PCT

(10) International Publication Number
WO 02/083860 A2

(51) International Patent Classification[7]: C12N

(21) International Application Number: PCT/US02/11644

(22) International Filing Date: 9 April 2002 (09.04.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/282,739 10 April 2001 (10.04.2001) US
60/286,630 25 April 2001 (25.04.2001) US

(71) Applicant: **AGENSYS, INC.** [US/US]; 1545 17th Street, Santa Monica, CA 90404 (US).

(72) Inventors: **CHALLITA-EID, Pia, M.**; 15745 Morrison Street, Encino, CA 91436 (US). **RAITANO, Arthur, B.**; 10807 Cushdon Avenue, Los Angeles, CA 90064 (US). **FARIS, Mary**; 2538 Almaden Court, Los Angeles, CA 90077 (US). **HUBERT, Rene, S.**; 1644 North Occidentia Boulevard, Los Angeles, CA 90026 (US). **MORRISON, Karen**; 1044 Yale Street, Santa Monica, CA 90403 (US). **MORRISON, Robert, Kendall**; 1044 Yale Street, Santa Monica, CA 90403 (US). **GE, Wangmao**; 4838 Hollow Corner Road, Apartment 314, Culver City, CA 90230 (US). **JAKOBOVITS, Aya**; 3135 Hutton Drive, Beverly Hills, CA 90210 (US).

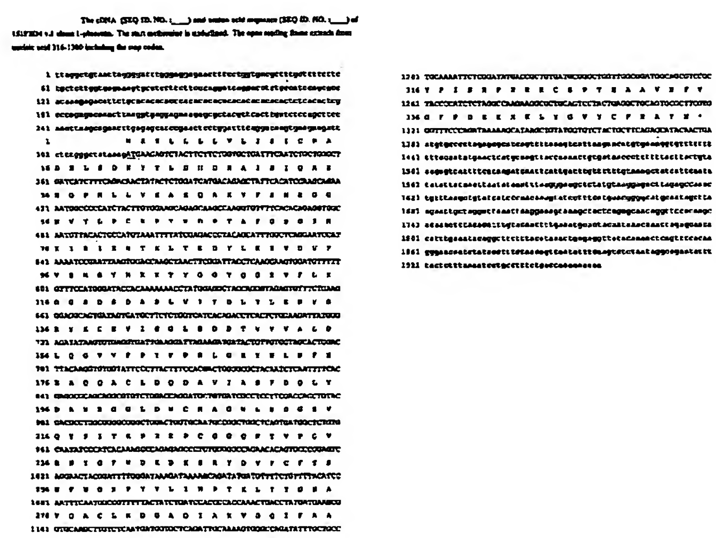
(74) Agents: **DEVERNOE, David, L.** et al.; Morrison & Foerster LLP, Suite 500, 3811 Valley Centre Drive, San Diego, CA 92130-2332 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,

[Continued on next page]

(54) Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 151P3D4 USEFUL IN TREATMENT AND DETECTION OF CANCER



(57) Abstract: A novel gene (designated 151P3D4) and its encoded protein, and variants thereof, are described wherein 151P3D4 exhibits tissue specific expression in normal adult tissue, and is aberrantly expressed in the cancers listed in Table 1. Consequently, 151P3D4 provides a diagnostic, prognostic, prophylactic and/or therapeutic target for cancer. The 151P3D4 gene or fragment thereof, or its encoded protein, or variants thereof, or a fragment thereof, can be used to elicit a humoral or cellular immune response; antibodies or T cells reactive with 151P3D4 can be used in active or passive immunization.

WO 02/083860 A2

GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 151P3D4 USEFUL IN TREATMENT AND DETECTION OF CANCER

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority from United States Serial No. 60/282,739 filed April 10, 2001, and United States Serial No. 60/286,630, filed April 25, 2001. The contents of these applications are hereby incorporated by reference herein in their entirety.

STATEMENT OF RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH

Not applicable.

FIELD OF THE INVENTION

The invention described herein relates to a gene and its encoded protein, termed 151P3D4, expressed in certain cancers, and to diagnostic and therapeutic methods and compositions useful in the management of cancers that express 151P3D4.

BACKGROUND OF THE INVENTION

Cancer is the second leading cause of human death next to coronary disease. Worldwide, millions of people die from cancer every year. In the United States alone, as reported by the American Cancer Society, cancer causes the death of well over a half-million people annually, with over 1.2 million new cases diagnosed per year. While deaths from heart disease have been declining significantly, those resulting from cancer generally are on the rise. In the early part of the next century, cancer is predicted to become the leading cause of death.

Worldwide, several cancers stand out as the leading killers. In particular, carcinomas of the lung, prostate, breast, colon, pancreas, and ovary represent the primary causes of cancer death. These and virtually all other carcinomas share a common lethal feature. With very few exceptions, metastatic disease from a carcinoma is fatal. Moreover, even for those cancer patients who initially survive their primary cancers, common experience has shown that their lives are dramatically altered. Many cancer patients experience strong anxieties driven by the awareness of the potential for recurrence or treatment failure. Many cancer patients experience physical debilitations following treatment. Furthermore, many cancer patients experience a recurrence.

Worldwide, prostate cancer is the fourth most prevalent cancer in men. In North America and Northern Europe, it is by far the most common cancer in males and is the second leading cause of cancer death in men. In the United States alone, well over 30,000 men die annually of this disease - second only to lung cancer. Despite the magnitude of these figures, there is still no effective treatment for metastatic prostate cancer. Surgical prostatectomy, radiation therapy, hormone ablation therapy, surgical castration and chemotherapy continue to be the main treatment modalities. Unfortunately, these treatments are ineffective for many and are often associated with undesirable consequences.

On the diagnostic front, the lack of a prostate tumor marker that can accurately detect early-stage, localized tumors remains a significant limitation in the diagnosis and management of this disease. Although the serum prostate specific antigen (PSA) assay has been a very useful tool, however its specificity and general utility is widely regarded as lacking in several important respects.

Progress in identifying additional specific markers for prostate cancer has been improved by the generation of prostate cancer xenografts that can recapitulate different stages of the disease in mice. The LAPC (Los Angeles Prostate Cancer) xenografts are prostate cancer xenografts that have survived passage in severe combined immune deficient (SCID) mice and have exhibited the capacity to mimic the transition from androgen dependence to androgen independence (Klein *et al.*, 1997, Nat. Med. 3:402). More recently identified prostate cancer markers include PCTA-1 (Su *et al.*, 1996, Proc. Natl. Acad. Sci. USA 93: 7252), prostate-specific membrane (PSM) antigen (Pinto *et al.*, Clin Cancer Res 1996 Sep 2 (9): 1445-51), STEAP (Hubert, *et al.*, Proc Natl Acad Sci U S A. 1999 Dec 7; 96(25): 14523-8) and prostate stem cell antigen (PSCA) (Reiter *et al.*, 1998, Proc. Natl. Acad. Sci. USA 95: 1735).

While previously identified markers such as PSA, PSM, PCTA and PSCA have facilitated efforts to diagnose and treat prostate cancer, there is need for the identification of additional markers and therapeutic targets for prostate and related cancers in order to further improve diagnosis and therapy.

Renal cell carcinoma (RCC) accounts for approximately 3 percent of adult malignancies. Once adenomas reach a diameter of 2 to 3 cm, malignant potential exists. In the adult, the two principal malignant renal tumors are renal cell adenocarcinoma and transitional cell carcinoma of the renal pelvis or ureter. The incidence of renal cell adenocarcinoma is estimated at more than 29,000 cases in the United States, and more than 11,600 patients died of this disease in 1998. Transitional cell carcinoma is less frequent, with an incidence of approximately 500 cases per year in the United States.

Surgery has been the primary therapy for renal cell adenocarcinoma for many decades. Until recently, metastatic disease has been refractory to any systemic therapy. With recent developments in systemic therapies, particularly immunotherapies, metastatic renal cell carcinoma may be approached aggressively in appropriate patients with a possibility of durable responses. Nevertheless, there is a remaining need for effective therapies for these patients.

Of all new cases of cancer in the United States, bladder cancer represents approximately 5 percent in men (fifth most common neoplasm) and 3 percent in women (eighth most common neoplasm). The incidence is increasing slowly, concurrent with an increasing older population. In 1998, there was an estimated 54,500 cases, including 39,500 in men and 15,000 in women. The age-adjusted incidence in the United States is 32 per 100,000 for men and 8 per 100,000 in women. The historic male/female ratio of 3:1 may be decreasing related to smoking patterns in women. There were an estimated 11,000 deaths from bladder cancer in 1998 (7,800 in men and 3,900 in women). Bladder cancer incidence and mortality strongly increase with age and will be an increasing problem as the population becomes more elderly.

Most bladder cancers recur in the bladder. Bladder cancer is managed with a combination of transurethral resection of the bladder (TUR) and intravesical chemotherapy or immunotherapy. The multifocal and recurrent nature of bladder cancer points out the limitations of TUR. Most muscle-invasive cancers are not cured by TUR alone. Radical cystectomy and urinary diversion is the most effective means to

eliminate the cancer but carry an undeniable impact on urinary and sexual function. There continues to be a significant need for treatment modalities that are beneficial for bladder cancer patients.

An estimated 130,200 cases of colorectal cancer occurred in 2000 in the United States, including 93,800 cases of colon cancer and 36,400 of rectal cancer. Colorectal cancers are the third most common cancers in men and women. Incidence rates declined significantly during 1992-1996 (-2.1% per year). Research suggests that these declines have been due to increased screening and polyp removal, preventing progression of polyps to invasive cancers. There were an estimated 56,300 deaths (47,700 from colon cancer, 8,600 from rectal cancer) in 2000, accounting for about 11% of all U.S. cancer deaths.

At present, surgery is the most common form of therapy for colorectal cancer, and for cancers that have not spread, it is frequently curative. Chemotherapy, or chemotherapy plus radiation, is given before or after surgery to most patients whose cancer has deeply perforated the bowel wall or has spread to the lymph nodes. A permanent colostomy (creation of an abdominal opening for elimination of body wastes) is occasionally needed for colon cancer and is infrequently required for rectal cancer. There continues to be a need for effective diagnostic and treatment modalities for colorectal cancer.

There were an estimated 164,100 new cases of lung and bronchial cancer in 2000, accounting for 14% of all U.S. cancer diagnoses. The incidence rate of lung and bronchial cancer is declining significantly in men, from a high of 86.5 per 100,000 in 1984 to 70.0 in 1996. In the 1990s, the rate of increase among women began to slow. In 1996, the incidence rate in women was 42.3 per 100,000.

Lung and bronchial cancer caused an estimated 156,900 deaths in 2000, accounting for 28% of all cancer deaths. During 1992–1996, mortality from lung cancer declined significantly among men (-1.7% per year) while rates for women were still significantly increasing (0.9% per year). Since 1987, more women have died each year of lung cancer than breast cancer, which, for over 40 years, was the major cause of cancer death in women. Decreasing lung cancer incidence and mortality rates most likely resulted from decreased smoking rates over the previous 30 years; however, decreasing smoking patterns among women lag behind those of men. Of concern, although the declines in adult tobacco use have slowed, tobacco use in youth is increasing again.

Treatment options for lung and bronchial cancer are determined by the type and stage of the cancer and include surgery, radiation therapy, and chemotherapy. For many localized cancers, surgery is usually the treatment of choice. Because the disease has usually spread by the time it is discovered, radiation therapy and chemotherapy are often needed in combination with surgery. Chemotherapy alone or combined with radiation is the treatment of choice for small cell lung cancer; on this regimen, a large percentage of patients experience remission, which in some cases is long-lasting. There is however, an ongoing need for effective treatment and diagnostic approaches for lung and bronchial cancers.

An estimated 182,800 new invasive cases of breast cancer were expected to occur among women in the United States during 2000. Additionally, about 1,400 new cases of breast cancer were expected to be diagnosed in men in 2000. After increasing about 4% per year in the 1980s, breast cancer incidence rates in women have leveled off in the 1990s to about 110.6 cases per 100,000.

In the U.S. alone, there were an estimated 41,200 deaths (40,800 women, 400 men) in 2000 due to breast cancer. Breast cancer ranks second among cancer deaths in women. According to the most recent

data, mortality rates declined significantly during 1992–1996 with the largest decreases in younger women, both white and black. These decreases were probably the result of earlier detection and improved treatment.

Taking into account the medical circumstances and the patient's preferences, treatment of breast cancer may involve lumpectomy (local removal of the tumor) and removal of the lymph nodes under the arm; mastectomy (surgical removal of the breast) and removal of the lymph nodes under the arm; radiation therapy; chemotherapy; or hormone therapy. Often, two or more methods are used in combination. Numerous studies have shown that, for early stage disease, long-term survival rates after lumpectomy plus radiotherapy are similar to survival rates after modified radical mastectomy. Significant advances in reconstruction techniques provide several options for breast reconstruction after mastectomy. Recently, such reconstruction has been done at the same time as the mastectomy.

Local excision of ductal carcinoma *in situ* (DCIS) with adequate amounts of surrounding normal breast tissue may prevent the local recurrence of the DCIS. Radiation to the breast and/or tamoxifen may reduce the chance of DCIS occurring in the remaining breast tissue. This is important because DCIS, if left untreated, may develop into invasive breast cancer. Nevertheless, there are serious side effects or sequelae to these treatments. There is, therefore, a need for efficacious breast cancer treatments.

There were an estimated 23,100 new cases of ovarian cancer in the United States in 2000. It accounts for 4% of all cancers among women and ranks second among gynecologic cancers. During 1992–1996, ovarian cancer incidence rates were significantly declining. Consequent to ovarian cancer, there were an estimated 14,000 deaths in 2000. Ovarian cancer causes more deaths than any other cancer of the female reproductive system.

Surgery, radiation therapy, and chemotherapy are treatment options for ovarian cancer. Surgery usually includes the removal of one or both ovaries, the fallopian tubes (salpingo-oophorectomy), and the uterus (hysterectomy). In some very early tumors, only the involved ovary will be removed, especially in young women who wish to have children. In advanced disease, an attempt is made to remove all intra-abdominal disease to enhance the effect of chemotherapy. There continues to be an important need for effective treatment options for ovarian cancer.

There were an estimated 28,300 new cases of pancreatic cancer in the United States in 2000. Over the past 20 years, rates of pancreatic cancer have declined in men. Rates among women have remained approximately constant but may be beginning to decline. Pancreatic cancer caused an estimated 28,200 deaths in 2000 in the United States. Over the past 20 years, there has been a slight but significant decrease in mortality rates among men (about –0.9% per year) while rates have increased slightly among women.

Surgery, radiation therapy, and chemotherapy are treatment options for pancreatic cancer. These treatment options can extend survival and/or relieve symptoms in many patients but are not likely to produce a cure for most. There is a significant need for additional therapeutic and diagnostic options for pancreatic cancer.

SUMMARY OF THE INVENTION

The present invention relates to a gene, designated 151P3D4, that has now been found to be over-expressed in the cancer(s) listed in Table I. Northern blot expression analysis of 151P3D4 gene expression in normal tissues shows a restricted expression pattern in adult tissues. The nucleotide (Figure 2) and amino acid (Figure 2, and Figure 3) sequences of 151P3D4 are provided. The tissue-related profile of 151P3D4 in normal adult tissues, combined with the over-expression observed in the tissues listed in Table I, shows that 151P3D4 is aberrantly over-expressed in at least some cancers, and thus serves as a useful diagnostic, prophylactic, prognostic, and/or therapeutic target for cancers of the tissue(s) such as those listed in Table I.

The invention provides polynucleotides corresponding or complementary to all or part of the 151P3D4 genes, mRNAs, and/or coding sequences, preferably in isolated form, including polynucleotides encoding 151P3D4-related proteins and fragments of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more than 25 contiguous amino acids; at least 30, 35, 40, 45, 50, 55, 60, 65, 70, 80, 85, 90, 95, 100 or more than 100 contiguous amino acids of a 151P3D4-related protein, as well as the peptides/proteins themselves; DNA, RNA, DNA/RNA hybrids, and related molecules, polynucleotides or oligonucleotides complementary or having at least a 90% homology to the 151P3D4 genes or mRNA sequences or parts thereof, and polynucleotides or oligonucleotides that hybridize to the 151P3D4 genes, mRNAs, or to 151P3D4-encoding polynucleotides. Also provided are means for isolating cDNAs and the genes encoding 151P3D4. Recombinant DNA molecules containing 151P3D4 polynucleotides, cells transformed or transduced with such molecules, and host-vector systems for the expression of 151P3D4 gene products are also provided. The invention further provides antibodies that bind to 151P3D4 proteins and polypeptide fragments thereof, including polyclonal and monoclonal antibodies, murine and other mammalian antibodies, chimeric antibodies, humanized and fully human antibodies, and antibodies labeled with a detectable marker or therapeutic agent. In certain embodiments there is a *proviso* that the entire nucleic acid sequence of Figure 2 is not encoded and/or the entire amino acid sequence of Figure 2 is not prepared. In certain embodiments, the entire nucleic acid sequence of Figure 2 is encoded and/or the entire amino acid sequence of Figure 2 is prepared, either of which are in respective human unit dose forms.

The invention further provides methods for detecting the presence and status of 151P3D4 polynucleotides and proteins in various biological samples, as well as methods for identifying cells that express 151P3D4. A typical embodiment of this invention provides methods for monitoring 151P3D4 gene products in a tissue or hematology sample having or suspected of having some form of growth dysregulation such as cancer.

The invention further provides various immunogenic or therapeutic compositions and strategies for treating cancers that express 151P3D4 such as cancers of tissues listed in Table I, including therapies aimed at inhibiting the transcription, translation, processing or function of 151P3D4 as well as cancer vaccines. In one aspect, the invention provides compositions, and methods comprising them, for treating a cancer that expresses 151P3D4 in a human subject wherein the composition comprises a carrier suitable for human use and a human unit dose of one or more than one agent that inhibits the production or function of 151P3D4. Preferably, the carrier is a uniquely human carrier. In another aspect of the invention, the agent is a moiety that is immunoreactive with 151P3D4 protein. Non-limiting examples of such moieties include, but are not limited to, antibodies (such as single chain, monoclonal, polyclonal, humanized, chimeric, or human

antibodies), functional equivalents thereof (whether naturally occurring or synthetic), and combinations thereof. The antibodies can be conjugated to a diagnostic or therapeutic moiety. In another aspect, the agent is a small molecule as defined herein.

In another aspect, the agent comprises one or more than one peptide which comprises a cytotoxic T lymphocyte (CTL) epitope that binds an HLA class I molecule in a human to elicit a CTL response to 151P3D4 and/or one or more than one peptide which comprises a helper T lymphocyte (HTL) epitope which binds an HLA class II molecule in a human to elicit an HTL response. The peptides of the invention may be on the same or on one or more separate polypeptide molecules. In a further aspect of the invention, the agent comprises one or more than one nucleic acid molecule that expresses one or more than one of the CTL or HTL response stimulating peptides as described above. In yet another aspect of the invention, the one or more than one nucleic acid molecule may express a moiety that is immunologically reactive with 151P3D4 as described above. The one or more than one nucleic acid molecule may also be, or encodes, a molecule that inhibits production of 151P3D4. Non-limiting examples of such molecules include, but are not limited to, those complementary to a nucleotide sequence essential for production of 151P3D4 (e.g. antisense sequences or molecules that form a triple helix with a nucleotide double helix essential for 151P3D4 production) or a ribozyme effective to lyse 151P3D4 mRNA.

Another embodiment of the invention is antibody epitopes which comprise a peptide regions, or an oligonucleotide encoding the peptide region, that has one two, three, four, or five of the following characteristics:

i) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Hydrophilicity profile of Figure 5;

ii) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or less than 0.5, 0.4, 0.3, 0.2, 0.1, or having a value equal to 0.0, in the Hydropathicity profile of Figure 6;

iii) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Percent Accessible Residues profile of Figure 7;

iv) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Average Flexibility profile of Figure 8; or

v) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Beta-turn profile of Figure 9.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. The 151P3D4 SSH sequence of 417 nucleotides.

Figure 2. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.1 clone 1-placenta (also called "151P3D4 v.1" or "151P3D4 variant 1") is shown in Figure 2A. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 2 (also called "151P3D4 v.2") is shown in Figure 2B. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 1-2166 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 3 (also called "151P3D4 v.3") is shown in Figure 2C. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 4 (also called "151P3D4 v.4") is shown in Figure 2D. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 5 (also called "151P3D4 v.5") is shown in Figure 2E. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 6 (also called "151P3D4 v.6") is shown in Figure 2F. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 7 (also called "151P3D4 v.7") is shown in Figure 2G. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 8 (also called "151P3D4 v.8") is shown in Figure 2H. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 9 (also called "151P3D4 v.9") is shown in Figure 2I. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 10 (also called "151P3D4 v.10") is shown in Figure 2J. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 variant 11 (also called "151P3D4 v.11") is shown in Figure 2K. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon. As used herein, a reference to 151P3D4 includes all variants thereof, including those shown in Figures 10 and 12.

Figure 3. Amino acid sequence of 151P3D4 v.1 (SEQ ID. NO. :____) is shown in Figure 3A; it has 354 amino acids. The amino acid sequence of 151P3D4 v.2 (SEQ ID. NO. :____) is shown in Figure 3B; it has 721 amino acids. As used herein, a reference to 151P3D4 includes all variants thereof, including those shown in Figures 11 and 12.

Figure 4. The nucleic acid sequence alignment of 151P3D4 v.1 with the mRNA for human cartilage link protein is shown in Figure 4A. The amino acid sequence alignments of 151P3D4 v.1 with human cartilage link protein (4B), mouse cartilage link protein (4C), 151P3D4 v.2 (4D), hypothetical protein XP_094318 (4E), bovine cartilage link protein (4F), and rat cartilage link protein (4G) are shown in Figures 4B-4G. The amino acid sequence alignments of 151P3D4 v.2 with human cartilage link protein is shown in Figure 4H. The clustal alignment of 151P3D4 v.1 and 151P3D4 v.2 is shown in Figure 4I.

Figure 5. Hydrophilicity amino acid profile of A) 151P3D4 v.1 and B) 151P3D4 v.2, determined by computer algorithm sequence analysis using the method of Hopp and Woods (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828) accessed on the Protscale website (www.expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 6. Hydropathicity amino acid profile of A) 151P3D4 v.1 and B) 151P3D4 v.2, determined by computer algorithm sequence analysis using the method of Kyte and Doolittle (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132) accessed on the ProtScale website (www.expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 7. Percent accessible residues amino acid profile of A) 151P3D4 v.1 and B) 151P3D4 v.2, determined by computer algorithm sequence analysis using the method of Janin (Janin J., 1979 Nature 277:491-492) accessed on the ProtScale website (www.expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 8. Average flexibility amino acid profile of A) 151P3D4 v.1 and B) 151P3D4 v.2, determined by computer algorithm sequence analysis using the method of Bhaskaran and Ponnuswamy (Bhaskaran R., and Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255) accessed on the ProtScale website (www.expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 9. Beta-turn amino acid profile of A) 151P3D4 v.1 and B) 151P3D4 v.2, determined by computer algorithm sequence analysis using the method of Deleage and Roux (Deleage, G., Roux B. 1987 Protein Engineering 1:289-294) accessed on the ProtScale website (www.expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 10. Schematic display of nucleotide variants of 151P3D4. Schematic alignment of Single Nucleotide Polymorphism (SNP) variants of 151P3D4. Variants 151P3D4 v.3 through v.11 are variants with single nucleotide differences. Though these SNP variants are shown separately, they could also occur in any combinations and in any one of the transcript variants that contains the base pairs. Numbers correspond to those of 151P3D4 v.1. The black boxes show the same sequence as 151P3D4 v.1. SNPs are indicated above the boxes.

Figure 11. Schematic alignment of protein variants of 151P3D4. Nucleotide variants 151P3D4 v.2 through v.9 in Figure 10 code for the same protein as 151P3D4 v.1. Variants 151P3D4 v.2 codes for a protein that shares 321 aa with 151P3D4 v.1. Boxes with the same fill pattern represent the same sequence. Numbers in "( )" underneath the boxes correspond to 151P3D4 v.1.

Figure 12. Schematic alignment of transcript variants of 151P3D4. Variant 151P3D4 v.2 is an alternative transcript, which shares the last three exons with 151P3D4 v.1. The first two exons of 151P3D4

v.1 are located in the sixth intron (between exons 6 and 7) of 151P3D4 v.2. Numbers in "( )" underneath the boxes correspond to those of 151P3D4 v.2. Boxes with the same fill pattern represent the same sequence.

Figure 13. Secondary structure prediction for 151P3D4 protein variants. The secondary structure of 151P3D4 protein variants 1 and 2 (Figures A and B, respectively) were predicted using the HNN - Hierarchical Neural Network method (Guermeur, 1997, http://pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_nn.html), accessed from the ExPasy molecular biology server (http://www.expasy.ch/tools/). This method predicts the presence and location of alpha helices, extended strands, and random coils from the primary protein sequence. The percent of the protein in a given secondary structure is also listed.

Figure 14. Expression of 151P3D4 by RT-PCR. First strand cDNA was prepared from vital pool 1 (liver, lung and kidney), vital pool 2 (pancreas, colon and stomach), bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, ovary cancer pool, breast cancer pool, and cancer metastasis pool. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 151P3D4, was performed at 26 and 30 cycles of amplification. Results show strong expression of 151P3D4 in ovary cancer pool. Expression of 151P3D4 was also detected in bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, breast cancer pool, cancer metastasis pool, vital pool 2, but not in vital pool 1.

Figure 15. Expression of 151P3D4 in normal tissues. Two multiple tissue northern blots (Clontech) both with 2 ug of mRNA/lane were probed with the 151P3D4 sequence. Size standards in kilobases (kb) are indicated on the side. Results show expression of 151P3D4 in small intestine and placenta. Lower level expression was also detected in heart and colon, but not in the other normal tissues tested.

Figure 16. Expression of 151P3D4 in bladder cancer patient tissues. RNA was extracted from normal bladder (NB), bladder cancer cell lines (CL: UM-UC-3, J82, SCaBER), bladder cancer patient tumors (T) and normal adjacent tissue (NAT). Northern blots with 10 ug of total RNA were probed with the 151P3D4 SSH sequence. Size standards in kilobases are indicated on the side. Results show expression of 151P3D4 in patient bladder cancer tissues, and in UM-UC-3 bladder cancer cell lines, but not in normal bladder nor in the other bladder cancer cell lines tested.

Figure 17. Expression of 151P3D4 in kidney cancer patient tissues. RNA was extracted from kidney cancer cell lines (CL: 769-P, A498, SW839), normal kidney (NK), kidney cancer patient tumors (T) and their normal adjacent tissues (NAT). Northern blots with 10 ug of total RNA were probed with the 151P3D4 SSH sequence. Size standards in kilobases are on the side. Results show expression of 151P3D4 in patient kidney tumor tissues, but not in normal kidney, nor in the cell lines tested.

Figure 18. Expression of 151P3D4 in ovary cancer patient tissues. RNA was extracted from ovary and cervical cancer cell lines (CL), normal ovary (N), and ovary cancer patient tumor (T). Northern blots with 10 ug of total RNA were probed with the 151P3D4 SSH sequence. Size standards in kilobases are on the side. Results show strong expression of 151P3D4 in patient ovary cancer tissues, but not in normal ovary nor in the ovary and cervical cancer cell lines.

Figure 19. Expression of 151P3D4 in stomach and uterus human cancer specimens. Expression of 151P3D4 was assayed in a panel of human stomach and uterus cancers (T) and their respective matched normal tissues (N) on RNA dot blots. 151P3D4 expression was seen in both stomach and uterus cancers.

Figure 20. 151P3D4 expression in 293T cells following transfection. 293T cells were transfected with either 151P3D4 .pcDNA3.1/mychis or pcDNA3.1/mychis vector control. Forty hours later, cell lysates were collected. Samples were run on an SDS-PAGE acrylamide gel, blotted and stained with anti-his antibody. The blot was developed using the ECL chemiluminescence kit and visualized by autoradiography. Results show expression of 151P3D4 from the 151P3D4 .pcDNA3.1/mychis mammalian expression construct in the lysates of 151P3D4 .pcDNA3.1/mychis transfected cells, but not from the control pcDNA3.1/mychis vector.

DETAILED DESCRIPTION OF THE INVENTION

<u>**Outline of Sections**</u>

I.) Definitions:

Unless otherwise defined, all terms of art, notations and other scientific terms or terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art. Many of the techniques and procedures described or referenced herein are well understood and commonly employed using conventional methodology by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2nd. edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer defined protocols and/or parameters unless otherwise noted.

The terms "advanced prostate cancer", "locally advanced prostate cancer", "advanced disease" and "locally advanced disease" mean prostate cancers that have extended through the prostate capsule, and are meant to include stage C disease under the American Urological Association (AUA) system, stage C1 - C2 disease under the Whitmore-Jewett system, and stage T3 - T4 and N+ disease under the TNM (tumor, node, metastasis) system. In general, surgery is not recommended for patients with locally advanced disease, and these patients have substantially less favorable outcomes compared to patients having clinically localized (organ-confined) prostate cancer. Locally advanced disease is clinically identified by palpable evidence of induration beyond the lateral border of the prostate, or asymmetry or induration above the prostate base. Locally advanced prostate cancer is presently diagnosed pathologically following radical prostatectomy if the tumor invades or penetrates the prostatic capsule, extends into the surgical margin, or invades the seminal vesicles.

"Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence 151P3D4 (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence 151P3D4. In addition, the phrase

includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

The term "analog" refers to a molecule which is structurally similar or shares similar or corresponding attributes with another molecule (e.g. a 151P3D4-related protein). For example an analog of a 151P3D4 protein can be specifically bound by an antibody or T cell that specifically binds to 151P3D4.

The term "antibody" is used in the broadest sense. Therefore an "antibody" can be naturally occurring or man-made such as monoclonal antibodies produced by conventional hybridoma technology. Anti-151P3D4 antibodies comprise monoclonal and polyclonal antibodies as well as fragments containing the antigen-binding domain and/or one or more complementarity determining regions of these antibodies.

An "antibody fragment" is defined as at least a portion of the variable region of the immunoglobulin molecule that binds to its target, i.e., the antigen-binding region. In one embodiment it specifically covers single anti-151P3D4 antibodies and clones thereof (including agonist, antagonist and neutralizing antibodies) and anti-151P3D4 antibody compositions with polyepitopic specificity.

The term "codon optimized sequences" refers to nucleotide sequences that have been optimized for a particular host species by replacing any codons having a usage frequency of less than about 20%. Nucleotide sequences that have been optimized for expression in a given host species by elimination of spurious polyadenylation sequences, elimination of exon/intron splicing signals, elimination of transposon-like repeats and/or optimization of GC content in addition to codon optimization are referred to herein as an "expression enhanced sequences."

The term "cytotoxic agent" refers to a substance that inhibits or prevents the expression activity of cells, function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes chemotherapeutic agents, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof. Examples of cytotoxic agents include, but are not limited to maytansinoids, yttrium, bismuth, ricin, ricin A-chain, doxorubicin, daunorubicin, taxol, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin, diphtheria toxin, Pseudomonas exotoxin (PE) A, PE40, abrin, abrin A chain, modeccin A chain, alpha-sarcin, gelonin, mitogellin, retstrictocin, phenomycin, enomycin, curicin, crotin, calicheamicin, sapaonaria officinalis inhibitor, and glucocorticoid and other chemotherapeutic agents, as well as radioisotopes such as At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32} and radioactive isotopes of Lu. Antibodies may also be conjugated to an anti-cancer pro-drug activating enzyme capable of converting the pro-drug to its active form.

The term "homolog" refers to a molecule which exhibits homology to another molecule, by for example, having sequences of chemical residues that are the same or similar at corresponding positions.

"Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g.*, Stites, *et al.*, IMMUNOLOGY, 8^{TH} ED., Lange Publishing, Los Altos, CA (1994).

The terms "hybridize", "hybridizing", "hybridizes" and the like, used in the context of polynucleotides, are meant to refer to conventional hybridization conditions, preferably such as hybridization

in 50% formamide/6XSSC/0.1% SDS/100 μg/ml ssDNA, in which temperatures for hybridization are above 37 degrees C and temperatures for washing in 0.1XSSC/0.1% SDS are above 55 degrees C.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. For example, a polynucleotide is said to be "isolated" when it is substantially separated from contaminant polynucleotides that correspond or are complementary to genes other than the 151P3D4 genes or that encode polypeptides other than 151P3D4 gene product or fragments thereof. A skilled artisan can readily employ nucleic acid isolation procedures to obtain an isolated 151P3D4 polynucleotide. A protein is said to be "isolated," for example, when physical, mechanical or chemical methods are employed to remove the 151P3D4 proteins from cellular constituents that are normally associated with the protein. A skilled artisan can readily employ standard purification methods to obtain an isolated 151P3D4 protein. Alternatively, an isolated protein can be prepared by chemical means.

The term "mammal" refers to any organism classified as a mammal, including mice, rats, rabbits, dogs, cats, cows, horses and humans. In one embodiment of the invention, the mammal is a mouse. In another embodiment of the invention, the mammal is a human.

The terms "metastatic prostate cancer" and "metastatic disease" mean prostate cancers that have spread to regional lymph nodes or to distant sites, and are meant to include stage D disease under the AUA system and stage TxNxM+ under the TNM system. As is the case with locally advanced prostate cancer, surgery is generally not indicated for patients with metastatic disease, and hormonal (androgen ablation) therapy is a preferred treatment modality. Patients with metastatic prostate cancer eventually develop an androgen-refractory state within 12 to 18 months of treatment initiation. Approximately half of these androgen-refractory patients die within 6 months after developing that status. The most common site for prostate cancer metastasis is bone. Prostate cancer bone metastases are often osteoblastic rather than osteolytic (i.e., resulting in net bone formation). Bone metastases are found most frequently in the spine, followed by the femur, pelvis, rib cage, skull and humerus. Other common sites for metastasis include lymph nodes, lung, liver and brain. Metastatic prostate cancer is typically diagnosed by open or laparoscopic pelvic lymphadenectomy, whole body radionuclide scans, skeletal radiography, and/or bone lesion biopsy.

The term "monoclonal antibody" refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the antibodies comprising the population are identical except for possible naturally occurring mutations that are present in minor amounts.

A "motif", as in biological motif of a 151P3D4-related protein, refers to any pattern of amino acids forming part of the primary sequence of a protein, that is associated with a particular function (e.g. protein-protein interaction, protein-DNA interaction, etc) or modification (e.g. that is phosphorylated, glycosylated or amidated), or localization (e.g. secretory sequence, nuclear localization sequence, etc.) or a sequence that is correlated with being immunogenic, either humorally or cellularly. A motif can be either contiguous or capable of being aligned to certain positions that are generally correlated with a certain function or property. In the context of HLA motifs, "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino

acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs for HLA binding are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

A "pharmaceutical excipient" comprises a material such as an adjuvant, a carrier, pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservative, and the like.

"Pharmaceutically acceptable" refers to a non-toxic, inert, and/or composition that is physiologically compatible with humans or other mammals.

The term "polynucleotide" means a polymeric form of nucleotides of at least 10 bases or base pairs in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide, and is meant to include single and double stranded forms of DNA and/or RNA. In the art, this term if often used interchangeably with "oligonucleotide". A polynucleotide can comprise a nucleotide sequence disclosed herein wherein thymidine (T), as shown for example in Figure 2, can also be uracil (U); this definition pertains to the differences between the chemical structures of DNA and RNA, in particular the observation that one of the four major bases in RNA is uracil (U) instead of thymidine (T).

The term "polypeptide" means a polymer of at least about 4, 5, 6, 7, or 8 amino acids. Throughout the specification, standard three letter or single letter designations for amino acids are used. In the art, this term is often used interchangeably with "peptide" or "protein".

An HLA "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding groove of an HLA molecule, with their side chains buried in specific pockets of the binding groove. In one embodiment, for example, the primary anchor residues for an HLA class I molecule are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 8, 9, 10, 11, or 12 residue peptide epitope in accordance with the invention. In another embodiment, for example, the primary anchor residues of a peptide that will bind an HLA class II molecule are spaced relative to each other, rather than to the termini of a peptide, where the peptide is generally of at least 9 amino acids in length. The primary anchor positions for each motif and supermotif are set forth in Table IV. For example, analog peptides can be created by altering the presence or absence of particular residues in the primary and/or secondary anchor positions shown in Table IV. Such analogs are used to modulate the binding affinity and/or population coverage of a peptide comprising a particular HLA motif or supermotif.

A "recombinant" DNA or RNA molecule is a DNA or RNA molecule that has been subjected to molecular manipulation *in vitro*.

Non-limiting examples of small molecules include compounds that bind or interact with 151P3D4, ligands including hormones, neuropeptides, chemokines, odorants, phospholipids, and functional equivalents thereof that bind and preferably inhibit 151P3D4 protein function. Such non-limiting small molecules preferably have a molecular weight of less than about 10 kDa, more preferably below about 9, about 8, about 7, about 6, about 5 or about 4 kDa. In certain embodiments, small molecules physically associate with, or

bind, 151P3D4 protein; are not found in naturally occurring metabolic pathways; and/or are more soluble in aqueous than non-aqueous solutions

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured nucleic acid sequences to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature that can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel *et al.*, Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, are identified by, but not limited to, those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42 °C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42 °C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium. citrate) and 50% formamide at 55 °C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55 °C. "Moderately stringent conditions" are described by, but not limited to, those in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/mL denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

An HLA "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles.

As used herein "to treat" or "therapeutic" and grammatically related terms, refer to any improvement of any consequence of disease, such as prolonged survival, less morbidity, and/or a lessening of side effects which are the byproducts of an alternative therapeutic modality; full eradication of disease is not required.

A "transgenic animal" (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A "transgene" is a DNA that is integrated into the genome of a cell from which a transgenic animal develops.

As used herein, an HLA or cellular immune response "vaccine" is a composition that contains or encodes one or more peptides of the invention. There are numerous embodiments of such vaccines, such as a cocktail of one or more individual peptides; one or more peptides of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such individual peptides or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150 or more, e.g., at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I peptides of the invention can be admixed with, or linked to, HLA class II peptides, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. HLA vaccines can also comprise peptide-pulsed antigen presenting cells, *e.g.*, dendritic cells.

The term "variant" refers to a molecule that exhibits a variation from a described type or norm, such as a protein that has one or more different amino acid residues in the corresponding position(s) of a specifically described protein (e.g. the 151P3D4 protein shown in Figure 2 or Figure 3. An analog is an example of a variant protein. Splice isoforms and single nucleotides polymorphisms (SNPs) are further examples of variants.

The "151P3D4-related proteins" of the invention include those specifically identified herein, as well as allelic variants, conservative substitution variants, analogs and homologs that can be isolated/generated and characterized without undue experimentation following the methods outlined herein or readily available in the art. Fusion proteins that combine parts of different 151P3D4 proteins or fragments thereof, as well as fusion proteins of a 151P3D4 protein and a heterologous polypeptide are also included. Such 151P3D4 proteins are collectively referred to as the 151P3D4-related proteins, the proteins of the invention, or 151P3D4. The term "151P3D4-related protein" refers to a polypeptide fragment or a 151P3D4 protein sequence of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more than 25 amino acids; or, at least 30, 35, 40, 45, 50, 55, 60, 65, 70, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, or 354 or more amino acids.

II.) 151P3D4 Polynucleotides

One aspect of the invention provides polynucleotides corresponding or complementary to all or part of a 151P3D4 gene, mRNA, and/or coding sequence, preferably in isolated form, including polynucleotides encoding a 151P3D4-related protein and fragments thereof, DNA, RNA, DNA/RNA hybrid, and related molecules, polynucleotides or oligonucleotides complementary to a 151P3D4 gene or mRNA sequence or a part thereof, and polynucleotides or oligonucleotides that hybridize to a 151P3D4 gene, mRNA, or to a 151P3D4 encoding polynucleotide (collectively, "151P3D4 polynucleotides"). In all instances when referred to in this section, T can also be U in Figure 2.

Embodiments of a 151P3D4 polynucleotide include: a 151P3D4 polynucleotide having the sequence shown in Figure 2, the nucleotide sequence of 151P3D4 as shown in Figure 2 wherein T is U; at least 10 contiguous nucleotides of a polynucleotide having the sequence as shown in Figure 2; or, at least 10

contiguous nucleotides of a polynucleotide having the sequence as shown in Figure 2 where T is U. For example, embodiments of 151P3D4 nucleotides comprise, without limitation:

(I) a polynucleotide comprising, consisting essentially of, or consisting of a sequence as shown in Figure 2 (SEQ ID NO: ____), wherein T can also be U;

(II) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2A (SEQ ID NO: ____), from nucleotide residue number 316 through nucleotide residue number 1380, including the stop codon, wherein T can also be U;

(III) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2B (SEQ ID NO: ____), from nucleotide residue number 1 through nucleotide residue number 2166, including the stop codon, wherein T can also be U;

(IV) a polynucleotide comprising, consisting essentially of, or consisting of the sequences as shown in Figures 2C-2K (SEQ ID NOs: ____), from nucleotide residue number 316 through nucleotide residue number 1380, including the a stop codon, wherein T can also be U;

(V) a polynucleotide that encodes a 151P3D4-related protein that is at least 90% homologous to an entire amino acid sequence shown in Figure 2A-K (SEQ ID NO: ____);

(VI) a polynucleotide that encodes a 151P3D4-related protein that is at least 90% identical to an entire amino acid sequence shown in Figure 2A-K (SEQ ID NO: ____);

(VII) a polynucleotide that encodes at least one peptide set forth in Tables V-XVIII and XXII-LI;

(VIII) a polynucleotide that encodes a peptide region of at least 5 amino acids of a peptide of Figure 3A in any whole number increment up to 354 that includes an amino acid position having a value greater than 0.5 in the Hydrophilicity profile of Figure 5A; or of Figure 3B in any whole number increment up to 721 that includes an amino acid position having a value greater than 0.5 in the Hydrophilicity profile of Figure 5B;

(XIX) a polynucleotide that encodes a peptide region of at least 5 amino acids of a peptide of Figure 3A in any whole number increment up to 354 that includes an amino acid position having a value less than 0.5 in the Hydropathicity profile of Figure 6A; or of Figure 3B in any whole number increment up to 721 that includes an amino acid position having a value less than 0.5 in the Hydropathicity profile of Figure 6B;

(X) a polynucleotide that encodes a peptide region of at least 5 amino acids of a peptide of Figure 3A in any whole number increment up to 354 that includes an amino acid position having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7A; or of Figure 3B in any whole number increment up to 721 that includes an amino acid position having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7B;

(XII) a polynucleotide that encodes a peptide region of at least 5 amino acids of a peptide of Figure 3A in any whole number increment up to 354 that includes an amino acid position having a value greater than 0.5 in the Average Flexibility profile of Figure 8A; or of Figure 3B in any whole number increment up to 721 that includes an amino acid position having a value greater than 0.5 in the Average Flexibility profile of Figure 8B;

(XIII) a polynucleotide that encodes a peptide region of at least 5 amino acids of a peptide of Figure 3A in any whole number increment up to 354 that includes an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figure 9A; or of Figure 3B in any whole number increment up to 721 that includes an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figure 9B;

(XIV) a polynucleotide that is fully complementary to a polynucleotide of any one of (I)-(XIII).

(XV) a peptide that is encoded by any of (I)-(XIV); and

(XVI) a polynucleotide of any of (I)-(XIV) or peptide of (XV) together with a pharmaceutical excipient and/or in a human unit dose form.

As used herein, a range is understood to specifically disclose all whole unit positions thereof.

Typical embodiments of the invention disclosed herein include 151P3D4 polynucleotides that encode specific portions of 151P3D4 mRNA sequences (and those which are complementary to such sequences) such as those that encode the proteins and/or fragments thereof, for example:

(a) 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, or 354 or more contiguous amino acids of 151P3D4.

(b) 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 625, 650, 675, 700, or 721 or more contiguous amino acids of 151P3D4 variant 2.

For example, representative embodiments of the invention disclosed herein include: polynucleotides and their encoded peptides themselves encoding about amino acid 1 to about amino acid 10 of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 10 to about amino acid 20 of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 20 to about amino acid 30 of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 30 to about amino acid 40 of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 40 to about amino acid 50 of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 50 to about amino acid 60 of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 60 to about amino acid 70 of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 70 to about amino acid 80

of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 80 to about amino acid 90 of the 151P3D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 90 to about amino acid 100 of the 151P3D4 protein shown in Figure 2 or Figure 3, in increments of about 10 amino acids, ending at the carboxyl terminal amino acid set forth in Figure 2 or Figure 3. Accordingly polynucleotides encoding portions of the amino acid sequence (of about 10 amino acids), of amino acids 100 through the carboxyl terminal amino acid of the 151P3D4 protein are embodiments of the invention. Wherein it is understood that each particular amino acid position discloses that position plus or minus five amino acid residues.

Polynucleotides encoding relatively long portions of a 151P3D4 protein are also within the scope of the invention. For example, polynucleotides encoding from about amino acid 1 (or 20 or 30 or 40 etc.) to about amino acid 20, (or 30, or 40 or 50 etc.) of the 151P3D4 protein "or variant" shown in Figure 2 or Figure 3 can be generated by a variety of techniques well known in the art. These polynucleotide fragments can include any portion of the 151P3D4 sequence as shown in Figure 2.

One embodiment of the invention comprises an HLA peptide, that occurs at least twice in Tables V-XVIII and XXII to LI collectively, or an oligonucleotide that encodes the HLA peptide. Another embodiment of the invention comprises an HLA peptide that occurs at least once in Tables V-XVIII and at least once in tables XXII to LI, or an oligonucleotide that encodes the HLA peptide. In another embodiment of the invention, typical polynucleotide fragments can encode one or more of the 151P3D4 protein or variant N-glycosylation sites, cAMP and cGMP-dependent protein kinase phosphorylation sites, casein kinase II phosphorylation sites or N-myristoylation site and amidation sites.

II.A.) Uses of 151P3D4 Polynucleotides

II.A.1.) Monitoring of Genetic Abnormalities

The polynucleotides of the preceding paragraphs have a number of different specific uses. The human 151P3D4 gene maps to the chromosomal location set forth in the Example entitled "Chromosomal Mapping of 151P3D4." For example, because the 151P3D4 gene maps to this chromosome, polynucleotides that encode different regions of the 151P3D4 proteins are used to characterize cytogenetic abnormalities of this chromosomal locale, such as abnormalities that are identified as being associated with various cancers. In certain genes, a variety of chromosomal abnormalities including rearrangements have been identified as frequent cytogenetic abnormalities in a number of different cancers (see e.g. Krajinovic *et al.*, Mutat. Res. 382(3-4): 81-83 (1998); Johansson *et al.*, Blood 86(10): 3905-3914 (1995) and Finger *et al.*, P.N.A.S. 85(23): 9158-9162 (1988)). Thus, polynucleotides encoding specific regions of the 151P3D4 proteins provide new tools that can be used to delineate, with greater precision than previously possible, cytogenetic abnormalities in the chromosomal region that encodes 151P3D4 that may contribute to the malignant phenotype. In this context, these polynucleotides satisfy a need in the art for expanding the sensitivity of chromosomal screening in order to identify more subtle and less common chromosomal abnormalities (see e.g. Evans *et al.*, Am. J. Obstet. Gynecol 171(4): 1055-1057 (1994)).

Furthermore, as 151P3D4 was shown to be highly expressed in bladder and other cancers, 151P3D4 polynucleotides are used in methods assessing the status of 151P3D4 gene products in normal versus

cancerous tissues. Typically, polynucleotides that encode specific regions of the 151P3D4 proteins are used to assess the presence of perturbations (such as deletions, insertions, point mutations, or alterations resulting in a loss of an antigen etc.) in specific regions of the 151P3D4 gene, such as regions containing one or more motifs. Exemplary assays include both RT-PCR assays as well as single-strand conformation polymorphism (SSCP) analysis (see, e.g., Marrogi *et al.*, J. Cutan. Pathol. 26(8): 369-378 (1999), both of which utilize polynucleotides encoding specific regions of a protein to examine these regions within the protein.

II.A.2.) Antisense Embodiments

Other specifically contemplated nucleic acid related embodiments of the invention disclosed herein are genomic DNA, cDNAs, ribozymes, and antisense molecules, as well as nucleic acid molecules based on an alternative backbone, or including alternative bases, whether derived from natural sources or synthesized, and include molecules capable of inhibiting the RNA or protein expression of 151P3D4. For example, antisense molecules can be RNAs or other molecules, including peptide nucleic acids (PNAs) or non-nucleic acid molecules such as phosphorothioate derivatives, that specifically bind DNA or RNA in a base pair-dependent manner. A skilled artisan can readily obtain these classes of nucleic acid molecules using the 151P3D4 polynucleotides and polynucleotide sequences disclosed herein.

Antisense technology entails the administration of exogenous oligonucleotides that bind to a target polynucleotide located within the cells. The term "antisense" refers to the fact that such oligonucleotides are complementary to their intracellular targets, e.g., 151P3D4. See for example, Jack Cohen, Oligodeoxynucleotides, Antisense Inhibitors of Gene Expression, CRC Press, 1989; and Synthesis 1:1-5 (1988). The 151P3D4 antisense oligonucleotides of the present invention include derivatives such as S-oligonucleotides (phosphorothioate derivatives or S-oligos, see, Jack Cohen, supra), which exhibit enhanced cancer cell growth inhibitory action. S-oligos (nucleoside phosphorothioates) are isoelectronic analogs of an oligonucleotide (O-oligo) in which a nonbridging oxygen atom of the phosphate group is replaced by a sulfur atom. The S-oligos of the present invention can be prepared by treatment of the corresponding O-oligos with 3H-1,2-benzodithiol-3-one-1,1-dioxide, which is a sulfur transfer reagent. See, *e.g.*, Iyer, R. P. *et al.*, J. Org. Chem. 55:4693-4698 (1990); and Iyer, R. P. *et al.*, J. Am. Chem. Soc. 112:1253-1254 (1990). Additional 151P3D4 antisense oligonucleotides of the present invention include morpholino antisense oligonucleotides known in the art (see, e.g., Partridge *et al.*, 1996, Antisense & Nucleic Acid Drug Development 6: 169-175).

The 151P3D4 antisense oligonucleotides of the present invention typically can be RNA or DNA that is complementary to and stably hybridizes with the first 100 5' codons or last 100 3' codons of a 151P3D4 genomic sequence or the corresponding mRNA. Absolute complementarity is not required, although high degrees of complementarity are preferred. Use of an oligonucleotide complementary to this region allows for the selective hybridization to 151P3D4 mRNA and not to mRNA specifying other regulatory subunits of protein kinase. In one embodiment, 151P3D4 antisense oligonucleotides of the present invention are 15 to 30-mer fragments of the antisense DNA molecule that have a sequence that hybridizes to 151P3D4 mRNA. Optionally, 151P3D4 antisense oligonucleotide is a 30-mer oligonucleotide that is complementary to a region in the first 10 5' codons or last 10 3' codons of 151P3D4. Alternatively, the antisense molecules are modified to employ ribozymes in the inhibition of 151P3D4 expression, see, e.g., L. A. Couture & D. T. Stinchcomb; *Trends Genet* 12: 510-515 (1996).

II.A.3.) Primers and Primer Pairs

Further specific embodiments of this nucleotides of the invention include primers and primer pairs, which allow the specific amplification of polynucleotides of the invention or of any specific parts thereof, and probes that selectively or specifically hybridize to nucleic acid molecules of the invention or to any part thereof. Probes can be labeled with a detectable marker, such as, for example, a radioisotope, fluorescent compound, bioluminescent compound, a chemiluminescent compound, metal chelator or enzyme. Such probes and primers are used to detect the presence of a 151P3D4 polynucleotide in a sample and as a means for detecting a cell expressing a 151P3D4 protein.

Examples of such probes include polypeptides comprising all or part of the human 151P3D4 cDNA sequence shown in Figure 2. Examples of primer pairs capable of specifically amplifying 151P3D4 mRNAs are also described in the Examples. As will be understood by the skilled artisan, a great many different primers and probes can be prepared based on the sequences provided herein and used effectively to amplify and/or detect a 151P3D4 mRNA.

The 151P3D4 polynucleotides of the invention are useful for a variety of purposes, including but not limited to their use as probes and primers for the amplification and/or detection of the 151P3D4 gene(s), mRNA(s), or fragments thereof; as reagents for the diagnosis and/or prognosis of prostate cancer and other cancers; as coding sequences capable of directing the expression of 151P3D4 polypeptides; as tools for modulating or inhibiting the expression of the 151P3D4 gene(s) and/or translation of the 151P3D4 transcript(s); and as therapeutic agents.

The present invention includes the use of any probe as described herein to identify and isolate a 151P3D4 or 151P3D4 related nucleic acid sequence from a naturally occurring source, such as humans or other mammals, as well as the isolated nucleic acid sequence *per se*, which would comprise all or most of the sequences found in the probe used.

II.A.4.) Isolation of 151P3D4-Encoding Nucleic Acid Molecules

The 151P3D4 cDNA sequences described herein enable the isolation of other polynucleotides encoding 151P3D4 gene product(s), as well as the isolation of polynucleotides encoding 151P3D4 gene product homologs, alternatively spliced isoforms, allelic variants, and mutant forms of a 151P3D4 gene product as well as polynucleotides that encode analogs of 151P3D4-related proteins. Various molecular cloning methods that can be employed to isolate full length cDNAs encoding a 151P3D4 gene are well known (see, for example, Sambrook, J. *et al.*, Molecular Cloning: A Laboratory Manual, 2d edition, Cold Spring Harbor Press, New York, 1989; Current Protocols in Molecular Biology. Ausubel *et al.*, Eds., Wiley and Sons, 1995). For example, lambda phage cloning methodologies can be conveniently employed, using commercially available cloning systems (e.g., Lambda ZAP Express, Stratagene). Phage clones containing 151P3D4 gene cDNAs can be identified by probing with a labeled 151P3D4 cDNA or a fragment thereof. For example, in one embodiment, a 151P3D4 cDNA (e.g., Figure 2) or a portion thereof can be synthesized and used as a probe to retrieve overlapping and full-length cDNAs corresponding to a 151P3D4 gene. A 151P3D4 gene itself can be isolated by screening genomic DNA libraries, bacterial artificial chromosome libraries (BACs), yeast artificial chromosome libraries (YACs), and the like, with 151P3D4 DNA probes or primers.

II.A.5.) Recombinant Nucleic Acid Molecules and Host-Vector Systems

The invention also provides recombinant DNA or RNA molecules containing a 151P3D4 polynucleotide, a fragment, analog or homologue thereof, including but not limited to phages, plasmids, phagemids, cosmids, YACs, BACs, as well as various viral and non-viral vectors well known in the art, and cells transformed or transfected with such recombinant DNA or RNA molecules. Methods for generating such molecules are well known (see, for example, Sambrook *et al.*, 1989, supra).

The invention further provides a host-vector system comprising a recombinant DNA molecule containing a 151P3D4 polynucleotide, fragment, analog or homologue thereof within a suitable prokaryotic or eukaryotic host cell. Examples of suitable eukaryotic host cells include a yeast cell, a plant cell, or an animal cell, such as a mammalian cell or an insect cell (e.g., a baculovirus-infectible cell such as an Sf9 or HighFive cell). Examples of suitable mammalian cells include various prostate cancer cell lines such as DU145 and TsuPr1, other transfectable or transducible prostate cancer cell lines, primary cells (PrEC), as well as a number of mammalian cells routinely used for the expression of recombinant proteins (e.g., COS, CHO, 293, 293T cells). More particularly, a polynucleotide comprising the coding sequence of 151P3D4 or a fragment, analog or homolog thereof can be used to generate 151P3D4 proteins or fragments thereof using any number of host-vector systems routinely used and widely known in the art.

A wide range of host-vector systems suitable for the expression of 151P3D4 proteins or fragments thereof are available, see for example, Sambrook *et al.*, 1989, supra; Current Protocols in Molecular Biology, 1995, supra). Preferred vectors for mammalian expression include but are not limited to pcDNA 3.1 myc-His-tag (Invitrogen) and the retroviral vector pSRαtkneo (Muller *et al.*, 1991, MCB 11:1785). Using these expression vectors, 151P3D4 can be expressed in several prostate cancer and non-prostate cell lines, including for example 293, 293T, rat-1, NIH 3T3 and TsuPr1. The host-vector systems of the invention are useful for the production of a 151P3D4 protein or fragment thereof. Such host-vector systems can be employed to study the functional properties of 151P3D4 and 151P3D4 mutations or analogs.

Recombinant human 151P3D4 protein or an analog or homolog or fragment thereof can be produced by mammalian cells transfected with a construct encoding a 151P3D4-related nucleotide. For example, 293T cells can be transfected with an expression plasmid encoding 151P3D4 or fragment, analog or homolog thereof, a 151P3D4-related protein is expressed in the 293T cells, and the recombinant 151P3D4 protein is isolated using standard purification methods (e.g., affinity purification using anti-151P3D4 antibodies). In another embodiment, a 151P3D4 coding sequence is subcloned into the retroviral vector pSRαMSVtkneo and used to infect various mammalian cell lines, such as NIH 3T3, TsuPr1, 293 and rat-1 in order to establish 151P3D4 expressing cell lines. Various other expression systems well known in the art can also be employed. Expression constructs encoding a leader peptide joined in frame to a 151P3D4 coding sequence can be used for the generation of a secreted form of recombinant 151P3D4 protein.

As discussed herein, redundancy in the genetic code permits variation in 151P3D4 gene sequences. In particular, it is known in the art that specific host species often have specific codon preferences, and thus one can adapt the disclosed sequence as preferred for a desired host. For example, preferred analog codon sequences typically have rare codons (i.e., codons having a usage frequency of less than about 20% in known sequences of the desired host) replaced with higher frequency codons. Codon preferences for a specific

species are calculated, for example, by utilizing codon usage tables available on the INTERNET such as at URL www.dna.affrc.go.jp/~nakamura/codon.html.

Additional sequence modifications are known to enhance protein expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon/intron splice site signals, transposon-like repeats, and/or other such well-characterized sequences that are deleterious to gene expression. The GC content of the sequence is adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. Where possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures. Other useful modifications include the addition of a translational initiation consensus sequence at the start of the open reading frame, as described in Kozak, *Mol. Cell Biol.*, 9:5073-5080 (1989). Skilled artisans understand that the general rule that eukaryotic ribosomes initiate translation exclusively at the 5' proximal AUG codon is abrogated only under rare conditions (see, e.g., Kozak PNAS 92(7): 2662-2666, (1995) and Kozak NAR 15(20): 8125-8148 (1987)).

III.) 151P3D4-related Proteins

Another aspect of the present invention provides 151P3D4-related proteins. Specific embodiments of 151P3D4 proteins comprise a polypeptide having all or part of the amino acid sequence of human 151P3D4 as shown in Figure 2 or Figure 3. Alternatively, embodiments of 151P3D4 proteins comprise variant, homolog or analog polypeptides that have alterations in the amino acid sequence of 151P3D4 shown in Figure 2 or Figure 3.

In general, naturally occurring allelic variants of human 151P3D4 share a high degree of structural identity and homology (e.g., 90% or more homology). Typically, allelic variants of a 151P3D4 protein contain conservative amino acid substitutions within the 151P3D4 sequences described herein or contain a substitution of an amino acid from a corresponding position in a homologue of 151P3D4. One class of 151P3D4 allelic variants are proteins that share a high degree of homology with at least a small region of a particular 151P3D4 amino acid sequence, but further contain a radical departure from the sequence, such as a non-conservative substitution, truncation, insertion or frame shift. In comparisons of protein sequences, the terms, similarity, identity, and homology each have a distinct meaning as appreciated in the field of genetics. Moreover, orthology and paralogy can be important concepts describing the relationship of members of a given protein family in one organism to the members of the same family in other organisms.

Amino acid abbreviations are provided in Table II. Conservative amino acid substitutions can frequently be made in a protein without altering either the conformation or the function of the protein. Proteins of the invention can comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 conservative substitutions. Such changes include substituting any of isoleucine (I), valine (V), and leucine (L) for any other of these hydrophobic amino acids; aspartic acid (D) for glutamic acid (E) and vice versa; glutamine (Q) for asparagine (N) and vice versa; and serine (S) for threonine (T) and vice versa. Other substitutions can also be considered conservative, depending on the environment of the particular amino acid and its role in the three-dimensional structure of the protein. For example, glycine (G) and alanine (A) can frequently be interchangeable, as can alanine (A) and valine (V). Methionine (M), which is relatively hydrophobic, can frequently be interchanged with leucine and isoleucine, and sometimes with valine. Lysine (K) and arginine (R) are frequently

interchangeable in locations in which the significant feature of the amino acid residue is its charge and the differing pK's of these two amino acid residues are not significant. Still other changes can be considered "conservative" in particular environments (see, e.g. Table III herein; pages 13-15 "Biochemistry" 2nd ED. Lubert Stryer ed (Stanford University); Henikoff *et al.*, PNAS 1992 Vol 89 10915-10919; Lei *et al.*, J Biol Chem 1995 May 19; 270(20):11882-6).

Embodiments of the invention disclosed herein include a wide variety of art-accepted variants or analogs of 151P3D4 proteins such as polypeptides having amino acid insertions, deletions and substitutions. 151P3D4 variants can be made using methods known in the art such as site-directed mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis (Carter *et al., Nucl. Acids Res., 13:*4331 (1986); Zoller *et al., Nucl. Acids Res., 10:*6487 (1987)), cassette mutagenesis (Wells *et al.*, Gene, 34:315 (1985)), restriction selection mutagenesis (Wells *et al., Philos. Trans. R. Soc. London SerA*, 317:415 (1986)) or other known techniques can be performed on the cloned DNA to produce the 151P3D4 variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence that is involved in a specific biological activity such as a protein-protein interaction. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions (Creighton, *The Proteins,* (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)). If alanine substitution does not yield adequate amounts of variant, an isosteric amino acid can be used.

As defined herein, 151P3D4 variants, analogs or homologs, have the distinguishing attribute of having at least one epitope that is "cross reactive" with a 151P3D4 protein having an amino acid sequence of Figure 3. As used in this sentence, "cross reactive" means that an antibody or T cell that specifically binds to a 151P3D4 variant also specifically binds to a 151P3D4 protein having an amino acid sequence set forth in Figure 3. A polypeptide ceases to be a variant of a protein shown in Figure 3, when it no longer contains any epitope capable of being recognized by an antibody or T cell that specifically binds to the starting 151P3D4 protein. Those skilled in the art understand that antibodies that recognize proteins bind to epitopes of varying size, and a grouping of the order of about four or five amino acids, contiguous or not, is regarded as a typical number of amino acids in a minimal epitope. See, e.g., Nair *et al.*, J. Immunol 2000 165(12): 6949-6955; Hebbes *et al.*, Mol Immunol (1989) 26(9):865-73; Schwartz *et al.*, J Immunol (1985) 135(4):2598-608.

Other classes of 151P3D4-related protein variants share 70%, 75%, 80%, 85% or 90% or more similarity with an amino acid sequence of Figure 3, or a fragment thereof. Another specific class of 151P3D4 protein variants or analogs comprise one or more of the 151P3D4 biological motifs described herein or presently known in the art. Thus, encompassed by the present invention are analogs of 151P3D4 fragments (nucleic or amino acid) that have altered functional (e.g. immunogenic) properties relative to the starting fragment. It is to be appreciated that motifs now or which become part of the art are to be applied to the nucleic or amino acid sequences of Figure 2 or Figure 3.

As discussed herein, embodiments of the claimed invention include polypeptides containing less than the full amino acid sequence of a 151P3D4 protein shown in Figure 2 or Figure 3. For example, representative embodiments of the invention comprise peptides/proteins having any 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more contiguous amino acids of a 151P3D4 protein shown in Figure 2 or Figure 3.

Moreover, representative embodiments of the invention disclosed herein include polypeptides consisting of about amino acid 1 to about amino acid 10 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 10 to about amino acid 20 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 20 to about amino acid 30 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 30 to about amino acid 40 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 40 to about amino acid 50 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 50 to about amino acid 60 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 60 to about amino acid 70 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 70 to about amino acid 80 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 80 to about amino acid 90 of a 151P3D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 90 to about amino acid 100 of a 151P3D4 protein shown in Figure 2 or Figure 3, etc. throughout the entirety of a 151P3D4 amino acid sequence. Moreover, polypeptides consisting of about amino acid 1 (or 20 or 30 or 40 etc.) to about amino acid 20, (or 130, or 140 or 150 etc.) of a 151P3D4 protein shown in Figure 2 or Figure 3 are embodiments of the invention. It is to be appreciated that the starting and stopping positions in this paragraph refer to the specified position as well as that position plus or minus 5 residues.

151P3D4-related proteins are generated using standard peptide synthesis technology or using chemical cleavage methods well known in the art. Alternatively, recombinant methods can be used to generate nucleic acid molecules that encode a 151P3D4-related protein. In one embodiment, nucleic acid molecules provide a means to generate defined fragments of a 151P3D4 protein (or variants, homologs or analogs thereof).

III.A.) Motif-bearing Protein Embodiments

Additional illustrative embodiments of the invention disclosed herein include 151P3D4 polypeptides comprising the amino acid residues of one or more of the biological motifs contained within a 151P3D4 polypeptide sequence set forth in Figure 2 or Figure 3. Various motifs are known in the art, and a protein can be evaluated for the presence of such motifs by a number of publicly available Internet sites (see, e.g., URL addresses: pfam.wustl.edu/; http://searchlauncher.bcm.tmc.edu/seq-search/struc-predict.html; psort.ims.u-tokyo.ac.jp/; www.cbs.dtu.dk/; www.ebi.ac.uk/interpro/scan.html; www.expasy.ch/tools/scnpsit1.html; Epimatrix™ and Epimer™, Brown University, www.brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html; and BIMAS, bimas.dcrt.nih.gov/.).

Motif bearing subsequences of all 151P3D4 variant proteins are set forth and identified in Tables V-XVIII and XXII-LII.

Table XIX sets forth several frequently occurring motifs based on pfam searches (see URL address pfam.wustl.edu/). The columns of Table XIX list (1) motif name abbreviation, (2) percent identity found

amongst the different member of the motif family, (3) motif name or description and (4) most common function; location information is included if the motif is relevant for location.

Polypeptides comprising one or more of the 151P3D4 motifs discussed above are useful in elucidating the specific characteristics of a malignant phenotype in view of the observation that the 151P3D4 motifs discussed above are associated with growth dysregulation and because 151P3D4 is overexpressed in certain cancers (See, e.g., Table I). Casein kinase II, cAMP and camp-dependent protein kinase, and Protein Kinase C, for example, are enzymes known to be associated with the development of the malignant phenotype (see e.g. Chen *et al.*, Lab Invest., 78(2): 165-174 (1998); Gaiddon *et al.*, Endocrinology 136(10): 4331-4338 (1995); Hall *et al.*, Nucleic Acids Research 24(6): 1119-1126 (1996); Peterziel *et al.*, Oncogene 18(46): 6322-6329 (1999) and O'Brian, Oncol. Rep. 5(2): 305-309 (1998)). Moreover, both glycosylation and myristoylation are protein modifications also associated with cancer and cancer progression (see e.g. Dennis *et al.*, Biochem. Biophys. Acta 1473(1):21-34 (1999); Raju *et al.*, Exp. Cell Res. 235(1): 145-154 (1997)). Amidation is another protein modification also associated with cancer and cancer progression (see e.g. Treston *et al.*, J. Natl. Cancer Inst. Monogr. (13): 169-175 (1992)).

In another embodiment, proteins of the invention comprise one or more of the immunoreactive epitopes identified in accordance with art-accepted methods, such as the peptides set forth in Tables V-XVIII and XXII-LI. CTL epitopes can be determined using specific algorithms to identify peptides within a 151P3D4 protein that are capable of optimally binding to specified HLA alleles (e.g., Table IV; Epimatrix™ and Epimer™, Brown University, URL www.brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html; and BIMAS, URL bimas.dcrt.nih.gov/.) Moreover, processes for identifying peptides that have sufficient binding affinity for HLA molecules and which are correlated with being immunogenic epitopes, are well known in the art, and are carried out without undue experimentation. In addition, processes for identifying peptides that are immunogenic epitopes, are well known in the art, and are carried out without undue experimentation either *in vitro* or *in vivo*.

Also known in the art are principles for creating analogs of such epitopes in order to modulate immunogenicity. For example, one begins with an epitope that bears a CTL or HTL motif (see, e.g., the HLA Class I and HLA Class II motifs/supermotifs of Table IV). The epitope is analoged by substituting out an amino acid at one of the specified positions, and replacing it with another amino acid specified for that position. For example, one can substitute out a deleterious residue in favor of any other residue, such as a preferred residue as defined in Table IV; substitute a less-preferred residue with a preferred residue as defined in Table IV; or substitute an originally-occurring preferred residue with another preferred residue as defined in Table IV. Substitutions can occur at primary anchor positions or at other positions in a peptide; see, e.g., Table IV.

A variety of references reflect the art regarding the identification and generation of epitopes in a protein of interest as well as analogs thereof. See, for example, WO 97/33602 to Chesnut *et al.*; Sette, Immunogenetics 1999 50(3-4): 201-212; Sette *et al.*, J. Immunol. 2001 166(2): 1389-1397; Sidney *et al.*, Hum. Immunol. 1997 58(1): 12-20; Kondo *et al.*, Immunogenetics 1997 45(4): 249-258; Sidney *et al.*, J. Immunol. 1996 157(8): 3480-90; and Falk *et al.*, Nature 351: 290-6 (1991); Hunt *et al.*, Science 255:1261-3 (1992); Parker *et al.*, J. Immunol. 149:3580-7 (1992); Parker *et al.*, J. Immunol. 152:163-75 (1994)); Kast *et*

al., 1994 152(8): 3904-12; Borras-Cuesta *et al.*, Hum. Immunol. 2000 61(3): 266-278; Alexander *et al.*, J. Immunol. 2000 164(3); 164(3): 1625-1633; Alexander *et al.*, PMID: 7895164, UI: 95202582; O'Sullivan *et al.*, J. Immunol. 1991 147(8): 2663-2669; Alexander *et al.*, Immunity 1994 1(9): 751-761 and Alexander *et al.*, Immunol. Res. 1998 18(2): 79-92.

Related embodiments of the invention include polypeptides comprising combinations of the different motifs set forth in Table XX, and/or, one or more of the predicted CTL epitopes of Tables V-XVII and XXII-XLVII, and/or, one or more of the predicted HTL epitopes of Tables XLVIII-LI, and/or, one or more of the T cell binding motifs known in the art. Preferred embodiments contain no insertions, deletions or substitutions either within the motifs or the intervening sequences of the polypeptides. In addition, embodiments which include a number of either N-terminal and/or C-terminal amino acid residues on either side of these motifs may be desirable (to, for example, include a greater portion of the polypeptide architecture in which the motif is located). Typically the number of N-terminal and/or C-terminal amino acid residues on either side of a motif is between about 1 to about 100 amino acid residues, preferably 5 to about 50 amino acid residues.

151P3D4-related proteins are embodied in many forms, preferably in isolated form. A purified 151P3D4 protein molecule will be substantially free of other proteins or molecules that impair the binding of 151P3D4 to antibody, T cell or other ligand. The nature and degree of isolation and purification will depend on the intended use. Embodiments of a 151P3D4-related proteins include purified 151P3D4-related proteins and functional, soluble 151P3D4-related proteins. In one embodiment, a functional, soluble 151P3D4 protein or fragment thereof retains the ability to be bound by antibody, T cell or other ligand.

The invention also provides 151P3D4 proteins comprising biologically active fragments of a 151P3D4 amino acid sequence shown in Figure 2 or Figure 3. Such proteins exhibit properties of the starting 151P3D4 protein, such as the ability to elicit the generation of antibodies that specifically bind an epitope associated with the starting 151P3D4 protein; to be bound by such antibodies; to elicit the activation of HTL or CTL; and/or, to be recognized by HTL or CTL that also specifically bind to the starting protein.

151P3D4-related polypeptides that contain particularly interesting structures can be predicted and/or identified using various analytical techniques well known in the art, including, for example, the methods of Chou-Fasman, Garnier-Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis, or on the basis of immunogenicity. Fragments that contain such structures are particularly useful in generating subunit-specific anti-151P3D4 antibodies, or T cells or in identifying cellular factors that bind to 151P3D4. For example, hydrophilicity profiles can be generated, and immunogenic peptide fragments identified, using the method of Hopp, T.P. and Woods, K.R., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828. Hydropathicity profiles can be generated, and immunogenic peptide fragments identified, using the method of Kyte, J. and Doolittle, R.F., 1982, J. Mol. Biol. 157:105-132. Percent (%) Accessible Residues profiles can be generated, and immunogenic peptide fragments identified, using the method of Janin J., 1979, Nature 277:491-492. Average Flexibility profiles can be generated, and immunogenic peptide fragments identified, using the method of Bhaskaran R., Ponnuswamy P.K., 1988, Int. J. Pept. Protein Res. 32:242-255. Beta-turn profiles can be generated, and immunogenic peptide fragments identified, using the method of Deleage, G., Roux B., 1987, Protein Engineering 1:289-294.

CTL epitopes can be determined using specific algorithms to identify peptides within a 151P3D4 protein that are capable of optimally binding to specified HLA alleles (e.g., by using the SYFPEITHI site at World Wide Web URL syfpeithi.bmi-heidelberg.com/; the listings in Table IV(A)-(E); Epimatrix™ and Epimer™, Brown University, URL (www.brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html); and BIMAS, URL bimas.dcrt.nih.gov/). Illustrating this, peptide epitopes from 151P3D4 that are presented in the context of human MHC Class I molecules, e.g., HLA-A1, A2, A3, A11, A24, B7 and B35 were predicted (see, e.g., Tables V-XVIII, XXII-LI). Specifically, the complete amino acid sequence of the 151P3D4 protein and relevant portions of other variants, i.e., for HLA Class I predictions 9 flanking residues on either side of a point mutation, and for HLA Class II predictions 14 flanking residues on either side of a point mutation, were entered into the HLA Peptide Motif Search algorithm found in the Bioinformatics and Molecular Analysis Section (BIMAS) web site listed above; in addition to the site SYFPEITHI, at URL syfpeithi.bmi-heidelberg.com/.

The HLA peptide motif search algorithm was developed by Dr. Ken Parker based on binding of specific peptide sequences in the groove of HLA Class I molecules, in particular HLA-A2 (see, e.g., Falk *et al.*, Nature 351: 290-6 (1991); Hunt *et al.*, Science 255:1261-3 (1992); Parker *et al.*, J. Immunol. 149:3580-7 (1992); Parker *et al.*, J. Immunol. 152:163-75 (1994)). This algorithm allows location and ranking of 8-mer, 9-mer, and 10-mer peptides from a complete protein sequence for predicted binding to HLA-A2 as well as numerous other HLA Class I molecules. Many HLA class I binding peptides are 8-, 9-, 10 or 11-mers. For example, for Class I HLA-A2, the epitopes preferably contain a leucine (L) or methionine (M) at position 2 and a valine (V) or leucine (L) at the C-terminus (see, e.g., Parker *et al.*, J. Immunol. 149:3580-7 (1992)). Selected results of 151P3D4 predicted binding peptides are shown in Tables V-XVIII and XXII-LI herein. In Tables V-XVIII and XXII-XLVII, selected candidates, 9-mers and 10-mers, for each family member are shown along with their location, the amino acid sequence of each specific peptide, and an estimated binding score. In Tables XLVIII-LI, selected candidates, 15-mers, for each family member are shown along with their location, the amino acid sequence of each specific peptide, and an estimated binding score. The binding score corresponds to the estimated half time of dissociation of complexes containing the peptide at 37°C at pH 6.5. Peptides with the highest binding score are predicted to be the most tightly bound to HLA Class I on the cell surface for the greatest period of time and thus represent the best immunogenic targets for T-cell recognition.

Actual binding of peptides to an HLA allele can be evaluated by stabilization of HLA expression on the antigen-processing defective cell line T2 (see, e.g., Xue *et al.*, Prostate 30:73-8 (1997) and Peshwa *et al.*, Prostate 36:129-38 (1998)). Immunogenicity of specific peptides can be evaluated *in vitro* by stimulation of CD8+ cytotoxic T lymphocytes (CTL) in the presence of antigen presenting cells such as dendritic cells.

It is to be appreciated that every epitope predicted by the BIMAS site, Epimer™ and Epimatrix™ sites, or specified by the HLA class I or class II motifs available in the art or which become part of the art such as set forth in Table IV (or determined using World Wide Web site URL syfpeithi.bmi-heidelberg.com/, or BIMAS, bimas.dcrt.nih.gov/) are to be "applied" to a 151P3D4 protein in accordance with the invention. As used in this context "applied" means that a 151P3D4 protein is evaluated, e.g., visually or by computer-based patterns finding methods, as appreciated by those of skill in the relevant art. Every subsequence of a

151P3D4 protein of 8, 9, 10, or 11 amino acid residues that bears an HLA Class I motif, or a subsequence of 9 or more amino acid residues that bear an HLA Class II motif are within the scope of the invention.

III.B.) Expression of 151P3D4-related Proteins

In an embodiment described in the examples that follow, 151P3D4 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 151P3D4 with a C-terminal 6XHis and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 151P3D4 protein in transfected cells. The secreted HIS-tagged 151P3D4 in the culture media can be purified, e.g., using a nickel column using standard techniques.

III.C.) Modifications of 151P3D4-related Proteins

Modifications of 151P3D4-related proteins such as covalent modifications are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a 151P3D4 polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of a 151P3D4 protein. Another type of covalent modification of a 151P3D4 polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of a protein of the invention. Another type of covalent modification of 151P3D4 comprises linking a 151P3D4 polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The 151P3D4-related proteins of the present invention can also be modified to form a chimeric molecule comprising 151P3D4 fused to another, heterologous polypeptide or amino acid sequence. Such a chimeric molecule can be synthesized chemically or recombinantly. A chimeric molecule can have a protein of the invention fused to another tumor-associated antigen or fragment thereof. Alternatively, a protein in accordance with the invention can comprise a fusion of fragments of a 151P3D4 sequence (amino or nucleic acid) such that a molecule is created that is not, through its length, directly homologous to the amino or nucleic acid sequences shown in Figure 2 or Figure 3. Such a chimeric molecule can comprise multiples of the same subsequence of 151P3D4. A chimeric molecule can comprise a fusion of a 151P3D4-related protein with a polyhistidine epitope tag, which provides an epitope to which immobilized nickel can selectively bind, with cytokines or with growth factors. The epitope tag is generally placed at the amino- or carboxyl-terminus of a 151P3D4 protein. In an alternative embodiment, the chimeric molecule can comprise a fusion of a 151P3D4-related protein with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a 151P3D4 polypeptide in place of at least one variable region within an Ig molecule. In a preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CHI, CH2 and CH3 regions of an IgGI molecule. For the production of immunoglobulin fusions see, e.g., U.S. Patent No. 5,428,130 issued June 27, 1995.

III.D.) Uses of 151P3D4-related Proteins

The proteins of the invention have a number of different specific uses. As 151P3D4 is highly expressed in prostate and other cancers, 151P3D4-related proteins are used in methods that assess the status of 151P3D4 gene products in normal versus cancerous tissues, thereby elucidating the malignant phenotype. Typically, polypeptides from specific regions of a 151P3D4 protein are used to assess the presence of perturbations (such as deletions, insertions, point mutations etc.) in those regions (such as regions containing one or more motifs). Exemplary assays utilize antibodies or T cells targeting 151P3D4-related proteins comprising the amino acid residues of one or more of the biological motifs contained within a 151P3D4 polypeptide sequence in order to evaluate the characteristics of this region in normal versus cancerous tissues or to elicit an immune response to the epitope. Alternatively, 151P3D4-related proteins that contain the amino acid residues of one or more of the biological motifs in a 151P3D4 protein are used to screen for factors that interact with that region of 151P3D4.

151P3D4 protein fragments/subsequences are particularly useful in generating and characterizing domain-specific antibodies (e.g., antibodies recognizing an extracellular or intracellular epitope of a 151P3D4 protein), for identifying agents or cellular factors that bind to 151P3D4 or a particular structural domain thereof, and in various therapeutic and diagnostic contexts, including but not limited to diagnostic assays, cancer vaccines and methods of preparing such vaccines.

Proteins encoded by the 151P3D4 genes, or by analogs, homologs or fragments thereof, have a variety of uses, including but not limited to generating antibodies and in methods for identifying ligands and other agents and cellular constituents that bind to a 151P3D4 gene product. Antibodies raised against a 151P3D4 protein or fragment thereof are useful in diagnostic and prognostic assays, and imaging methodologies in the management of human cancers characterized by expression of 151P3D4 protein, such as those listed in Table I. Such antibodies can be expressed intracellularly and used in methods of treating patients with such cancers. 151P3D4-related nucleic acids or proteins are also used in generating HTL or CTL responses.

Various immunological assays useful for the detection of 151P3D4 proteins are used, including but not limited to various types of radioimmunoassays, enzyme-linked immunosorbent assays (ELISA), enzyme-linked immunofluorescent assays (ELIFA), immunocytochemical methods, and the like. Antibodies can be labeled and used as immunological imaging reagents capable of detecting 151P3D4-expressing cells (e.g., in radioscintigraphic imaging methods). 151P3D4 proteins are also particularly useful in generating cancer vaccines, as further described herein.

IV.) 151P3D4 Antibodies

Another aspect of the invention provides antibodies that bind to 151P3D4-related proteins. Preferred antibodies specifically bind to a 151P3D4-related protein and do not bind (or bind weakly) to peptides or proteins that are not 151P3D4-related proteins. For example, antibodies that bind 151P3D4 can bind 151P3D4-related proteins such as the homologs or analogs thereof.

151P3D4 antibodies of the invention are particularly useful in cancer (see, e.g., Table I) diagnostic and prognostic assays, and imaging methodologies. Similarly, such antibodies are useful in the treatment,

diagnosis, and/or prognosis of other cancers, to the extent 151P3D4 is also expressed or overexpressed in these other cancers. Moreover, intracellularly expressed antibodies (e.g., single chain antibodies) are therapeutically useful in treating cancers in which the expression of 151P3D4 is involved, such as advanced or metastatic prostate cancers.

The invention also provides various immunological assays useful for the detection and quantification of 151P3D4 and mutant 151P3D4-related proteins. Such assays can comprise one or more 151P3D4 antibodies capable of recognizing and binding a 151P3D4-related protein, as appropriate. These assays are performed within various immunological assay formats well known in the art, including but not limited to various types of radioimmunoassays, enzyme-linked immunosorbent assays (ELISA), enzyme-linked immunofluorescent assays (ELIFA), and the like.

Immunological non-antibody assays of the invention also comprise T cell immunogenicity assays (inhibitory or stimulatory) as well as major histocompatibility complex (MHC) binding assays.

In addition, immunological imaging methods capable of detecting prostate cancer and other cancers expressing 151P3D4 are also provided by the invention, including but not limited to radioscintigraphic imaging methods using labeled 151P3D4 antibodies. Such assays are clinically useful in the detection, monitoring, and prognosis of 151P3D4 expressing cancers such as prostate cancer.

151P3D4 antibodies are also used in methods for purifying a 151P3D4-related protein and for isolating 151P3D4 homologues and related molecules. For example, a method of purifying a 151P3D4-related protein comprises incubating a 151P3D4 antibody, which has been coupled to a solid matrix, with a lysate or other solution containing a 151P3D4-related protein under conditions that permit the 151P3D4 antibody to bind to the 151P3D4-related protein; washing the solid matrix to eliminate impurities; and eluting the 151P3D4-related protein from the coupled antibody. Other uses of 151P3D4 antibodies in accordance with the invention include generating anti-idiotypic antibodies that mimic a 151P3D4 protein.

Various methods for the preparation of antibodies are well known in the art. For example, antibodies can be prepared by immunizing a suitable mammalian host using a 151P3D4-related protein, peptide, or fragment, in isolated or immunoconjugated form (Antibodies: A Laboratory Manual, CSH Press, Eds., Harlow, and Lane (1988); Harlow, Antibodies, Cold Spring Harbor Press, NY (1989)). In addition, fusion proteins of 151P3D4 can also be used, such as a 151P3D4 GST-fusion protein. In a particular embodiment, a GST fusion protein comprising all or most of the amino acid sequence of Figure 2 or Figure 3 is produced, then used as an immunogen to generate appropriate antibodies. In another embodiment, a 151P3D4-related protein is synthesized and used as an immunogen.

In addition, naked DNA immunization techniques known in the art are used (with or without purified 151P3D4-related protein or 151P3D4 expressing cells) to generate an immune response to the encoded immunogen (for review, see Donnelly *et al.*, 1997, Ann. Rev. Immunol. 15: 617-648).

The amino acid sequence of a 151P3D4 protein as shown in Figure 2 or Figure 3 can be analyzed to select specific regions of the 151P3D4 protein for generating antibodies. For example, hydrophobicity and hydrophilicity analyses of a 151P3D4 amino acid sequence are used to identify hydrophilic regions in the 151P3D4 structure. Regions of a 151P3D4 protein that show immunogenic structure, as well as other regions and domains, can readily be identified using various other methods known in the art, such as Chou-Fasman, Garnier-

Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis. Hydrophilicity profiles can be generated using the method of Hopp, T.P. and Woods, K.R., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828. Hydropathicity profiles can be generated using the method of Kyte, J. and Doolittle, R.F., 1982, J. Mol. Biol. 157:105-132. Percent (%) Accessible Residues profiles can be generated using the method of Janin J., 1979, Nature 277:491-492. Average Flexibility profiles can be generated using the method of Bhaskaran R., Ponnuswamy P.K., 1988, Int. J. Pept. Protein Res. 32:242-255. Beta-turn profiles can be generated using the method of Deleage, G., Roux B., 1987, Protein Engineering 1:289-294. Thus, each region identified by any of these programs or methods is within the scope of the present invention. Methods for the generation of 151P3D4 antibodies are further illustrated by way of the examples provided herein. Methods for preparing a protein or polypeptide for use as an immunogen are well known in the art. Also well known in the art are methods for preparing immunogenic conjugates of a protein with a carrier, such as BSA, KLH or other carrier protein. In some circumstances, direct conjugation using, for example, carbodiimide reagents are used; in other instances linking reagents such as those supplied by Pierce Chemical Co., Rockford, IL, are effective. Administration of a 151P3D4 immunogen is often conducted by injection over a suitable time period and with use of a suitable adjuvant, as is understood in the art. During the immunization schedule, titers of antibodies can be taken to determine adequacy of antibody formation.

151P3D4 monoclonal antibodies can be produced by various means well known in the art. For example, immortalized cell lines that secrete a desired monoclonal antibody are prepared using the standard hybridoma technology of Kohler and Milstein or modifications that immortalize antibody-producing B cells, as is generally known. Immortalized cell lines that secrete the desired antibodies are screened by immunoassay in which the antigen is a 151P3D4-related protein. When the appropriate immortalized cell culture is identified, the cells can be expanded and antibodies produced either from *in vitro* cultures or from ascites fluid.

The antibodies or fragments of the invention can also be produced, by recombinant means. Regions that bind specifically to the desired regions of a 151P3D4 protein can also be produced in the context of chimeric or complementarity determining region (CDR) grafted antibodies of multiple species origin. Humanized or human 151P3D4 antibodies can also be produced, and are preferred for use in therapeutic contexts. Methods for humanizing murine and other non-human antibodies, by substituting one or more of the non-human antibody CDRs for corresponding human antibody sequences, are well known (see for example, Jones *et al.*, 1986, Nature 321: 522-525; Riechmann *et al.*, 1988, Nature 332: 323-327; Verhoeyen *et al.*, 1988, Science 239: 1534-1536). See also, Carter *et al.*, 1993, Proc. Natl. Acad. Sci. USA 89: 4285 and Sims *et al.*, 1993, J. Immunol. 151: 2296.

Methods for producing fully human monoclonal antibodies include phage display and transgenic methods (for review, see Vaughan *et al.*, 1998, Nature Biotechnology 16: 535-539). Fully human 151P3D4 monoclonal antibodies can be generated using cloning technologies employing large human Ig gene combinatorial libraries (i.e., phage display) (Griffiths and Hoogenboom, Building an *in vitro* immune system: human antibodies from phage display libraries. In: Protein Engineering of Antibody Molecules for Prophylactic and Therapeutic Applications in Man, Clark, M. (Ed.), Nottingham Academic, pp 45-64 (1993); Burton and Barbas, Human Antibodies from combinatorial libraries. Id., pp 65-82). Fully human 151P3D4 monoclonal antibodies can also be produced using transgenic mice engineered to contain human immunoglobulin gene loci as described in PCT Patent Application WO98/24893, Kucherlapati and Jakobovits *et al.*, published December 3,

1997 (see also, Jakobovits, 1998, Exp. Opin. Invest. Drugs 7(4): 607-614; U.S. patents 6,162,963 issued 19 December 2000; 6,150,584 issued 12 November 2000; and, 6,114598 issued 5 September 2000). This method avoids the *in vitro* manipulation required with phage display technology and efficiently produces high affinity authentic human antibodies.

Reactivity of 151P3D4 antibodies with a 151P3D4-related protein can be established by a number of well known means, including Western blot, immunoprecipitation, ELISA, and FACS analyses using, as appropriate, 151P3D4-related proteins, 151P3D4-expressing cells or extracts thereof. A 151P3D4 antibody or fragment thereof can be labeled with a detectable marker or conjugated to a second molecule. Suitable detectable markers include, but are not limited to, a radioisotope, a fluorescent compound, a bioluminescent compound, chemiluminescent compound, a metal chelator or an enzyme. Further, bi-specific antibodies specific for two or more 151P3D4 epitopes are generated using methods generally known in the art. Homodimeric antibodies can also be generated by cross-linking techniques known in the art (e.g., Wolff *et al.*, Cancer Res. 53: 2560-2565).

V.) 151P3D4 Cellular Immune Responses

The mechanism by which T cells recognize antigens has been delineated. Efficacious peptide epitope vaccine compositions of the invention induce a therapeutic or prophylactic immune responses in very broad segments of the world-wide population. For an understanding of the value and efficacy of compositions of the invention that induce cellular immune responses, a brief review of immunology-related technology is provided.

A complex of an HLA molecule and a peptidic antigen acts as the ligand recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P. *et al.*, *Nature* 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601, 1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are set forth in Table IV (*see* also, *e.g.*, Southwood, *et al.*, *J. Immunol.* 160:3363, 1998; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI, access via World Wide Web at URL syfpeithi.bmi-heidelberg.com/; Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al.*, *Cell* 74:929-937, 1993; Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; Sidney *et al.*, *J. Immunol.* 157:3480-3490, 1996; Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics 1999 Nov; 50(3-4):201-12,* Review).

Furthermore, x-ray crystallographic analyses of HLA-peptide complexes have revealed pockets within the peptide binding cleft/groove of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands; these residues in turn determine the HLA binding capacity of the peptides in which they are present. (*See, e.g.*, Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al.*, *Immunity* 4:203, 1996; Fremont *et al.*, *Immunity* 8:305, 1998; Stern *et al.*, *Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al.*, *Nature* 364:33, 1993; Guo, H. C. *et al.*, *Proc. Natl.*

Acad. Sci. USA 90:8053, 1993; Guo, H. C. *et al., Nature* 360:364, 1992; Silver, M. L. *et al., Nature* 360:367, 1992; Matsumura, M. *et al., Science* 257:927, 1992; Madden *et al., Cell* 70:1035, 1992; Fremont, D. H. *et al., Science* 257:919, 1992; Saper, M. A. , Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that are correlated with binding to particular HLA antigen(s).

Thus, by a process of HLA motif identification, candidates for epitope-based vaccines have been identified; such candidates can be further evaluated by HLA-peptide binding assays to determine binding affinity and/or the time period of association of the epitope and its corresponding HLA molecule. Additional confirmatory work can be performed to select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, and/or immunogenicity.

Various strategies can be utilized to evaluate cellular immunogenicity, including:

1) Evaluation of primary T cell cultures from normal individuals (*see, e.g.*, Wentworth, P. A. *et al., Mol. Immunol.* 32:603, 1995; Celis, E. *et al., Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al., J. Immunol.* 158:1796, 1997; Kawashima, I. *et al., Human Immunol.* 59:1, 1998). This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several weeks. T cells specific for the peptide become activated during this time and are detected using, *e.g.*, a lymphokine- or ^{51}Cr-release assay involving peptide sensitized target cells.

2) Immunization of HLA transgenic mice (*see, e.g.*, Wentworth, P. A. *et al., J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al., Int. Immunol.* 8:651, 1996; Alexander, J. *et al., J. Immunol.* 159:4753, 1997). For example, in such methods peptides in incomplete Freund's adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, *e.g.*, a ^{51}Cr-release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.

3) Demonstration of recall T cell responses from immune individuals who have been either effectively vaccinated and/or from chronically ill patients (*see, e.g.*, Rehermann, B. *et al., J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al., Immunity* 7:97, 1997; Bertoni, R. *et al., J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al., J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al., J. Virol.* 71:6011, 1997). Accordingly, recall responses are detected by culturing PBL from subjects that have been exposed to the antigen due to disease and thus have generated an immune response "naturally", or from patients who were vaccinated against the antigen. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.

VI.) 151P3D4 Transgenic Animals

Nucleic acids that encode a 151P3D4-related protein can also be used to generate either transgenic animals or "knock out" animals that, in turn, are useful in the development and screening of therapeutically useful reagents. In accordance with established techniques, cDNA encoding 151P3D4 can be used to clone genomic DNA that encodes 151P3D4. The cloned genomic sequences can then be used to generate transgenic animals containing cells that express DNA that encode 151P3D4. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 issued 12 April 1988, and 4,870,009 issued 26 September 1989. Typically, particular cells would be targeted for 151P3D4 transgene incorporation with tissue-specific enhancers.

Transgenic animals that include a copy of a transgene encoding 151P3D4 can be used to examine the effect of increased expression of DNA that encodes 151P3D4. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this aspect of the invention, an animal is treated with a reagent and a reduced incidence of a pathological condition, compared to untreated animals that bear the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of 151P3D4 can be used to construct a 151P3D4 "knock out" animal that has a defective or altered gene encoding 151P3D4 as a result of homologous recombination between the endogenous gene encoding 151P3D4 and altered genomic DNA encoding 151P3D4 introduced into an embryonic cell of the animal. For example, cDNA that encodes 151P3D4 can be used to clone genomic DNA encoding 151P3D4 in accordance with established techniques. A portion of the genomic DNA encoding 151P3D4 can be deleted or replaced with another gene, such as a gene encoding a selectable marker that can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector (see, e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected (see, e.g., Li *et al.*, Cell, 69:915 (1992)). The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras (see, e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal, and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knock out animals can be characterized, for example, for their ability to defend against certain pathological conditions or for their development of pathological conditions due to absence of a 151P3D4 polypeptide.

VII.) Methods for the Detection of 151P3D4

Another aspect of the present invention relates to methods for detecting 151P3D4 polynucleotides and 151P3D4-related proteins, as well as methods for identifying a cell that expresses 151P3D4. The expression

profile of 151P3D4 makes it a diagnostic marker for metastasized disease. Accordingly, the status of 151P3D4 gene products provides information useful for predicting a variety of factors including susceptibility to advanced stage disease, rate of progression, and/or tumor aggressiveness. As discussed in detail herein, the status of 151P3D4 gene products in patient samples can be analyzed by a variety protocols that are well known in the art including immunohistochemical analysis, the variety of Northern blotting techniques including *in situ* hybridization, RT-PCR analysis (for example on laser capture micro-dissected samples), Western blot analysis and tissue array analysis.

More particularly, the invention provides assays for the detection of 151P3D4 polynucleotides in a biological sample, such as serum, bone, prostate, and other tissues, urine, semen, cell preparations, and the like. Detectable 151P3D4 polynucleotides include, for example, a 151P3D4 gene or fragment thereof, 151P3D4 mRNA, alternative splice variant 151P3D4 mRNAs, and recombinant DNA or RNA molecules that contain a 151P3D4 polynucleotide. A number of methods for amplifying and/or detecting the presence of 151P3D4 polynucleotides are well known in the art and can be employed in the practice of this aspect of the invention.

In one embodiment, a method for detecting a 151P3D4 mRNA in a biological sample comprises producing cDNA from the sample by reverse transcription using at least one primer; amplifying the cDNA so produced using a 151P3D4 polynucleotides as sense and antisense primers to amplify 151P3D4 cDNAs therein; and detecting the presence of the amplified 151P3D4 cDNA. Optionally, the sequence of the amplified 151P3D4 cDNA can be determined.

In another embodiment, a method of detecting a 151P3D4 gene in a biological sample comprises first isolating genomic DNA from the sample; amplifying the isolated genomic DNA using 151P3D4 polynucleotides as sense and antisense primers; and detecting the presence of the amplified 151P3D4 gene. Any number of appropriate sense and antisense probe combinations can be designed from a 151P3D4 nucleotide sequence (see, e.g., Figure 2) and used for this purpose.

The invention also provides assays for detecting the presence of a 151P3D4 protein in a tissue or other biological sample such as serum, semen, bone, prostate, urine, cell preparations, and the like. Methods for detecting a 151P3D4-related protein are also well known and include, for example, immunoprecipitation, immunohistochemical analysis, Western blot analysis, molecular binding assays, ELISA, ELIFA and the like. For example, a method of detecting the presence of a 151P3D4-related protein in a biological sample comprises first contacting the sample with a 151P3D4 antibody, a 151P3D4-reactive fragment thereof, or a recombinant protein containing an antigen binding region of a 151P3D4 antibody; and then detecting the binding of 151P3D4-related protein in the sample.

Methods for identifying a cell that expresses 151P3D4 are also within the scope of the invention. In one embodiment, an assay for identifying a cell that expresses a 151P3D4 gene comprises detecting the presence of 151P3D4 mRNA in the cell. Methods for the detection of particular mRNAs in cells are well known and include, for example, hybridization assays using complementary DNA probes (such as *in situ* hybridization using labeled 151P3D4 riboprobes, Northern blot and related techniques) and various nucleic acid amplification assays (such as RT-PCR using complementary primers specific for 151P3D4, and other amplification type detection methods, such as, for example, branched DNA, SISBA, TMA and the like). Alternatively, an assay for identifying a cell that expresses a 151P3D4 gene comprises detecting the presence of 151P3D4-related protein in the cell or

secreted by the cell. Various methods for the detection of proteins are well known in the art and are employed for the detection of 151P3D4-related proteins and cells that express 151P3D4-related proteins.

151P3D4 expression analysis is also useful as a tool for identifying and evaluating agents that modulate 151P3D4 gene expression. For example, 151P3D4 expression is significantly upregulated in prostate cancer, and is expressed in cancers of the tissues listed in Table I. Identification of a molecule or biological agent that inhibits 151P3D4 expression or over-expression in cancer cells is of therapeutic value. For example, such an agent can be identified by using a screen that quantifies 151P3D4 expression by RT-PCR, nucleic acid hybridization or antibody binding.

VIII.) Methods for Monitoring the Status of 151P3D4-related Genes and Their Products

Oncogenesis is known to be a multistep process where cellular growth becomes progressively dysregulated and cells progress from a normal physiological state to precancerous and then cancerous states (see, e.g., Alers *et al.*, Lab Invest. 77(5): 437-438 (1997) and Isaacs *et al.*, Cancer Surv. 23: 19-32 (1995)). In this context, examining a biological sample for evidence of dysregulated cell growth (such as aberrant 151P3D4 expression in cancers) allows for early detection of such aberrant physiology, before a pathologic state such as cancer has progressed to a stage that therapeutic options are more limited and or the prognosis is worse. In such examinations, the status of 151P3D4 in a biological sample of interest can be compared, for example, to the status of 151P3D4 in a corresponding normal sample (e.g. a sample from that individual or alternatively another individual that is not affected by a pathology). An alteration in the status of 151P3D4 in the biological sample (as compared to the normal sample) provides evidence of dysregulated cellular growth. In addition to using a biological sample that is not affected by a pathology as a normal sample, one can also use a predetermined normative value such as a predetermined normal level of mRNA expression (see, e.g., Grever *et al.*, J. Comp. Neurol. 1996 Dec 9; 376(2): 306-14 and U.S. Patent No. 5,837,501) to compare 151P3D4 status in a sample.

The term "status" in this context is used according to its art accepted meaning and refers to the condition or state of a gene and its products. Typically, skilled artisans use a number of parameters to evaluate the condition or state of a gene and its products. These include, but are not limited to the location of expressed gene products (including the location of 151P3D4 expressing cells) as well as the level, and biological activity of expressed gene products (such as 151P3D4 mRNA, polynucleotides and polypeptides). Typically, an alteration in the status of 151P3D4 comprises a change in the location of 151P3D4 and/or 151P3D4 expressing cells and/or an increase in 151P3D4 mRNA and/or protein expression.

151P3D4 status in a sample can be analyzed by a number of means well known in the art, including without limitation, immunohistochemical analysis, *in situ* hybridization, RT-PCR analysis on laser capture micro-dissected samples, Western blot analysis, and tissue array analysis. Typical protocols for evaluating the status of a 151P3D4 gene and gene products are found, for example in Ausubel *et al.* eds., 1995, Current Protocols In Molecular Biology, Units 2 (Northern Blotting), 4 (Southern Blotting), 15 (Immunoblotting) and 18 (PCR Analysis). Thus, the status of 151P3D4 in a biological sample is evaluated by various methods utilized by skilled artisans including, but not limited to genomic Southern analysis (to examine, for example perturbations in a 151P3D4 gene), Northern analysis and/or PCR analysis of 151P3D4 mRNA (to examine,

for example alterations in the polynucleotide sequences or expression levels of 151P3D4 mRNAs), and, Western and/or immunohistochemical analysis (to examine, for example alterations in polypeptide sequences, alterations in polypeptide localization within a sample, alterations in expression levels of 151P3D4 proteins and/or associations of 151P3D4 proteins with polypeptide binding partners). Detectable 151P3D4 polynucleotides include, for example, a 151P3D4 gene or fragment thereof, 151P3D4 mRNA, alternative splice variants, 151P3D4 mRNAs, and recombinant DNA or RNA molecules containing a 151P3D4 polynucleotide.

The expression profile of 151P3D4 makes it a diagnostic marker for local and/or metastasized disease, and provides information on the growth or oncogenic potential of a biological sample. In particular, the status of 151P3D4 provides information useful for predicting susceptibility to particular disease stages, progression, and/or tumor aggressiveness. The invention provides methods and assays for determining 151P3D4 status and diagnosing cancers that express 151P3D4, such as cancers of the tissues listed in Table I. For example, because 151P3D4 mRNA is so highly expressed in prostate and other cancers relative to normal prostate tissue, assays that evaluate the levels of 151P3D4 mRNA transcripts or proteins in a biological sample can be used to diagnose a disease associated with 151P3D4 dysregulation, and can provide prognostic information useful in defining appropriate therapeutic options.

The expression status of 151P3D4 provides information including the presence, stage and location of dysplastic, precancerous and cancerous cells, predicting susceptibility to various stages of disease, and/or for gauging tumor aggressiveness. Moreover, the expression profile makes it useful as an imaging reagent for metastasized disease. Consequently, an aspect of the invention is directed to the various molecular prognostic and diagnostic methods for examining the status of 151P3D4 in biological samples such as those from individuals suffering from, or suspected of suffering from a pathology characterized by dysregulated cellular growth, such as cancer.

As described above, the status of 151P3D4 in a biological sample can be examined by a number of well-known procedures in the art. For example, the status of 151P3D4 in a biological sample taken from a specific location in the body can be examined by evaluating the sample for the presence or absence of 151P3D4 expressing cells (e.g. those that express 151P3D4 mRNAs or proteins). This examination can provide evidence of dysregulated cellular growth, for example, when 151P3D4-expressing cells are found in a biological sample that does not normally contain such cells (such as a lymph node), because such alterations in the status of 151P3D4 in a biological sample are often associated with dysregulated cellular growth. Specifically, one indicator of dysregulated cellular growth is the metastases of cancer cells from an organ of origin (such as the prostate) to a different area of the body (such as a lymph node). In this context, evidence of dysregulated cellular growth is important for example because occult lymph node metastases can be detected in a substantial proportion of patients with prostate cancer, and such metastases are associated with known predictors of disease progression (see, e.g., Murphy *et al.*, Prostate 42(4): 315-317 (2000);Su *et al.*, Semin. Surg. Oncol. 18(1): 17-28 (2000) and Freeman *et al.*, J Urol 1995 Aug 154(2 Pt 1):474-8).

In one aspect, the invention provides methods for monitoring 151P3D4 gene products by determining the status of 151P3D4 gene products expressed by cells from an individual suspected of having a disease associated with dysregulated cell growth (such as hyperplasia or cancer) and then comparing the status so determined to the status of 151P3D4 gene products in a corresponding normal sample. The presence

of aberrant 151P3D4 gene products in the test sample relative to the normal sample provides an indication of the presence of dysregulated cell growth within the cells of the individual.

In another aspect, the invention provides assays useful in determining the presence of cancer in an individual, comprising detecting a significant increase in 151P3D4 mRNA or protein expression in a test cell or tissue sample relative to expression levels in the corresponding normal cell or tissue. The presence of 151P3D4 mRNA can, for example, be evaluated in tissues including but not limited to those listed in Table I. The presence of significant 151P3D4 expression in any of these tissues is useful to indicate the emergence, presence and/or severity of a cancer, since the corresponding normal tissues do not express 151P3D4 mRNA or express it at lower levels.

In a related embodiment, 151P3D4 status is determined at the protein level rather than at the nucleic acid level. For example, such a method comprises determining the level of 151P3D4 protein expressed by cells in a test tissue sample and comparing the level so determined to the level of 151P3D4 expressed in a corresponding normal sample. In one embodiment, the presence of 151P3D4 protein is evaluated, for example, using immunohistochemical methods. 151P3D4 antibodies or binding partners capable of detecting 151P3D4 protein expression are used in a variety of assay formats well known in the art for this purpose.

In a further embodiment, one can evaluate the status of 151P3D4 nucleotide and amino acid sequences in a biological sample in order to identify perturbations in the structure of these molecules. These perturbations can include insertions, deletions, substitutions and the like. Such evaluations are useful because perturbations in the nucleotide and amino acid sequences are observed in a large number of proteins associated with a growth dysregulated phenotype (see, e.g., Marrogi *et al.*, 1999, J. Cutan. Pathol. 26(8):369-378). For example, a mutation in the sequence of 151P3D4 may be indicative of the presence or promotion of a tumor. Such assays therefore have diagnostic and predictive value where a mutation in 151P3D4 indicates a potential loss of function or increase in tumor growth.

A wide variety of assays for observing perturbations in nucleotide and amino acid sequences are well known in the art. For example, the size and structure of nucleic acid or amino acid sequences of 151P3D4 gene products are observed by the Northern, Southern, Western, PCR and DNA sequencing protocols discussed herein. In addition, other methods for observing perturbations in nucleotide and amino acid sequences such as single strand conformation polymorphism analysis are well known in the art (see, e.g., U.S. Patent Nos. 5,382,510 issued 7 September 1999, and 5,952,170 issued 17 January 1995).

Additionally, one can examine the methylation status of a 151P3D4 gene in a biological sample. Aberrant demethylation and/or hypermethylation of CpG islands in gene 5' regulatory regions frequently occurs in immortalized and transformed cells, and can result in altered expression of various genes. For example, promoter hypermethylation of the pi-class glutathione S-transferase (a protein expressed in normal prostate but not expressed in >90% of prostate carcinomas) appears to permanently silence transcription of this gene and is the most frequently detected genomic alteration in prostate carcinomas (De Marzo *et al.*, Am. J. Pathol. 155(6): 1985-1992 (1999)). In addition, this alteration is present in at least 70% of cases of high-grade prostatic intraepithelial neoplasia (PIN) (Brooks *et al.*, Cancer Epidemiol. Biomarkers Prev., 1998, 7:531-536). In another example, expression of the LAGE-I tumor specific gene (which is not expressed in normal prostate but is expressed in 25-50% of prostate cancers) is induced by deoxy-azacytidine in lymphoblastoid

cells, suggesting that tumoral expression is due to demethylation (Lethe *et al.*, Int. J. Cancer 76(6): 903-908 (1998)). A variety of assays for examining methylation status of a gene are well known in the art. For example, one can utilize, in Southern hybridization approaches, methylation-sensitive restriction enzymes that cannot cleave sequences that contain methylated CpG sites to assess the methylation status of CpG islands. In addition, MSP (methylation specific PCR) can rapidly profile the methylation status of all the CpG sites present in a CpG island of a given gene. This procedure involves initial modification of DNA by sodium bisulfite (which will convert all unmethylated cytosines to uracil) followed by amplification using primers specific for methylated versus unmethylated DNA. Protocols involving methylation interference can also be found for example in Current Protocols In Molecular Biology, Unit 12, Frederick M. Ausubel *et al.* eds., 1995.

Gene amplification is an additional method for assessing the status of 151P3D4. Gene amplification is measured in a sample directly, for example, by conventional Southern blotting or Northern blotting to quantitate the transcription of mRNA (Thomas, 1980, Proc. Natl. Acad. Sci. USA, 77:5201-5205), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies are employed that recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn are labeled and the assay carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Biopsied tissue or peripheral blood can be conveniently assayed for the presence of cancer cells using for example, Northern, dot blot or RT-PCR analysis to detect 151P3D4 expression. The presence of RT-PCR amplifiable 151P3D4 mRNA provides an indication of the presence of cancer. RT-PCR assays are well known in the art. RT-PCR detection assays for tumor cells in peripheral blood are currently being evaluated for use in the diagnosis and management of a number of human solid tumors. In the prostate cancer field, these include RT-PCR assays for the detection of cells expressing PSA and PSM (Verkaik *et al.*, 1997, Urol. Res. 25:373-384; Ghossein *et al.*, 1995, J. Clin. Oncol. 13:1195-2000; Heston *et al.*, 1995, Clin. Chem. 41:1687-1688).

A further aspect of the invention is an assessment of the susceptibility that an individual has for developing cancer. In one embodiment, a method for predicting susceptibility to cancer comprises detecting 151P3D4 mRNA or 151P3D4 protein in a tissue sample, its presence indicating susceptibility to cancer, wherein the degree of 151P3D4 mRNA expression correlates to the degree of susceptibility. In a specific embodiment, the presence of 151P3D4 in prostate or other tissue is examined, with the presence of 151P3D4 in the sample providing an indication of prostate cancer susceptibility (or the emergence or existence of a prostate tumor). Similarly, one can evaluate the integrity 151P3D4 nucleotide and amino acid sequences in a biological sample, in order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like. The presence of one or more perturbations in 151P3D4 gene products in the sample is an indication of cancer susceptibility (or the emergence or existence of a tumor).

The invention also comprises methods for gauging tumor aggressiveness. In one embodiment, a method for gauging aggressiveness of a tumor comprises determining the level of 151P3D4 mRNA or 151P3D4 protein expressed by tumor cells, comparing the level so determined to the level of 151P3D4 mRNA or 151P3D4 protein expressed in a corresponding normal tissue taken from the same individual or a normal tissue reference sample, wherein the degree of 151P3D4 mRNA or 151P3D4 protein expression in the tumor sample relative to the normal

sample indicates the degree of aggressiveness. In a specific embodiment, aggressiveness of a tumor is evaluated by determining the extent to which 151P3D4 is expressed in the tumor cells, with higher expression levels indicating more aggressive tumors. Another embodiment is the evaluation of the integrity of 151P3D4 nucleotide and amino acid sequences in a biological sample, in order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like. The presence of one or more perturbations indicates more aggressive tumors.

Another embodiment of the invention is directed to methods for observing the progression of a malignancy in an individual over time. In one embodiment, methods for observing the progression of a malignancy in an individual over time comprise determining the level of 151P3D4 mRNA or 151P3D4 protein expressed by cells in a sample of the tumor, comparing the level so determined to the level of 151P3D4 mRNA or 151P3D4 protein expressed in an equivalent tissue sample taken from the same individual at a different time, wherein the degree of 151P3D4 mRNA or 151P3D4 protein expression in the tumor sample over time provides information on the progression of the cancer. In a specific embodiment, the progression of a cancer is evaluated by determining 151P3D4 expression in the tumor cells over time, where increased expression over time indicates a progression of the cancer. Also, one can evaluate the integrity 151P3D4 nucleotide and amino acid sequences in a biological sample in order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like, where the presence of one or more perturbations indicates a progression of the cancer.

The above diagnostic approaches can be combined with any one of a wide variety of prognostic and diagnostic protocols known in the art. For example, another embodiment of the invention is directed to methods for observing a coincidence between the expression of 151P3D4 gene and 151P3D4 gene products (or perturbations in 151P3D4 gene and 151P3D4 gene products) and a factor that is associated with malignancy, as a means for diagnosing and prognosticating the status of a tissue sample. A wide variety of factors associated with malignancy can be utilized, such as the expression of genes associated with malignancy (e.g. PSA, PSCA and PSM expression for prostate cancer etc.) as well as gross cytological observations (see, e.g., Bocking *et al.*, 1984, Anal. Quant. Cytol. 6(2):74-88; Epstein, 1995, Hum. Pathol. 26(2):223-9; Thorson *et al.*, 1998, Mod. Pathol. 11(6):543-51; Baisden *et al.*, 1999, Am. J. Surg. Pathol. 23(8):918-24). Methods for observing a coincidence between the expression of 151P3D4 gene and 151P3D4 gene products (or perturbations in 151P3D4 gene and 151P3D4 gene products) and another factor that is associated with malignancy are useful, for example, because the presence of a set of specific factors that coincide with disease provides information crucial for diagnosing and prognosticating the status of a tissue sample.

In one embodiment, methods for observing a coincidence between the expression of 151P3D4 gene and 151P3D4 gene products (or perturbations in 151P3D4 gene and 151P3D4 gene products) and another factor associated with malignancy entails detecting the overexpression of 151P3D4 mRNA or protein in a tissue sample, detecting the overexpression of PSA mRNA or protein in a tissue sample (or PSCA or PSM expression), and observing a coincidence of 151P3D4 mRNA or protein and PSA mRNA or protein overexpression (or PSCA or PSM expression). In a specific embodiment, the expression of 151P3D4 and PSA mRNA in prostate tissue is examined, where the coincidence of 151P3D4 and PSA mRNA overexpression in the sample indicates the existence of prostate cancer, prostate cancer susceptibility or the emergence or status of a prostate tumor.

Methods for detecting and quantifying the expression of 151P3D4 mRNA or protein are described herein, and standard nucleic acid and protein detection and quantification technologies are well known in the art. Standard methods for the detection and quantification of 151P3D4 mRNA include *in situ* hybridization using labeled 151P3D4 riboprobes, Northern blot and related techniques using 151P3D4 polynucleotide probes, RT-PCR analysis using primers specific for 151P3D4, and other amplification type detection methods, such as, for example, branched DNA, SISBA, TMA and the like. In a specific embodiment, semi-quantitative RT-PCR is used to detect and quantify 151P3D4 mRNA expression. Any number of primers capable of amplifying 151P3D4 can be used for this purpose, including but not limited to the various primer sets specifically described herein. In a specific embodiment, polyclonal or monoclonal antibodies specifically reactive with the wild-type 151P3D4 protein can be used in an immunohistochemical assay of biopsied tissue.

IX.) Identification of Molecules That Interact With 151P3D4

The 151P3D4 protein and nucleic acid sequences disclosed herein allow a skilled artisan to identify proteins, small molecules and other agents that interact with 151P3D4, as well as pathways activated by 151P3D4 via any one of a variety of art accepted protocols. For example, one can utilize one of the so-called interaction trap systems (also referred to as the "two-hybrid assay"). In such systems, molecules interact and reconstitute a transcription factor which directs expression of a reporter gene, whereupon the expression of the reporter gene is assayed. Other systems identify protein-protein interactions *in vivo* through reconstitution of a eukaryotic transcriptional activator, see, e.g., U.S. Patent Nos. 5,955,280 issued 21 September 1999, 5,925,523 issued 20 July 1999, 5,846,722 issued 8 December 1998 and 6,004,746 issued 21 December 1999. Algorithms are also available in the art for genome-based predictions of protein function (see, e.g., Marcotte, *et al.*, Nature 402: 4 November 1999, 83-86).

Alternatively one can screen peptide libraries to identify molecules that interact with 151P3D4 protein sequences. In such methods, peptides that bind to 151P3D4 are identified by screening libraries that encode a random or controlled collection of amino acids. Peptides encoded by the libraries are expressed as fusion proteins of bacteriophage coat proteins, the bacteriophage particles are then screened against the 151P3D4 protein(s).

Accordingly, peptides having a wide variety of uses, such as therapeutic, prognostic or diagnostic reagents, are thus identified without any prior information on the structure of the expected ligand or receptor molecule. Typical peptide libraries and screening methods that can be used to identify molecules that interact with 151P3D4 protein sequences are disclosed for example in U.S. Patent Nos. 5,723,286 issued 3 March 1998 and 5,733,731 issued 31 March 1998.

Alternatively, cell lines that express 151P3D4 are used to identify protein-protein interactions mediated by 151P3D4. Such interactions can be examined using immunoprecipitation techniques (see, e.g., Hamilton B.J., *et al.* Biochem. Biophys. Res. Commun. 1999, 261:646-51). 151P3D4 protein can be immunoprecipitated from 151P3D4-expressing cell lines using anti-151P3D4 antibodies. Alternatively, antibodies against His-tag can be used in a cell line engineered to express fusions of 151P3D4 and a His-tag (vectors mentioned above). The immunoprecipitated complex can be examined for protein association by

procedures such as Western blotting, ^{35}S-methionine labeling of proteins, protein microsequencing, silver staining and two-dimensional gel electrophoresis.

Small molecules and ligands that interact with 151P3D4 can be identified through related embodiments of such screening assays. For example, small molecules can be identified that interfere with protein function, including molecules that interfere with 151P3D4's ability to mediate phosphorylation and de-phosphorylation, interaction with DNA or RNA molecules as an indication of regulation of cell cycles, second messenger signaling or tumorigenesis. Similarly, small molecules that modulate 151P3D4-related ion channel, protein pump, or cell communication functions are identified and used to treat patients that have a cancer that expresses 151P3D4 (see, e.g., Hille, B., Ionic Channels of Excitable Membranes 2nd Ed., Sinauer Assoc., Sunderland, MA, 1992). Moreover, ligands that regulate 151P3D4 function can be identified based on their ability to bind 151P3D4 and activate a reporter construct. Typical methods are discussed for example in U.S. Patent No. 5,928,868 issued 27 July 1999, and include methods for forming hybrid ligands in which at least one ligand is a small molecule. In an illustrative embodiment, cells engineered to express a fusion protein of 151P3D4 and a DNA-binding protein are used to co-express a fusion protein of a hybrid ligand/small molecule and a cDNA library transcriptional activator protein. The cells further contain a reporter gene, the expression of which is conditioned on the proximity of the first and second fusion proteins to each other, an event that occurs only if the hybrid ligand binds to target sites on both hybrid proteins. Those cells that express the reporter gene are selected and the unknown small molecule or the unknown ligand is identified. This method provides a means of identifying modulators which activate or inhibit 151P3D4.

An embodiment of this invention comprises a method of screening for a molecule that interacts with a 151P3D4 amino acid sequence shown in Figure 2 or Figure 3, comprising the steps of contacting a population of molecules with a 151P3D4 amino acid sequence, allowing the population of molecules and the 151P3D4 amino acid sequence to interact under conditions that facilitate an interaction, determining the presence of a molecule that interacts with the 151P3D4 amino acid sequence, and then separating molecules that do not interact with the 151P3D4 amino acid sequence from molecules that do. In a specific embodiment, the method further comprises purifying, characterizing and identifying a molecule that interacts with the 151P3D4 amino acid sequence. The identified molecule can be used to modulate a function performed by 151P3D4. In a preferred embodiment, the 151P3D4 amino acid sequence is contacted with a library of peptides.

X.) Therapeutic Methods and Compositions

The identification of 151P3D4 as a protein that is normally expressed in a restricted set of tissues, but which is also expressed in prostate and other cancers, opens a number of therapeutic approaches to the treatment of such cancers. As contemplated herein, 151P3D4 functions as a transcription factor involved in activating tumor-promoting genes or repressing genes that block tumorigenesis.

Accordingly, therapeutic approaches that inhibit the activity of a 151P3D4 protein are useful for patients suffering from a cancer that expresses 151P3D4. These therapeutic approaches generally fall into two classes. One class comprises various methods for inhibiting the binding or association of a 151P3D4

protein with its binding partner or with other proteins. Another class comprises a variety of methods for inhibiting the transcription of a 151P3D4 gene or translation of 151P3D4 mRNA.

X.A.) Anti-Cancer Vaccines

The invention provides cancer vaccines comprising a 151P3D4-related protein or 151P3D4-related nucleic acid. In view of the expression of 151P3D4, cancer vaccines prevent and/or treat 151P3D4-expressing cancers with minimal or no effects on non-target tissues. The use of a tumor antigen in a vaccine that generates humoral and/or cell-mediated immune responses as anti-cancer therapy is well known in the art and has been employed in prostate cancer using human PSMA and rodent PAP immunogens (Hodge *et al.*, 1995, Int. J. Cancer 63:231-237; Fong *et al.*, 1997, J. Immunol. 159:3113-3117).

Such methods can be readily practiced by employing a 151P3D4-related protein, or a 151P3D4-encoding nucleic acid molecule and recombinant vectors capable of expressing and presenting the 151P3D4 immunogen (which typically comprises a number of antibody or T cell epitopes). Skilled artisans understand that a wide variety of vaccine systems for delivery of immunoreactive epitopes are known in the art (see, e.g., Heryln *et al.*, Ann Med 1999 Feb 31(1):66-78; Maruyama *et al.*, Cancer Immunol Immunother 2000 Jun 49(3):123-32) Briefly, such methods of generating an immune response (e.g. humoral and/or cell-mediated) in a mammal, comprise the steps of: exposing the mammal's immune system to an immunoreactive epitope (e.g. an epitope present in a 151P3D4 protein shown in Figure 3 or analog or homolog thereof) so that the mammal generates an immune response that is specific for that epitope (e.g. generates antibodies that specifically recognize that epitope). In a preferred method, a 151P3D4 immunogen contains a biological motif, see e.g., Tables V-XVIII and XXII-LI, or a peptide of a size range from 151P3D4 indicated in Figure 5, Figure 6, Figure 7, Figure 8, and Figure 9.

The entire 151P3D4 protein, immunogenic regions or epitopes thereof can be combined and delivered by various means. Such vaccine compositions can include, for example, lipopeptides (*e.g.*,Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991: Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.*, Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In:

Concepts in vaccine development, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

In patients with 151P3D4-associated cancer, the vaccine compositions of the invention can also be used in conjunction with other treatments used for cancer, *e.g.*, surgery, chemotherapy, drug therapies, radiation therapies, *etc.* including use in combination with immune adjuvants such as IL-2, IL-12, GM-CSF, and the like.

Cellular Vaccines:

CTL epitopes can be determined using specific algorithms to identify peptides within 151P3D4 protein that bind corresponding HLA alleles (see e.g., Table IV; Epimer™ and Epimatrix™, Brown University (URL www.brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html); and, BIMAS, (URL bimas.dcrt.nih.gov/; SYFPEITHI at URL syfpeithi.bmi-heidelberg.com/). In a preferred embodiment, a 151P3D4 immunogen contains one or more amino acid sequences identified using techniques well known in the art, such as the sequences shown in Tables V-XVIII and XXII-LI or a peptide of 8, 9, 10 or 11 amino acids specified by an HLA Class I motif/supermotif (e.g., Table IV (A), Table IV (D), or Table IV (E)) and/or a peptide of at least 9 amino acids that comprises an HLA Class II motif/supermotif (e.g., Table IV (B) or Table IV (C)). As is appreciated in the art, the HLA Class I binding groove is essentially closed ended so that peptides of only a particular size range can fit into the groove and be bound, generally HLA Class I epitopes are 8, 9, 10, or 11 amino acids long. In contrast, the HLA Class II binding groove is essentially open ended; therefore a peptide of about 9 or more amino acids can be bound by an HLA Class II molecule. Due to the binding groove differences between HLA Class I and II, HLA Class I motifs are length specific, i.e., position two of a Class I motif is the second amino acid in an amino to carboxyl direction of the peptide. The amino acid positions in a Class II motif are relative only to each other, not the overall peptide, i.e., additional amino acids can be attached to the amino and/or carboxyl termini of a motif-bearing sequence. HLA Class II epitopes are often 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids long, or longer than 25 amino acids.

Antibody-based Vaccines

A wide variety of methods for generating an immune response in a mammal are known in the art (for example as the first step in the generation of hybridomas). Methods of generating an immune response in a mammal comprise exposing the mammal's immune system to an immunogenic epitope on a protein (e.g. a 151P3D4 protein) so that an immune response is generated. A typical embodiment consists of a method for generating an immune response to 151P3D4 in a host, by contacting the host with a sufficient amount of at least one 151P3D4 B cell or cytotoxic T-cell epitope or analog thereof; and at least one periodic interval thereafter re-contacting the host with the 151P3D4 B cell or cytotoxic T-cell epitope or analog thereof. A specific embodiment consists of a method of generating an immune response against a 151P3D4-related protein or a man-made multiepitopic peptide comprising: administering 151P3D4 immunogen (e.g. a 151P3D4 protein or a peptide fragment thereof, a 151P3D4 fusion protein or analog etc.) in a vaccine preparation to a human or another mammal. Typically, such vaccine preparations further contain a suitable

adjuvant (see, e.g., U.S. Patent No. 6,146,635) or a universal helper epitope such as a PADRE™ peptide (Epimmune Inc., San Diego, CA; see, e.g., Alexander *et al.*, J. Immmol. 2000 164(3); 164(3): 1625-1633; Alexander *et al.*, Immunity 1994 1(9): 751-761 and Alexander *et al.*, Immunol. Res. 1998 18(2): 79-92). An alternative method comprises generating an immune response in an individual against a 151P3D4 immunogen by: administering *in vivo* to muscle or skin of the individual's body a DNA molecule that comprises a DNA sequence that encodes a 151P3D4 immunogen, the DNA sequence operatively linked to regulatory sequences which control the expression of the DNA sequence; wherein the DNA molecule is taken up by cells, the DNA sequence is expressed in the cells and an immune response is generated against the immunogen (see, e.g., U.S. Patent No. 5,962,428). Optionally a genetic vaccine facilitator such as anionic lipids; saponins; lectins; estrogenic compounds; hydroxylated lower alkyls; dimethyl sulfoxide; and urea is also administered. In addition, an antiidiotypic antibody can be administered that mimics 151P3D4, in order to generate a response to the target antigen.

Nucleic Acid Vaccines:

Vaccine compositions of the invention include nucleic acid-mediated modalities. DNA or RNA that encode protein(s) of the invention can be administered to a patient. Genetic immunization methods can be employed to generate prophylactic or therapeutic humoral and cellular immune responses directed against cancer cells expressing 151P3D4. Constructs comprising DNA encoding a 151P3D4-related protein/immunogen and appropriate regulatory sequences can be injected directly into muscle or skin of an individual, such that the cells of the muscle or skin take-up the construct and express the encoded 151P3D4 protein/immunogen. Alternatively, a vaccine comprises a 151P3D4-related protein. Expression of the 151P3D4-related protein immunogen results in the generation of prophylactic or therapeutic humoral and cellular immunity against cells that bear a 151P3D4 protein. Various prophylactic and therapeutic genetic immunization techniques known in the art can be used (for review, see information and references published at Internet address www.genweb.com). Nucleic acid-based delivery is described, for instance, in Wolff *et. al., Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.,* U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, proteins of the invention can be expressed via viral or bacterial vectors. Various viral gene delivery systems that can be used in the practice of the invention include, but are not limited to, vaccinia, fowlpox, canarypox, adenovirus, influenza, poliovirus, adeno-associated virus, lentivirus, and sindbis virus (see, e.g., Restifo, 1996, Curr. Opin. Immunol. 8:658-663; Tsang *et al.* J. Natl. Cancer Inst. 87:982-990 (1995)). Non-viral delivery systems can also be employed by introducing naked DNA encoding a 151P3D4-related protein into the patient (e.g., intramuscularly or intradermally) to induce an anti-tumor response.

Vaccinia virus is used, for example, as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into a host, the recombinant vaccinia virus expresses the protein immunogenic peptide, and thereby elicits a host immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille

Calmette Guerin). BCG vectors are described in Stover *et al., Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

Thus, gene delivery systems are used to deliver a 151P3D4-related nucleic acid molecule. In one embodiment, the full-length human 151P3D4 cDNA is employed. In another embodiment, 151P3D4 nucleic acid molecules encoding specific cytotoxic T lymphocyte (CTL) and/or antibody epitopes are employed.

Ex Vivo Vaccines

Various *ex vivo* strategies can also be employed to generate an immune response. One approach involves the use of antigen presenting cells (APCs) such as dendritic cells (DC) to present 151P3D4 antigen to a patient's immune system. Dendritic cells express MHC class I and II molecules, B7 co-stimulator, and IL-12, and are thus highly specialized antigen presenting cells. In prostate cancer, autologous dendritic cells pulsed with peptides of the prostate-specific membrane antigen (PSMA) are being used in a Phase I clinical trial to stimulate prostate cancer patients' immune systems (Tjoa *et al.*, 1996, Prostate 28:65-69; Murphy *et al.*, 1996, Prostate 29:371-380). Thus, dendritic cells can be used to present 151P3D4 peptides to T cells in the context of MHC class I or II molecules. In one embodiment, autologous dendritic cells are pulsed with 151P3D4 peptides capable of binding to MHC class I and/or class II molecules. In another embodiment, dendritic cells are pulsed with the complete 151P3D4 protein. Yet another embodiment involves engineering the overexpression of a 151P3D4 gene in dendritic cells using various implementing vectors known in the art, such as adenovirus (Arthur *et al.*, 1997, Cancer Gene Ther. 4:17-25), retrovirus (Henderson *et al.*, 1996, Cancer Res. 56:3763-3770), lentivirus, adeno-associated virus, DNA transfection (Ribas *et al.*, 1997, Cancer Res. 57:2865-2869), or tumor-derived RNA transfection (Ashley *et al.*, 1997, J. Exp. Med. 186:1177-1182). Cells that express 151P3D4 can also be engineered to express immune modulators, such as GM-CSF, and used as immunizing agents.

X.B.) 151P3D4 as a Target for Antibody-based Therapy

151P3D4 is an attractive target for antibody-based therapeutic strategies. A number of antibody strategies are known in the art for targeting both extracellular and intracellular molecules (see, e.g., complement and ADCC mediated killing as well as the use of intrabodies). Because 151P3D4 is expressed by cancer cells of various lineages relative to corresponding normal cells, systemic administration of 151P3D4-immunoreactive compositions are prepared that exhibit excellent sensitivity without toxic, non-specific and/or non-target effects caused by binding of the immunoreactive composition to non-target organs and tissues. Antibodies specifically reactive with domains of 151P3D4 are useful to treat 151P3D4-expressing cancers systemically, either as conjugates with a toxin or therapeutic agent, or as naked antibodies capable of inhibiting cell proliferation or function.

151P3D4 antibodies can be introduced into a patient such that the antibody binds to 151P3D4 and modulates a function, such as an interaction with a binding partner, and consequently mediates destruction of the tumor cells and/or inhibits the growth of the tumor cells. Mechanisms by which such antibodies exert a therapeutic effect can include complement-mediated cytolysis, antibody-dependent cellular cytotoxicity, modulation of the physiological function of 151P3D4, inhibition of ligand binding or signal transduction

pathways, modulation of tumor cell differentiation, alteration of tumor angiogenesis factor profiles, and/or apoptosis.

Those skilled in the art understand that antibodies can be used to specifically target and bind immunogenic molecules such as an immunogenic region of a 151P3D4 sequence shown in Figure 2 or Figure 3. In addition, skilled artisans understand that it is routine to conjugate antibodies to cytotoxic agents (see, e.g., Slevers *et al.* Blood 93:11 3678-3684 (June 1, 1999)). When cytotoxic and/or therapeutic agents are delivered directly to cells, such as by conjugating them to antibodies specific for a molecule expressed by that cell (e.g. 151P3D4), the cytotoxic agent will exert its known biological effect (i.e. cytotoxicity) on those cells.

A wide variety of compositions and methods for using antibody-cytotoxic agent conjugates to kill cells are known in the art. In the context of cancers, typical methods entail administering to an animal having a tumor a biologically effective amount of a conjugate comprising a selected cytotoxic and/or therapeutic agent linked to a targeting agent (e.g. an anti-151P3D4 antibody) that binds to a marker (e.g. 151P3D4) expressed, accessible to binding or localized on the cell surfaces. A typical embodiment is a method of delivering a cytotoxic and/or therapeutic agent to a cell expressing 151P3D4, comprising conjugating the cytotoxic agent to an antibody that immunospecifically binds to a 151P3D4 epitope, and, exposing the cell to the antibody-agent conjugate. Another illustrative embodiment is a method of treating an individual suspected of suffering from metastasized cancer, comprising a step of administering parenterally to said individual a pharmaceutical composition comprising a therapeutically effective amount of an antibody conjugated to a cytotoxic and/or therapeutic agent.

Cancer immunotherapy using anti-151P3D4 antibodies can be done in accordance with various approaches that have been successfully employed in the treatment of other types of cancer, including but not limited to colon cancer (Arlen *et al.*, 1998, Crit. Rev. Immunol. 18:133-138), multiple myeloma (Ozaki *et al.*, 1997, Blood 90:3179-3186, Tsunenari *et al.*, 1997, Blood 90:2437-2444), gastric cancer (Kasprzyk *et al.*, 1992, Cancer Res. 52:2771-2776), B-cell lymphoma (Funakoshi *et al.*, 1996, J. Immunother. Emphasis Tumor Immunol. 19:93-101), leukemia (Zhong *et al.*, 1996, Leuk. Res. 20:581-589), colorectal cancer (Moun *et al.*, 1994, Cancer Res. 54:6160-6166; Velders *et al.*, 1995, Cancer Res. 55:4398-4403), and breast cancer (Shepard *et al.*, 1991, J. Clin. Immunol. 11:117-127). Some therapeutic approaches involve conjugation of naked antibody to a toxin or radioisotope, such as the conjugation of Y^{91} or I^{131} to anti-CD20 antibodies (e.g., Zevalin™, IDEC Pharmaceuticals Corp. or Bexxar™, Coulter Pharmaceuticals), while others involve co-administration of antibodies and other therapeutic agents, such as Herceptin™ (trastuzumab) with paclitaxel (Genentech, Inc.). The antibodies can be conjugated to a therapeutic agent. To treat prostate cancer, for example, 151P3D4 antibodies can be administered in conjunction with radiation, chemotherapy or hormone ablation. Also, antibodies can be conjugated to a toxin such as calicheamicin (e.g., Mylotarg™, Wyeth-Ayerst, Madison, NJ, a recombinant humanized IgG_4 kappa antibody conjugated to antitumor antibiotic calicheamicin) or a maytansinoid (e.g., taxane-based Tumor-Activated Prodrug, TAP, platform, ImmunoGen, Cambridge, MA, also see e.g., US Patent 5,416,064).

Although 151P3D4 antibody therapy is useful for all stages of cancer, antibody therapy can be particularly appropriate in advanced or metastatic cancers. Treatment with the antibody therapy of the invention is indicated for patients who have received one or more rounds of chemotherapy. Alternatively,

antibody therapy of the invention is combined with a chemotherapeutic or radiation regimen for patients who have not received chemotherapeutic treatment. Additionally, antibody therapy can enable the use of reduced dosages of concomitant chemotherapy, particularly for patients who do not tolerate the toxicity of the chemotherapeutic agent very well. Fan et al. (Cancer Res. 53:4637-4642, 1993), Prewett et al. (International J. of Onco. 9:217-224, 1996), and Hancock et al. (Cancer Res. 51:4575-4580, 1991) describe the use of various antibodies together with chemotherapeutic agents.

Although 151P3D4 antibody therapy is useful for all stages of cancer, antibody therapy can be particularly appropriate in advanced or metastatic cancers. Treatment with the antibody therapy of the invention is indicated for patients who have received one or more rounds of chemotherapy. Alternatively, antibody therapy of the invention is combined with a chemotherapeutic or radiation regimen for patients who have not received chemotherapeutic treatment. Additionally, antibody therapy can enable the use of reduced dosages of concomitant chemotherapy, particularly for patients who do not tolerate the toxicity of the chemotherapeutic agent very well.

Cancer patients can be evaluated for the presence and level of 151P3D4 expression, preferably using immunohistochemical assessments of tumor tissue, quantitative 151P3D4 imaging, or other techniques that reliably indicate the presence and degree of 151P3D4 expression. Immunohistochemical analysis of tumor biopsies or surgical specimens is preferred for this purpose. Methods for immunohistochemical analysis of tumor tissues are well known in the art.

Anti-151P3D4 monoclonal antibodies that treat prostate and other cancers include those that initiate a potent immune response against the tumor or those that are directly cytotoxic. In this regard, anti-151P3D4 monoclonal antibodies (mAbs) can elicit tumor cell lysis by either complement-mediated or antibody-dependent cell cytotoxicity (ADCC) mechanisms, both of which require an intact Fc portion of the immunoglobulin molecule for interaction with effector cell Fc receptor sites on complement proteins. In addition, anti-151P3D4 mAbs that exert a direct biological effect on tumor growth are useful to treat cancers that express 151P3D4. Mechanisms by which directly cytotoxic mAbs act include: inhibition of cell growth, modulation of cellular differentiation, modulation of tumor angiogenesis factor profiles, and the induction of apoptosis. The mechanism(s) by which a particular anti-151P3D4 mAb exerts an anti-tumor effect is evaluated using any number of *in vitro* assays that evaluate cell death such as ADCC, ADMMC, complement-mediated cell lysis, and so forth, as is generally known in the art.

In some patients, the use of murine or other non-human monoclonal antibodies, or human/mouse chimeric mAbs can induce moderate to strong immune responses against the non-human antibody. This can result in clearance of the antibody from circulation and reduced efficacy. In the most severe cases, such an immune response can lead to the extensive formation of immune complexes which, potentially, can cause renal failure. Accordingly, preferred monoclonal antibodies used in the therapeutic methods of the invention are those that are either fully human or humanized and that bind specifically to the target 151P3D4 antigen with high affinity but exhibit low or no antigenicity in the patient.

Therapeutic methods of the invention contemplate the administration of single anti-151P3D4 mAbs as well as combinations, or cocktails, of different mAbs. Such mAb cocktails can have certain advantages inasmuch as they contain mAbs that target different epitopes, exploit different effector mechanisms or

combine directly cytotoxic mAbs with mAbs that rely on immune effector functionality. Such mAbs in combination can exhibit synergistic therapeutic effects. In addition, anti-151P3D4 mAbs can be administered concomitantly with other therapeutic modalities, including but not limited to various chemotherapeutic agents, androgen-blockers, immune modulators (e.g., IL-2, GM-CSF), surgery or radiation. The anti-151P3D4 mAbs are administered in their "naked" or unconjugated form, or can have a therapeutic agent(s) conjugated to them.

Anti-151P3D4 antibody formulations are administered via any route capable of delivering the antibodies to a tumor cell. Routes of administration include, but are not limited to, intravenous, intraperitoneal, intramuscular, intratumor, intradermal, and the like. Treatment generally involves repeated administration of the anti-151P3D4 antibody preparation, via an acceptable route of administration such as intravenous injection (IV), typically at a dose in the range of about 0.1, .2, .3, .4, .5, .6, .7, .8, .9., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or 25 mg/kg body weight. In general, doses in the range of 10-1000 mg mAb per week are effective and well tolerated.

Based on clinical experience with the Herceptin™ mAb in the treatment of metastatic breast cancer, an initial loading dose of approximately 4 mg/kg patient body weight IV, followed by weekly doses of about 2 mg/kg IV of the anti-151P3D4 mAb preparation represents an acceptable dosing regimen. Preferably, the initial loading dose is administered as a 90 minute or longer infusion. The periodic maintenance dose is administered as a 30 minute or longer infusion, provided the initial dose was well tolerated. As appreciated by those of skill in the art, various factors can influence the ideal dose regimen in a particular case. Such factors include, for example, the binding affinity and half life of the Ab or mAbs used, the degree of 151P3D4 expression in the patient, the extent of circulating shed 151P3D4 antigen, the desired steady-state antibody concentration level, frequency of treatment, and the influence of chemotherapeutic or other agents used in combination with the treatment method of the invention, as well as the health status of a particular patient.

Optionally, patients should be evaluated for the levels of 151P3D4 in a given sample (e.g. the levels of circulating 151P3D4 antigen and/or 151P3D4 expressing cells) in order to assist in the determination of the most effective dosing regimen, etc. Such evaluations are also used for monitoring purposes throughout therapy, and are useful to gauge therapeutic success in combination with the evaluation of other parameters (for example, urine cytology and/or ImmunoCyt levels in bladder cancer therapy, or by analogy, serum PSA levels in prostate cancer therapy).

Anti-idiotypic anti-151P3D4 antibodies can also be used in anti-cancer therapy as a vaccine for inducing an immune response to cells expressing a 151P3D4-related protein. In particular, the generation of anti-idiotypic antibodies is well known in the art; this methodology can readily be adapted to generate anti-idiotypic anti-151P3D4 antibodies that mimic an epitope on a 151P3D4-related protein (see, for example, Wagner *et al.*, 1997, Hybridoma 16: 33-40; Foon *et al.*, 1995, J. Clin. Invest. 96:334-342; Herlyn *et al.*, 1996, Cancer Immunol. Immunother. 43:65-76). Such an anti-idiotypic antibody can be used in cancer vaccine strategies.

X.C.) 151P3D4 as a Target for Cellular Immune Responses

Vaccines and methods of preparing vaccines that contain an immunogenically effective amount of one or more HLA-binding peptides as described herein are further embodiments of the invention.

Furthermore, vaccines in accordance with the invention encompass compositions of one or more of the claimed peptides. A peptide can be present in a vaccine individually. Alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition can be a naturally occurring region of an antigen or can be prepared, *e.g.*, recombinantly or by chemical synthesis.

Carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (*i.e.*, acceptable) diluent such as water, or saline, preferably phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinlyseryl- serine (P_3CSS). Moreover, an adjuvant such as a synthetic cytosine-phosphorothiolated-guanine-containing (CpG) oligonucleotides has been found to increase CTL responses 10- to 100-fold. (see, e.g. Davila and Celis, J. Immunol. 165:539-547 (2000))

Upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to later development of cells that express or overexpress 151P3D4 antigen, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some embodiments, it may be desirable to combine the class I peptide components with components that induce or facilitate neutralizing antibody and or helper T cell responses directed to the target antigen. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a cross reactive HTL epitope such as PADRE™ (Epimmune, San Diego, CA) molecule (described *e.g.*, in U.S. Patent Number 5,736,142).

A vaccine of the invention can also include antigen-presenting cells (APC), such as dendritic cells (DC), as a vehicle to present peptides of the invention. Vaccine compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*. For example, dendritic cells are transfected, *e.g.*, with a minigene in accordance with the invention, or are pulsed with peptides. The dendritic cell can then be administered to a patient to elicit immune responses *in vivo*. Vaccine compositions, either DNA- or peptide-based, can also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polyepitopic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine

and/or to be encoded by nucleic acids such as a minigene. It is preferred that each of the following principles be balanced in order to make the selection. The multiple epitopes to be incorporated in a given vaccine composition may be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with tumor clearance. For HLA Class I this includes 3-4 epitopes that come from at least one tumor associated antigen (TAA). For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one TAA (*see, e.g.*, Rosenberg *et al.*, *Science* 278:1447-1450). Epitopes from one TAA may be used in combination with epitopes from one or more additional TAAs to produce a vaccine that targets tumors with varying expression patterns of frequently-expressed TAAs.

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, often 200 nM or less; and for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often useful to select analogs because the patient may have developed tolerance to the native epitope.

5.) Of particular relevance are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A nested peptide sequence can comprise B cell, HLA class I and/or HLA class II epitopes. When providing nested epitopes, a general objective is to provide the greatest number of epitopes per sequence. Thus, an aspect is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a multi-epitopic sequence, such as a sequence comprising nested epitopes, it is generally important to screen the sequence in order to insure that it does not have pathological or other deleterious biological properties.

6.) If a polyepitopic protein is created, or when creating a minigene, an objective is to generate the smallest peptide that encompasses the epitopes of interest. This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial polyepitopic peptide, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can, for example, be introduced to avoid junctional epitopes (an epitope recognized by the immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

7.) Where the sequences of multiple variants of the same target protein are present, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

X.C.1. *Minigene Vaccines*

A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention.

The use of multi-epitope minigenes is described below and in, Ishioka *et al., J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al., J. Immunol.* 157:822, 1996; Whitton, J. L. *et al., J. Virol.* 67:348, 1993; Hanke, R. *et al., Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding supermotif- and/or motif-bearing epitopes derived 151P3D4, the PADRE® universal helper T cell epitope or multiple HTL epitopes from 151P3D4 (see e.g., Tables V-XVIII and XXII to LI), and an endoplasmic reticulum-translocating signal sequence can be engineered. A vaccine may also comprise epitopes that are derived from other TAAs.

The immunogenicity of a multi-epitopic minigene can be confirmed in transgenic mice to evaluate the magnitude of CTL induction responses against the epitopes tested. Further, the immunogenicity of DNA-encoded epitopes *in vivo* can be correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. Thus, these experiments can show that the minigene serves to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the encoded epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous polypeptide sequence is created. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in the minigene sequence include: HLA class I epitopes, HLA class II epitopes, antibody epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (*e.g.* TGF-β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well-known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize

the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al., Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (^{51}Cr) labeled and used as target cells for epitope-specific CTL lines; cytolysis, detected by ^{51}Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (i.p.) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytolysis of peptide-loaded, ^{51}Cr-labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is confirmed in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

Minigenes can also be delivered using other bacterial or viral delivery systems well known in the art, *e.g.*, an expression construct encoding epitopes of the invention can be incorporated into a viral vector such as vaccinia.

X.C.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising CTL peptides of the invention can be modified, e.g., analoged, to provide desired attributes, such as improved serum half life, broadened population coverage or enhanced immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response.

Although a CTL peptide can be directly linked to a T helper peptide, often CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues. The CTL peptide epitope can be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO: ___), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO: ___), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; SEQ ID NO: ___). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa (SEQ ID NO: ___), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

HTL peptide epitopes can also be modified to alter their biological properties. For example, they can be modified to include D-amino acids to increase their resistance to proteases and thus extend their serum half life, or they can be conjugated to other molecules such as lipids, proteins, carbohydrates, and the like to increase their biological activity. For example, a T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

X.C.3. Combinations of CTL Peptides with T Cell Priming Agents

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes B lymphocytes or T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo*. For example, palmitic acid residues can be attached to the ε-and α-amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either

directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. In a preferred embodiment, a particularly effective immunogenic composition comprises palmitic acid attached to ε- and α- amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinlyseryl- serine (P_3CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see, e.g.*, Deres, *et al., Nature* 342:561, 1989). Peptides of the invention can be coupled to P_3CSS, for example, and the lipopeptide administered to an individual to specifically prime an immune response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P_3CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

X.C.4. Vaccine Compositions Comprising DC Pulsed with CTL and/or HTL Peptides

An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Pharmacia-Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes complexed with HLA molecules on their surfaces.

The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to 151P3D4. Optionally, a helper T cell (HTL) peptide, such as a natural or artificial loosely restricted HLA Class II peptide, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention is used to treat a cancer which expresses or overexpresses 151P3D4.

X.D. <u>Adoptive Immunotherapy</u>

Antigenic 151P3D4-related peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cell (e.g., a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells.

X.E. <u>Administration of Vaccines for Therapeutic or Prophylactic Purposes</u>

Pharmaceutical and vaccine compositions of the invention are typically used to treat and/or prevent a cancer that expresses or overexpresses 151P3D4. In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective B cell, CTL and/or HTL response to the antigen and to cure or at least partially arrest or slow symptoms and/or complications.

An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

For pharmaceutical compositions, the immunogenic peptides of the invention, or DNA encoding them, are generally administered to an individual already bearing a tumor that expresses 151P3D4. The peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences. Patients can be treated with the immunogenic peptides separately or in conjunction with other treatments, such as surgery, as appropriate.

For therapeutic use, administration should generally begin at the first diagnosis of 151P3D4-associated cancer. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. The embodiment of the vaccine composition (*i.e.*, including, but not limited to embodiments such as peptide cocktails, polyepitopic polypeptides, minigenes, or TAA-specific CTLs or pulsed dendritic cells) delivered to the patient may vary according to the stage of the disease or the patient's health status. For example, in a patient with a tumor that expresses 151P3D4, a vaccine comprising 151P3D4-specific CTL may be more efficacious in killing tumor cells in patient with advanced disease than alternative embodiments.

It is generally important to provide an amount of the peptide epitope delivered by a mode of administration sufficient to effectively stimulate a cytotoxic T cell response; compositions which stimulate helper T cell responses can also be given in accordance with this embodiment of the invention.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg. Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide pursuant to a boosting regimen over weeks to months may be administered depending upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood. Administration should continue until at least clinical symptoms or laboratory tests indicate that the neoplasia, has been eliminated or reduced and for a period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

In certain embodiments, the peptides and compositions of the present invention are employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

The vaccine compositions of the invention can also be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg. Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 μg to about 50,000 μg of peptide administered at

defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine can be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, nasal, intrathecal, or local (*e.g.* as a cream or topical ointment) administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier.

A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well-known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration.

The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

A human unit dose form of a composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, in one embodiment an aqueous carrier, and is administered in a volume/quantity that is known by those of skill in the art to be used for administration of such compositions to humans (*see, e.g.*, Remington's Pharmaceutical Sciences, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985). For example a peptide dose for initial immunization can be from about 1 to about 50,000 μg, generally 100-5,000 μg, for a 70 kg patient. For example, for nucleic acids an initial immunization may be performed using an expression vector in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be recombinant fowlpox virus administered at a dose of $5\text{-}10^7$ to $5\text{x}10^9$ pfu.

For antibodies, a treatment generally involves repeated administration of the anti-151P3D4 antibody preparation, via an acceptable route of administration such as intravenous injection (IV), typically at a dose in the range of about 0.1 to about 10 mg/kg body weight. In general, doses in the range of 10-500 mg mAb per week are effective and well tolerated. Moreover, an initial loading dose of approximately 4 mg/kg patient body weight IV, followed by weekly doses of about 2 mg/kg IV of the anti- 151P3D4 mAb preparation represents an acceptable dosing regimen. As appreciated by those of skill in the art, various factors can influence the ideal dose in a particular case. Such factors include, for example, half life of a composition, the

binding affinity of an Ab, the immunogenicity of a substance, the degree of 151P3D4 expression in the patient, the extent of circulating shed 151P3D4 antigen, the desired steady-state concentration level, frequency of treatment, and the influence of chemotherapeutic or other agents used in combination with the treatment method of the invention, as well as the health status of a particular patient. Non-limiting preferred human unit doses are, for example, 500μg - 1mg, 1mg - 50mg, 50mg - 100mg, 100mg - 200mg, 200mg - 300mg, 400mg - 500mg, 500mg - 600mg, 600mg - 700mg, 700mg - 800mg, 800mg - 900mg, 900mg - 1g, or 1mg - 700mg. In certain embodiments, the dose is in a range of 2-5 mg/kg body weight, e.g., with follow on weekly doses of 1-3 mg/kg; 0.5mg, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10mg/kg body weight followed, e.g., in two, three or four weeks by weekly doses; 0.5 - 10mg/kg body weight, e.g., followed in two, three or four weeks by weekly doses; 225, 250, 275, 300, 325, 350, 375, 400mg m^2 of body area weekly; 1-600mg m^2 of body area weekly; 225-400mg m^2 of body area weekly; these does can be followed by weekly doses for 2, 3, 4, 5, 6, 7, 8, 9, 19, 11, 12 or more weeks.

In one embodiment, human unit dose forms of polynucleotides comprise a suitable dosage range or effective amount that provides any therapeutic effect. As appreciated by one of ordinary skill in the art a therapeutic effect depends on a number of factors, including the sequence of the polynucleotide, molecular weight of the polynucleotide and route of administration. Dosages are generally selected by the physician or other health care professional in accordance with a variety of parameters known in the art, such as severity of symptoms, history of the patient and the like. Generally, for a polynucleotide of about 20 bases, a dosage range may be selected from, for example, an independently selected lower limit such as about 0.1, 0.25, 0.5, 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400 or 500 mg/kg up to an independently selected upper limit, greater than the lower limit, of about 60, 80, 100, 200, 300, 400, 500, 750, 1000, 1500, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000 or 10,000 mg/kg. For example, a dose may be about any of the following: 0.1 to 100 mg/kg, 0.1 to 50 mg/kg, 0.1 to 25 mg/kg, 0.1 to 10 mg/kg, 1 to 500 mg/kg, 100 to 400 mg/kg, 200 to 300 mg/kg, 1 to 100 mg/kg, 100 to 200 mg/kg, 300 to 400 mg/kg, 400 to 500 mg/kg, 500 to 1000 mg/kg, 500 to 5000 mg/kg, or 500 to 10,000 mg/kg. Generally, parenteral routes of administration may require higher doses of polynucleotide compared to more direct application to the nucleotide to diseased tissue, as do polynucleotides of increasing length.

In one embodiment, human unit dose forms of T-cells comprise a suitable dosage range or effective amount that provides any therapeutic effect. As appreciated by one of ordinary skill in the art, a therapeutic effect depends on a number of factors. Dosages are generally selected by the physician or other health care professional in accordance with a variety of parameters known in the art, such as severity of symptoms, history of the patient and the like. A dose may be about 10^4 cells to about 10^6 cells, about 10^6 cells to about 10^8 cells, about 10^8 to about 10^{11} cells, or about 10^8 to about 5×10^{10} cells. A dose may also about 10^6 cells/m^2 to about 10^{10} cells/m^2, or about 10^6 cells/m^2 to about 10^8 cells/m^2 .

Proteins(s) of the invention, and/or nucleic acids encoding the protein(s), can also be administered via liposomes, which may also serve to: 1) target the proteins(s) to a particular tissue, such as lymphoid tissue; 2) to target selectively to diseases cells; or, 3) to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as

part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are about 0.01%-20% by weight, preferably about 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from about 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute about 0.1%-20% by weight of the composition, preferably about 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

XI.) Diagnostic and Prognostic Embodiments of 151P3D4.

As disclosed herein, 151P3D4 polynucleotides, polypeptides, reactive cytotoxic T cells (CTL), reactive helper T cells (HTL) and anti-polypeptide antibodies are used in well known diagnostic, prognostic and therapeutic assays that examine conditions associated with dysregulated cell growth such as cancer, in particular the cancers listed in Table I (see, e.g., both its specific pattern of tissue expression as well as its overexpression in certain cancers as described for example in the Example entitled "Expression analysis of 151P3D4 in normal tissues, and patient specimens").

151P3D4 can be analogized to a prostate associated antigen PSA, the archetypal marker that has been used by medical practitioners for years to identify and monitor the presence of prostate cancer (see, e.g., Merrill *et al.*, J. Urol. 163(2): 503-5120 (2000); Polascik *et al.*, J. Urol. Aug; 162(2):293-306 (1999) and Fortier *et al.*, J. Nat. Cancer Inst. 91(19): 1635-1640(1999)). A variety of other diagnostic markers are also used in similar contexts including p53 and K-ras (see, e.g., Tulchinsky *et al.*, Int J Mol Med 1999 Jul 4(1):99-102 and Minimoto *et al.*, Cancer Detect Prev 2000;24(1):1-12). Therefore, this disclosure of 151P3D4 polynucleotides and polypeptides (as well as 151P3D4 polynucleotide probes and anti-151P3D4 antibodies used to identify the presence of these molecules) and their properties allows skilled artisans to utilize these molecules in methods that are analogous to those used, for example, in a variety of diagnostic assays directed to examining conditions associated with cancer.

Typical embodiments of diagnostic methods which utilize the 151P3D4 polynucleotides, polypeptides, reactive T cells and antibodies are analogous to those methods from well-established diagnostic assays which employ, e.g., PSA polynucleotides, polypeptides, reactive T cells and antibodies. For example, just as PSA polynucleotides are used as probes (for example in Northern analysis, see, e.g., Sharief *et al.*, Biochem. Mol. Biol. Int. 33(3):567-74(1994)) and primers (for example in PCR analysis, see, e.g., Okegawa *et al.*, J. Urol. 163(4): 1189-1190 (2000)) to observe the presence and/or the level of PSA mRNAs in methods of monitoring PSA overexpression or the metastasis of prostate cancers, the 151P3D4 polynucleotides described herein can be utilized in the same way to detect 151P3D4 overexpression or the metastasis of prostate and other cancers expressing this gene. Alternatively, just as PSA polypeptides are used to generate antibodies specific for PSA which can then be used to observe the presence and/or the level of PSA proteins in methods to monitor PSA protein overexpression (see, e.g., Stephan *et al.*, Urology 55(4):560-3 (2000)) or the metastasis of prostate cells (see, e.g., Alanen *et al.*, Pathol. Res. Pract. 192(3):233-7 (1996)), the 151P3D4 polypeptides described herein can be utilized to generate antibodies for use in detecting 151P3D4 overexpression or the metastasis of prostate cells and cells of other cancers expressing this gene.

Specifically, because metastases involves the movement of cancer cells from an organ of origin (such as the lung or prostate gland etc.) to a different area of the body (such as a lymph node), assays which examine a biological sample for the presence of cells expressing 151P3D4 polynucleotides and/or polypeptides can be used to provide evidence of metastasis. For example, when a biological sample from tissue that does not normally contain 151P3D4-expressing cells (lymph node) is found to contain 151P3D4-expressing cells such as the 151P3D4 expression seen in LAPC4 and LAPC9, xenografts isolated from lymph node and bone metastasis, respectively, this finding is indicative of metastasis.

Alternatively 151P3D4 polynucleotides and/or polypeptides can be used to provide evidence of cancer, for example, when cells in a biological sample that do not normally express 151P3D4 or express 151P3D4 at a different level are found to express 151P3D4 or have an increased expression of 151P3D4 (see, e.g., the 151P3D4 expression in the cancers listed in Table I and in patient samples etc. shown in the accompanying Figures). In such assays, artisans may further wish to generate supplementary evidence of metastasis by testing the biological sample for the presence of a second tissue restricted marker (in addition to 151P3D4) such as PSA, PSCA etc. (see, e.g., Alanen *et al.*, Pathol. Res. Pract. 192(3): 233-237 (1996)).

Just as PSA polynucleotide fragments and polynucleotide variants are employed by skilled artisans for use in methods of monitoring PSA, 151P3D4 polynucleotide fragments and polynucleotide variants are used in an analogous manner. In particular, typical PSA polynucleotides used in methods of monitoring PSA are probes or primers which consist of fragments of the PSA cDNA sequence. Illustrating this, primers used to PCR amplify a PSA polynucleotide must include less than the whole PSA sequence to function in the polymerase chain reaction. In the context of such PCR reactions, skilled artisans generally create a variety of different polynucleotide fragments that can be used as primers in order to amplify different portions of a polynucleotide of interest or to optimize amplification reactions (see, e.g., Caetano-Anolles, G. Biotechniques 25(3): 472-476, 478-480 (1998); Robertson *et al.*, Methods Mol. Biol. 98:121-154 (1998)). An additional illustration of the use of such fragments is provided in the Example entitled "Expression analysis of 151P3D4 in normal tissues, and patient specimens," where a 151P3D4 polynucleotide fragment is used as a probe to show the expression of 151P3D4 RNAs in cancer cells. In addition, variant polynucleotide sequences are typically used as primers and probes for the corresponding mRNAs in PCR and Northern analyses (see, e.g., Sawai *et al.*, Fetal Diagn. Ther. 1996 Nov-Dec 11(6):407-13 and Current Protocols In Molecular Biology, Volume 2, Unit 2, Frederick M. Ausubel *et al.* eds., 1995)). Polynucleotide fragments and variants are useful in this context where they are capable of binding to a target polynucleotide sequence (e.g., a 151P3D4 polynucleotide shown in Figure 2 or variant thereof) under conditions of high stringency.

Furthermore, PSA polypeptides which contain an epitope that can be recognized by an antibody or T cell that specifically binds to that epitope are used in methods of monitoring PSA. 151P3D4 polypeptide fragments and polypeptide analogs or variants can also be used in an analogous manner. This practice of using polypeptide fragments or polypeptide variants to generate antibodies (such as anti-PSA antibodies or T cells) is typical in the art with a wide variety of systems such as fusion proteins being used by practitioners (see, e.g., Current Protocols In Molecular Biology, Volume 2, Unit 16, Frederick M. Ausubel *et al.* eds., 1995). In this context, each epitope(s) functions to provide the architecture with which an antibody or T cell is reactive. Typically, skilled artisans create a variety of different polypeptide fragments that can be used in order to generate immune responses specific for different portions of a polypeptide of interest (see, e.g., U.S. Patent No. 5,840,501 and U.S. Patent No. 5,939,533). For example it may be preferable to utilize a polypeptide comprising one of the 151P3D4 biological motifs discussed herein or a motif-bearing subsequence which is readily identified by one of skill in the art based on motifs available in the art. Polypeptide fragments, variants or analogs are typically useful in this context as long as they comprise an epitope capable of generating an antibody or T cell specific for a target polypeptide sequence (e.g. a 151P3D4 polypeptide shown in Figure 3).

As shown herein, the 151P3D4 polynucleotides and polypeptides (as well as the 151P3D4 polynucleotide probes and anti-151P3D4 antibodies or T cells used to identify the presence of these molecules) exhibit specific properties that make them useful in diagnosing cancers such as those listed in Table I. Diagnostic assays that measure the presence of 151P3D4 gene products, in order to evaluate the presence or onset of a disease condition described herein, such as prostate cancer, are used to identify patients for preventive measures or further monitoring, as has been done so successfully with PSA. Moreover, these materials satisfy a need in the art for molecules having similar or complementary characteristics to PSA in

situations where, for example, a definite diagnosis of metastasis of prostatic origin cannot be made on the basis of a test for PSA alone (see, e.g., Alanen *et al.*, Pathol. Res. Pract. 192(3): 233-237 (1996)), and consequently, materials such as 151P3D4 polynucleotides and polypeptides (as well as the 151P3D4 polynucleotide probes and anti-151P3D4 antibodies used to identify the presence of these molecules) need to be employed to confirm a metastases of prostatic origin.

Finally, in addition to their use in diagnostic assays, the 151P3D4 polynucleotides disclosed herein have a number of other utilities such as their use in the identification of oncogenetic associated chromosomal abnormalities in the chromosomal region to which the 151P3D4 gene maps (see the Example entitled "Chromosomal Mapping of 151P3D4" below). Moreover, in addition to their use in diagnostic assays, the 151P3D4-related proteins and polynucleotides disclosed herein have other utilities such as their use in the forensic analysis of tissues of unknown origin (see, e.g., Takahama K Forensic Sci Int 1996 Jun 28;80(1-2): 63-9).

Additionally, 151P3D4-related proteins or polynucleotides of the invention can be used to treat a pathologic condition characterized by the over-expression of 151P3D4. For example, the amino acid or nucleic acid sequence of Figure 2 or Figure 3, or fragments of either, can be used to generate an immune response to a 151P3D4 antigen. Antibodies or other molecules that react with 151P3D4 can be used to modulate the function of this molecule, and thereby provide a therapeutic benefit.

XII.) Inhibition of 151P3D4 Protein Function

The invention includes various methods and compositions for inhibiting the binding of 151P3D4 to its binding partner or its association with other protein(s) as well as methods for inhibiting 151P3D4 function.

XII.A.) Inhibition of 151P3D4 With Intracellular Antibodies

In one approach, a recombinant vector that encodes single chain antibodies that specifically bind to 151P3D4 are introduced into 151P3D4 expressing cells via gene transfer technologies. Accordingly, the encoded single chain anti-151P3D4 antibody is expressed intracellularly, binds to 151P3D4 protein, and thereby inhibits its function. Methods for engineering such intracellular single chain antibodies are well known. Such intracellular antibodies, also known as "intrabodies", are specifically targeted to a particular compartment within the cell, providing control over where the inhibitory activity of the treatment is focused. This technology has been successfully applied in the art (for review, see Richardson and Marasco, 1995, TIBTECH vol. 13). Intrabodies have been shown to virtually eliminate the expression of otherwise abundant cell surface receptors (see, e.g., Richardson *et al.*, 1995, Proc. Natl. Acad. Sci. USA 92: 3137-3141; Beerli *et al.*, 1994, J. Biol. Chem. 289: 23931-23936; Deshane *et al.*, 1994, Gene Ther. 1: 332-337).

Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL amino acid motif. Intrabodies

intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.

In one embodiment, intrabodies are used to capture 151P3D4 in the nucleus, thereby preventing its activity within the nucleus. Nuclear targeting signals are engineered into such 151P3D4 intrabodies in order to achieve the desired targeting. Such 151P3D4 intrabodies are designed to bind specifically to a particular 151P3D4 domain. In another embodiment, cytosolic intrabodies that specifically bind to a 151P3D4 protein are used to prevent 151P3D4 from gaining access to the nucleus, thereby preventing it from exerting any biological activity within the nucleus (e.g., preventing 151P3D4 from forming transcription complexes with other factors).

In order to specifically direct the expression of such intrabodies to particular cells, the transcription of the intrabody is placed under the regulatory control of an appropriate tumor-specific promoter and/or enhancer. In order to target intrabody expression specifically to prostate, for example, the PSA promoter and/or promoter/enhancer can be utilized (See, for example, U.S. Patent No. 5,919,652 issued 6 July 1999).

XII.B.) Inhibition of 151P3D4 with Recombinant Proteins

In another approach, recombinant molecules bind to 151P3D4 and thereby inhibit 151P3D4 function. For example, these recombinant molecules prevent or inhibit 151P3D4 from accessing/binding to its binding partner(s) or associating with other protein(s). Such recombinant molecules can, for example, contain the reactive part(s) of a 151P3D4 specific antibody molecule. In a particular embodiment, the 151P3D4 binding domain of a 151P3D4 binding partner is engineered into a dimeric fusion protein, whereby the fusion protein comprises two 151P3D4 ligand binding domains linked to the Fc portion of a human IgG, such as human IgG1. Such IgG portion can contain, for example, the C_H2 and C_H3 domains and the hinge region, but not the C_H1 domain. Such dimeric fusion proteins are administered in soluble form to patients suffering from a cancer associated with the expression of 151P3D4, whereby the dimeric fusion protein specifically binds to 151P3D4 and blocks 151P3D4 interaction with a binding partner. Such dimeric fusion proteins are further combined into multimeric proteins using known antibody linking technologies.

XII.C.) Inhibition of 151P3D4 Transcription or Translation

The present invention also comprises various methods and compositions for inhibiting the transcription of the 151P3D4 gene. Similarly, the invention also provides methods and compositions for inhibiting the translation of 151P3D4 mRNA into protein.

In one approach, a method of inhibiting the transcription of the 151P3D4 gene comprises contacting the 151P3D4 gene with a 151P3D4 antisense polynucleotide. In another approach, a method of inhibiting 151P3D4 mRNA translation comprises contacting a 151P3D4 mRNA with an antisense polynucleotide. In another approach, a 151P3D4 specific ribozyme is used to cleave a 151P3D4 message, thereby inhibiting translation. Such antisense and ribozyme based methods can also be directed to the regulatory regions of the 151P3D4 gene, such as 151P3D4 promoter and/or enhancer elements. Similarly, proteins capable of inhibiting a 151P3D4 gene transcription factor are used to inhibit 151P3D4 mRNA transcription. The various

polynucleotides and compositions useful in the aforementioned methods have been described above. The use of antisense and ribozyme molecules to inhibit transcription and translation is well known in the art.

Other factors that inhibit the transcription of 151P3D4 by interfering with 151P3D4 transcriptional activation are also useful to treat cancers expressing 151P3D4. Similarly, factors that interfere with 151P3D4 processing are useful to treat cancers that express 151P3D4. Cancer treatment methods utilizing such factors are also within the scope of the invention.

XII.D.) General Considerations for Therapeutic Strategies

Gene transfer and gene therapy technologies can be used to deliver therapeutic polynucleotide molecules to tumor cells synthesizing 151P3D4 (i.e., antisense, ribozyme, polynucleotides encoding intrabodies and other 151P3D4 inhibitory molecules). A number of gene therapy approaches are known in the art. Recombinant vectors encoding 151P3D4 antisense polynucleotides, ribozymes, factors capable of interfering with 151P3D4 transcription, and so forth, can be delivered to target tumor cells using such gene therapy approaches.

The above therapeutic approaches can be combined with any one of a wide variety of surgical, chemotherapy or radiation therapy regimens. The therapeutic approaches of the invention can enable the use of reduced dosages of chemotherapy (or other therapies) and/or less frequent administration, an advantage for all patients and particularly for those that do not tolerate the toxicity of the chemotherapeutic agent well.

The anti-tumor activity of a particular composition (e.g., antisense, ribozyme, intrabody), or a combination of such compositions, can be evaluated using various *in vitro* and *in vivo* assay systems. *In vitro* assays that evaluate therapeutic activity include cell growth assays, soft agar assays and other assays indicative of tumor promoting activity, binding assays capable of determining the extent to which a therapeutic composition will inhibit the binding of 151P3D4 to a binding partner, etc.

In vivo, the effect of a 151P3D4 therapeutic composition can be evaluated in a suitable animal model. For example, xenogenic prostate cancer models can be used, wherein human prostate cancer explants or passaged xenograft tissues are introduced into immune compromised animals, such as nude or SCID mice (Klein *et al.*, 1997, Nature Medicine 3: 402-408). For example, PCT Patent Application WO98/16628 and U.S. Patent 6,107,540 describe various xenograft models of human prostate cancer capable of recapitulating the development of primary tumors, micrometastasis, and the formation of osteoblastic metastases characteristic of late stage disease. Efficacy can be predicted using assays that measure inhibition of tumor formation, tumor regression or metastasis, and the like.

In vivo assays that evaluate the promotion of apoptosis are useful in evaluating therapeutic compositions. In one embodiment, xenografts from tumor bearing mice treated with the therapeutic composition can be examined for the presence of apoptotic foci and compared to untreated control xenograft-bearing mice. The extent to which apoptotic foci are found in the tumors of the treated mice provides an indication of the therapeutic efficacy of the composition.

The therapeutic compositions used in the practice of the foregoing methods can be formulated into pharmaceutical compositions comprising a carrier suitable for the desired delivery method. Suitable carriers include any material that when combined with the therapeutic composition retains the anti-tumor function of the therapeutic composition and is generally non-reactive with the patient's immune system. Examples include, but are not limited to, any of a number of standard pharmaceutical carriers such as sterile phosphate

buffered saline solutions, bacteriostatic water, and the like (see, generally, Remington's Pharmaceutical Sciences 16th Edition, A. Osal., Ed., 1980).

Therapeutic formulations can be solubilized and administered via any route capable of delivering the therapeutic composition to the tumor site. Potentially effective routes of administration include, but are not limited to, intravenous, parenteral, intraperitoneal, intramuscular, intratumor, intradermal, intraorgan, orthotopic, and the like. A preferred formulation for intravenous injection comprises the therapeutic composition in a solution of preserved bacteriostatic water, sterile unpreserved water, and/or diluted in polyvinylchloride or polyethylene bags containing 0.9% sterile Sodium Chloride for Injection, USP. Therapeutic protein preparations can be lyophilized and stored as sterile powders, preferably under vacuum, and then reconstituted in bacteriostatic water (containing for example, benzyl alcohol preservative) or in sterile water prior to injection.

Dosages and administration protocols for the treatment of cancers using the foregoing methods will vary with the method and the target cancer, and will generally depend on a number of other factors appreciated in the art.

XIII.) Kits

For use in the diagnostic and therapeutic applications described herein, kits are also within the scope of the invention. Such kits can comprise a carrier, package or container that is compartmentalized to receive one or more containers such as vials, tubes, and the like, each of the container(s) comprising one of the separate elements to be used in the method. For example, the container(s) can comprise a probe that is or can be detectably labeled. Such probe can be an antibody or polynucleotide specific for a 151P3D4-related protein or a 151P3D4 gene or message, respectively. Where the method utilizes nucleic acid hybridization to detect the target nucleic acid, the kit can also have containers containing nucleotide(s) for amplification of the target nucleic acid sequence and/or a container comprising a reporter-means, such as a biotin-binding protein, such as avidin or streptavidin, bound to a reporter molecule, such as an enzymatic, florescent, or radioisotope label. The kit can include all or part of the amino acid sequence of Figure 2 or Figure 3 or analogs thereof, or a nucleic acid molecules that encodes such amino acid sequences.

The kit of the invention will typically comprise the container described above and one or more other containers comprising materials desirable from a commercial and user standpoint, including buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

A label can be present on the container to indicate that the composition is used for a specific therapy or non-therapeutic application, and can also indicate directions for either *in vivo* or *in vitro* use, such as those described above. Directions and or other information can also be included on an insert which is included with the kit.

EXAMPLES:

Various aspects of the invention are further described and illustrated by way of the several examples that follow, none of which are intended to limit the scope of the invention.

Example 1: SSH-Generated Isolation of a cDNA Fragment of the 151P3D4 Gene

To isolate genes that are over-expressed in bladder cancer we used the Suppression Subtractive Hybridization (SSH) procedure using cDNA derived from the LNCaP prostate cancer cell line.

The 151P3D4 SSH cDNA sequence was derived from a subtraction consisting of two different populations of LNCaP cells. The 151P3D4 SSH cDNA sequence of 417 bp is listed in Figure 1.

The full-length 151P3D4 v.1 clone 1-placenta was cloned from normal placenta cDNA, revealing an ORF of 354 amino acids (Figure 2 and Figure 3). Other variants of 151P3D4 were also identified and these are listed in Figures 2 and 3.

Materials and Methods

Human Tissues:

The patient cancer and normal tissues were purchased from different sources such as the NDRI (Philadelphia, PA). mRNA for some normal tissues were purchased from Clontech, Palo Alto, CA.

RNA Isolation:

Tissues were homogenized in Trizol reagent (Life Technologies, Gibco BRL) using 10 ml/ g tissue isolate total RNA. Poly A RNA was purified from total RNA using Qiagen's Oligotex mRNA Mini and Midi kits. Total and mRNA were quantified by spectrophotometric analysis (O.D. 260/280 nm) and analyzed by gel electrophoresis.

Oligonucleotides:

The following HPLC purified oligonucleotides were used.

DPNCDN (cDNA synthesis primer):

5'TTTTGATCAAGCTT$_{30}$3' (SEQ ID NO: ___)

Adaptor 1:

5'CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAG3' (SEQ ID NO: ___)

3'GGCCCGTCCTAG5' (SEQ ID NO: ___)

Adaptor 2:

5'GTAATACGACTCACTATAGGGCAGCGTGGTCGCGGCCGAG3' (SEQ ID NO:___)

3'CGGCTCCTAG5' (SEQ ID NO: ___)

PCR primer 1:

5'CTAATACGACTCACTATAGGGC3' (SEQ ID NO: ___)

Nested primer (NP)1:

5'TCGAGCGGCCGCCCGGGCAGGA3' (SEQ ID NO: ___)

Nested primer (NP)2:

5'AGCGTGGTCGCGGCCGAGGA3' (SEQ ID NO: ___)

Suppression Subtractive Hybridization:

Suppression Subtractive Hybridization (SSH) was used to identify cDNAs corresponding to genes that may be differentially expressed in prostate cancer. The SSH reaction utilized cDNA from two different clones of LNCaP cells.

The gene 151P3D4 was derived from one population of LNCaP cells minus another population of LNCaP cells cDNA subtraction. The 151P3D4 SSH DNA sequence (Figure 1) was identified.

The cDNA derived from one population of LNCaP cells was used as the source of the "driver" cDNA, while the cDNA from another population of LNCaP cells was used as the source of the "tester" cDNA. Double stranded cDNAs corresponding to tester and driver cDNAs were synthesized from 2 µg of poly(A)$^+$ RNA isolated from the relevant tissue, as described above, using CLONTECH's PCR-Select cDNA Subtraction Kit and 1 ng of oligonucleotide DPNCDN as primer. First- and second-strand synthesis were carried out as described in the Kit's user manual protocol (CLONTECH Protocol No. PT1117-1, Catalog No. K1804-1). The resulting cDNA was digested with Dpn II for 3 hrs at 37°C. Digested cDNA was extracted with phenol/chloroform (1:1) and ethanol precipitated.

Driver cDNA was generated by combining in a 1:1 ratio Dpn II digested cDNA from the relevant source (see above). Tester cDNA was generated by diluting 1 µl of Dpn II digested cDNA from the relevant source (see above) (400 ng) in 5 µl of water. The diluted cDNA (2 µl, 160 ng) was then ligated to 2 µl of Adaptor 1 and Adaptor 2 (10 µM), in separate ligation reactions, in a total volume of 10 µl at 16°C overnight, using 400 u of T4 DNA ligase (CLONTECH). Ligation was terminated with 1 µl of 0.2 M EDTA and heating at 72°C for 5 min.

The first hybridization was performed by adding 1.5 µl (600 ng) of driver cDNA to each of two tubes containing 1.5 µl (20 ng) Adaptor 1- and Adaptor 2- ligated tester cDNA. In a final volume of 4 µl, the samples were overlaid with mineral oil, denatured in an MJ Research thermal cycler at 98°C for 1.5 minutes, and then were allowed to hybridize for 8 hrs at 68°C. The two hybridizations were then mixed together with an additional 1 µl of fresh denatured driver cDNA and were allowed to hybridize overnight at 68°C. The second hybridization was then diluted in 200 µl of 20 mM Hepes, pH 8.3, 50 mM NaCl, 0.2 mM EDTA, heated at 70°C for 7 min. and stored at -20°C.

PCR Amplification, Cloning and Sequencing of Gene Fragments Generated from SSH:

To amplify gene fragments resulting from SSH reactions, two PCR amplifications were performed. In the primary PCR reaction 1 µl of the diluted final hybridization mix was added to 1 µl of PCR primer 1 (10 µM), 0.5 µl dNTP mix (10 µM), 2.5 µl 10 x reaction buffer (CLONTECH) and 0.5 µl 50 x Advantage cDNA polymerase Mix (CLONTECH) in a final volume of 25 µl. PCR 1 was conducted using the following conditions: 75°C for 5 min., 94°C for 25 sec., then 27 cycles of 94°C for 10 sec, 66°C for 30 sec, 72°C for 1.5 min. Five separate primary PCR

reactions were performed for each experiment. The products were pooled and diluted 1:10 with water. For the secondary PCR reaction, 1 μl from the pooled and diluted primary PCR reaction was added to the same reaction mix as used for PCR 1, except that primers NP1 and NP2 (10 μM) were used instead of PCR primer 1. PCR 2 was performed using 10-12 cycles of 94°C for 10 sec, 68°C for 30 sec, and 72°C for 1.5 minutes. The PCR products were analyzed using 2% agarose gel electrophoresis.

The PCR products were inserted into pCR2.1 using the T/A vector cloning kit (Invitrogen). Transformed *E. coli* were subjected to blue/white and ampicillin selection. White colonies were picked and arrayed into 96 well plates and were grown in liquid culture overnight. To identify inserts, PCR amplification was performed on 1 ml of bacterial culture using the conditions of PCR1 and NP1 and NP2 as primers. PCR products were analyzed using 2% agarose gel electrophoresis.

Bacterial clones were stored in 20% glycerol in a 96 well format. Plasmid DNA was prepared, sequenced, and subjected to nucleic acid homology searches of the GenBank, dBest, and NCI-CGAP databases.

RT-PCR Expression Analysis:

First strand cDNAs can be generated from 1 μg of mRNA with oligo (dT)12-18 priming using the Gibco-BRL Superscript Preamplification system. The manufacturer's protocol was used which included an incubation for 50 min at 42°C with reverse transcriptase followed by RNAse H treatment at 37°C for 20 min. After completing the reaction, the volume can be increased to 200 μl with water prior to normalization. First strand cDNAs from 16 different normal human tissues can be obtained from Clontech.

Normalization of the first strand cDNAs from multiple tissues was performed by using the primers 5'atatcgccgcgctcgtcgtcgacaa3' (SEQ ID NO: ___) and 5'agccacacgcagctcattgtagaagg 3' (SEQ ID NO: ___) to amplify β-actin. First strand cDNA (5 μl) were amplified in a total volume of 50 μl containing 0.4 μM primers, 0.2 μM each dNTPs, 1XPCR buffer (Clontech, 10 mM Tris-HCL, 1.5 mM $MgCl_2$, 50 mM KCl, pH8.3) and 1X Klentaq DNA polymerase (Clontech). Five μl of the PCR reaction can be removed at 18, 20, and 22 cycles and used for agarose gel electrophoresis. PCR was performed using an MJ Research thermal cycler under the following conditions: initial denaturation can be at 94°C for 15 sec, followed by a 18, 20, and 22 cycles of 94°C for 15, 65°C for 2 min, 72°C for 5 sec. A final extension at 72°C was carried out for 2 min. After agarose gel electrophoresis, the band intensities of the 283 b.p. β-actin bands from multiple tissues were compared by visual inspection. Dilution factors for the first strand cDNAs were calculated to result in equal β-actin band intensities in all tissues after 22 cycles of PCR. Three rounds of normalization can be required to achieve equal band intensities in all tissues after 22 cycles of PCR.

To determine expression levels of the 151P3D4 gene, 5 μl of normalized first strand cDNA were analyzed by PCR using 26, and 30 cycles of amplification. Semi-quantitative expression analysis can be achieved by comparing the PCR products at cycle numbers that give light band intensities. The primers used for RT-PCR were designed using the 151P3D4 SSH sequence and are listed below:

151P3D4.1

5'- CCCACCAAACTGACCTATGATGAA - 3' (SEQ ID NO:)

151P3D4.2

5'- TGTATGCTCTGAAGCAGTAGACACC - 3' (SEQ ID NO:)

A typical RT-PCR expression study is shown in Figure 14. First strand cDNA was prepared from vital pool 1 (liver, lung and kidney), vital pool 2 (pancreas, colon and stomach), bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, ovary cancer pool, breast cancer pool, and cancer metastasis pool. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 151P3D4, was performed at 26 and 30 cycles of amplification. Results show strong expression of 151P3D4 in ovary cancer pool. Expression of 151P3D4 was also detected in bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, breast cancer pool, cancer metastasis pool, vital pool 2, but not in vital pool 1.

Example 2: Full Length Cloning of 151P3D4

To isolate genes that are expressed in prostate cancer, we used the Suppression Subtractive Hybridization (SSH) procedure using cDNA derived from two different populations of LNCaP cells.

The 151P3D4 SSH cDNA sequence was derived from a subtraction consisting of one population of LNCaP cells minus another population of LNCaP cells. The 151P3D4 SSH cDNA sequence of 417 bp is listed in Figure 1.

The full-length 151P3D4 v.1 (151P3D4 clone 1-placenta) was cloned from normal placenta cDNA, revealing an ORF of 354 amino acids (Figure 2 and Figure 3). 151P3D4 v.1 showed 99% identity over 1492 nucleotides with the human mRNA for cartilage link protein (gi463246) (Figure 4A). 151P3D4 v.1 protein showed 100% identity over 354 amino acids with the human cartilage link protein (Figure 4B). Also, 151P3D4 v.1 was 96% identical over 355 amino acids with the mouse link protein (gi4218976) (Figure 4C).

Other variants of 151P3D4 were also identified and these are listed in Figures 2 and 3. 151P3D4 v.2 codes for a novel protein that contains sequences not present in 151P3D4 v.1. These are from amino acids 1 to 400. Amino acids 401 to 721 of 151P3D4 v.2 align with 151P3D4 v.1 at positions 34 to 354 (Figure 4D). A small portion of 151P3D4 v.2 demonstrates homology to the hypothetical protein XP_094318 (Figure 4E). The two proteins show 99% identity over 168 amino acids. The other variants 151P3D4 v.3 through v.11 each differ from 151P3D4 v.1 by one nucleotide (Figure 10).

Example 3: Chromosomal Mapping of 151P3D4

Chromosomal localization can implicate genes in disease pathogenesis. Several chromosome mapping approaches are available including fluorescent *in situ* hybridization (FISH), human/hamster radiation hybrid (RH) panels (Walter et al., 1994; Nature Genetics 7:22; Research Genetics, Huntsville Al), human-rodent somatic cell hybrid panels such as is available from the Coriell Institute (Camden, New Jersey), and genomic viewers utilizing BLAST homologies to sequenced and mapped genomic clones (NCBI, Bethesda, Maryland).

151P3D4 maps to chromosome 5q13-q14.1 using 151P3D4 sequence and the NCBI BLAST tool: (http://www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs).

Example 4: Expression Analysis of 151P3D4 in Normal Tissues and Patient Specimens

Expression analysis by RT-PCR demonstrated that 151P3D4 is strongly expressed in cancer patient specimens (Figure 14). First strand cDNA was prepared from vital pool 1 (liver, lung and kidney), vital pool 2 (pancreas, colon and stomach), bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, ovary cancer pool, breast cancer pool, and cancer metastasis pool. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 151P3D4, was performed at 26 and 30 cycles of amplification. Results show strong expression of 151P3D4 in ovary cancer pool. Expression of 151P3D4 was also detected in bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, breast cancer pool, cancer metastasis pool, vital pool 2, but not in vital pool 1.

Extensive northern blot analysis of 151P3D4 in multiple human normal tissues is shown in Figure 15. Two multiple tissue northern blots (Clontech) both with 2 ug of mRNA/lane were probed with the 151P3D4 SSH sequence. Size standards in kilobases (kb) are indicated on the side. Results show expression of 151P3D4 in small intestine and placenta. Lower level expression was also detected in heart and colon, but not in the other normal tissues tested.

Expression of 151P3D4 in patient bladder cancer specimens is shown in Figure 16. RNA was extracted from normal bladder (NB), bladder cancer cell lines (CL; UM-UC-3, J82, SCaBER), bladder cancer patient tumors (T) and normal adjacent tissue (NAT). Northern blots with 10 ug of total RNA were probed with the 151P3D4 SSH sequence. Size standards in kilobases are indicated on the side. Results show expression of 151P3D4 in patient bladder cancer tissues, and in UM-UC-3 bladder cancer cell lines, but not in normal bladder nor in the other bladder cancer cell lines tested.

Figure 17 shows that 151P3D4 was expressed in kidney cancer patient specimens. RNA was extracted from kidney cancer cell lines (CL: 769-P, A498, SW839), normal kidney (NK), kidney cancer patient tumors (T) and their normal adjacent tissues (NAT). Northern blots with 10 ug of total RNA were probed with the 151P3D4 SSH sequence. Size standards in kilobases are on the side. Results show expression of 151P3D4 in patient kidney tumor tissues, but not in normal kidney, nor in the cell lines tested.

Expression of 151P3D4 was also detected in ovary cancer patient specimen (Figure 18). RNA was extracted from ovary and cervical cancer cell lines (CL), normal ovary (N), and ovary cancer patient tumor (T). Northern blots with 10 ug of total RNA were probed with the 151P3D4 SSH sequence. Size standards in kilobases are on the side. Results show strong expression of 151P3D4 in patient ovary cancer tissues, but not in normal ovary nor in the ovary and cervical cancer cell lines.

Figure 19 shows that 151P3D4 was also expressed in stomach cancers and in uterus cancers. Expression of 151P3D4 was assayed in a panel of human stomach and uterus cancers (T) and their respective matched normal tissues (N) on RNA dot blots. 151P3D4 expression was seen in both stomach and uterus cancers.

The restricted expression of 151P3D4 in normal tissues and the expression detected in human cancers suggest that 151P3D4 is a potential therapeutic target and a diagnostic marker for human cancers.

Example 5: Transcript Variants of 151P3D4

Transcript variants are variants of matured mRNA from the same gene by alternative transcription or alternative splicing. Alternative transcripts are transcripts from the same gene but start transcription at different points. Splice variants are mRNA variants spliced differently from the same transcript. In eukaryotes, when a multi-exon gene is transcribed from genomic DNA, the initial RNA is spliced to produce functional mRNA, which has only exons and is used for translation into an amino acid sequence. Accordingly, a given gene can have zero to many alternative transcripts and each transcript can have zero to many splice variants. Each transcript variant has a unique exon makeup, and can have different coding and/or non-coding (5' or 3' end) portions, from the original transcript. Transcript variants can code for similar or different proteins with the same or a similar function or may encode proteins with different functions, and may be expressed in the same tissue at the same time, or at different tissue, or at different times, proteins encoded by transcript variants can have similar or different cellular or extracellular localizations, i.e., be secreted.

Transcript variants are identified by a variety of art-accepted methods. For example, alternative transcripts and splice variants are identified in a full-length cloning experiment, or by use of full-length transcript and EST sequences. First, all human ESTs were grouped into clusters which show direct or indirect identity with each other. Second, ESTs in the same cluster were further grouped into sub-clusters and assembled into a consensus sequence. The original gene sequence is compared to the consensus sequence(s) or other full-length sequences. Each consensus sequence is a potential splice variant for that gene (see, e.g., http://www.doubletwist.com/products/c11_agentsOverview.jhtml). Even when a variant is identified that is not a full-length clone, that portion of the variant is very useful for antigen generation and for further cloning of the full-length splice variant, using techniques known in the art.

Moreover, computer programs are available in the art that identify transcript variants based on genomic sequences. Genomic-based transcript variant identification programs include FgenesH (A. Salamov and V. Solovyev, "Ab initio gene finding in Drosophila genomic DNA," Genome Research. 2000 April;10(4):516-22); Grail (http://compbio.ornl.gov/Grail-bin/EmptyGrailForm) and GenScan (http://genes.mit.edu/GENSCAN.html). For a general discussion of splice variant identification protocols see., e.g., Southan, C., A genomic perspective on human proteases, FEBS Lett. 2001 Jun 8; 498(2-3):214-8; de Souza, S.J., *et al.*, Identification of human chromosome 22 transcribed sequences with ORF expressed sequence tags, Proc. Natl Acad Sci U S A. 2000 Nov 7; 97(23):12690-3.

To further confirm the parameters of a transcript variant, a variety of techniques are available in the art, such as full-length cloning, proteomic validation, PCR-based validation, and 5' RACE validation, etc. (see e.g., Proteomic Validation: Brennan, S.O., *et al.*, Albumin banks peninsula: a new termination variant characterized by electrospray mass spectrometry, Biochem Biophys Acta. 1999 Aug 17;1433(1-2):321-6; Ferranti P, *et al.*, Differential splicing of pre-messenger RNA produces multiple forms of mature caprine alpha(s1)-casein, Eur J Biochem. 1997 Oct 1;249(1):1-7. For PCR-based Validation: Wellmann S, *et al.*, Specific reverse transcription-PCR quantification of vascular endothelial growth factor (VEGF) splice variants by LightCycler technology, Clin Chem. 2001 Apr;47(4):654-60; Jia, H.P., *et al.*, Discovery of new human beta-defensins using a genomics-based approach, Gene. 2001 Jan 24; 263(1-2):211-8. For PCR-based

and 5' RACE Validation: Brigle, K.E., *et al.*, Organization of the murine reduced folate carrier gene and identification of variant splice forms, Biochem Biophys Acta. 1997 Aug 7; 1353(2): 191-8).

It is known in the art that genomic regions are modulated in cancers. When the genomic region to which a gene maps is modulated in a particular cancer, the alternative transcripts or splice variants of the gene are modulated as well. Disclosed herein is that 151P3D4 has a particular expression profile. Alternative transcripts and splice variants of 151P3D4 that are structurally and/or functionally similar to 151P3D4 share this expression pattern, thus serving as tumor associated markers/antigens.

The exon composition of the original transcript, designated as 151P3D4 v.1, is shown in Table LII (A). Using the full-length gene and EST sequences, one alternative transcript was identified, designated as 151P3D4 v.2. Compared with 151P3D4 v.1, transcript variant 151P3D4 v.2 has 10 exons, as shown in Table LII (B) and Figure 12. Exons 8 and 9 are the same as exons 3 and 4 of 151P3D4 v.1, and exon 10 is the coding portion of exon 5 of 151P3D4 v.1. Each different combination of exons in spatial order, e.g. exons 2 and 3, is a potential splice variant. Figure 12 shows the schematic alignment of exons of the two transcript variants.

Table LIII shows nucleotide sequence of the transcript variant, 151P3D4 v.2 (see also Figure 2B). Table LIV shows the alignment of the transcript variant 151P3D4 v.2 with nucleic acid sequence of 151P3D4 v.1. Figure 3B provides the amino acid translation of the transcript variant 151P3D4 v.2 for the identified reading frame orientation. Table LV displays alignments of the amino acid sequence encoded by the transcript variant 151P3D4 v.2 with that of 151P3D4 v.1.

Example 6: Single Nucleotide Polymorphisms of 151P3D4

Single Nucleotide Polymorphism (SNP) is a single base pair variation in nucleotide sequences. At a specific point of the genome, there are four possible nucleotide base pairs: A/T, C/G, G/C and T/A. Genotype refers to the base pair make-up of one or more spots in the genome of an individual, while haplotype refers to base pair make-up of more than one varied spots on the same DNA molecule (chromosome in higher organism). SNPs that occur on a cDNA are called cSNPs. These cSNPs may change amino acids of the protein encoded by the gene and thus change the functions of the protein. Some SNPs cause inherited diseases and some others contribute to quantitative variations in phenotype and reactions to environmental factors including diet and drugs among individuals. Therefore, SNPs and/or combinations of alleles (called haplotypes) have many applications including diagnosis of inherited diseases, determination of drug reactions and dosage, identification of genes responsible for disearses and discovery of genetic relationship between individuals (P. Nowotny, J. M. Kwon and A. M. Goate, " SNP analysis to dissect human traits," Curr. Opin. Neurobiol. 2001 Oct; 11(5):637-641; M. Pirmohamed and B. K. Park, "Genetic susceptibility to adverse drug reactions," Trends Pharmacol. Sci. 2001 Jun; 22(6):298-305; J. H. Riley, C. J. Allan, E. Lai and A. Roses, "The use of single nucleotide polymorphisms in the isolation of common disease genes," Pharmacogenomics. 2000 Feb; 1(1):39-47; R. Judson, J. C. Stephens and A. Windemuth, "The predictive power of haplotypes in clinical response," Pharmacogenomics. 2000 feb; 1(1):15-26).

SNPs are identified by a variety of art-accepted methods (P. Bean, "The promising voyage of SNP target discovery," Am. Clin. Lab. 2001 Oct-Nov; 20(9):18-20; K. M. Weiss, "In search of human variation,"

Genome Res. 1998 Jul; 8(7):691-697; M. M. She, "Enabling large-scale pharmacogenetic studies by high-throughput mutation detection and genotyping technologies," Clin. Chem. 2001 Feb; 47(2):164-172). For example, SNPs are identified by sequencing DNA fragments that show polymorphism by gel-based methods such as restriction fragment length polymorphism (RFLP) and denaturing gradient gel electrophoresis (DGGE). They can also be discovered by direct sequencing of DNA samples pooled from different individuals or by comparing sequences from different DNA samples. With the rapid accumulation of sequence data in public and private databases, one can discover SNPs by comparing sequences using computer programs (Z. Gu, L. Hillier and P. Y. Kwok, "Single nucleotide polymorphism hunting in cyberspace," Hum. Mutat. 1998; 12(4):221-225). SNPs can be verified and genotype or haplotype of an individual can be determined by a variety of methods including direct sequencing and high throughput microarrays (P. Y. Kwok, "Methods for genotyping single nucleotide polymorphisms," Annu. Rev. Genomics Hum. Genet. 2001; 2:235-258; M. Kokoris, K. Dix, K. Moynihan, J. Mathis, B. Erwin, P. Grass, B. Hines and A. Duesterhoeft, "High-throughput SNP genotyping with the Masscode system," Mol. Diagn. 2000 Dec; 5(4):329-340).

Using the methods described above, nine SNPs were identified in the original transcript, 151P3D4 v.1, at positions 154 (A/G), 218 (C/G), 219 (G/C), 999 (C/G), 1326 (C/T), 1399 (T/C), 1400 (C/T), 1653 (T/C) and 1726 (A/G). The transcripts or proteins with alternative alleles were designated as variants 151P3D4 v.3, v.4, v.5, v.6, v.7, v.8, v.9, v.10 and v.11. Figures 10 and 12 show the schematic alignment of the nucleotide variants. Figure 11 shows the schematic alignment of protein variants, corresponding to nucleotide variants. Nucleotide variants that code for the same amino acid sequence as variant 1 are not shown in Figure 11. These alleles of the SNPs, though shown separately here, can occur in different combinations (haplotypes) and in any one of the transcript variants that contains the sequence context of the SNPs, e.g., 151P3D4 v.7.

Example 7: Production of Recombinant 151P3D4 in Prokaryotic Systems

To express recombinant 151P3D4 and 151P3D4 variants in prokaryotic cells, the full or partial length 151P3D4 and 151P3D4 variant cDNA sequences are cloned into any one of a variety of expression vectors known in the art. One or more of the following regions of 151P3D4 variants are expressed: the full length sequence presented in Figures 2 and 3, or any 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous amino acids from 151P3D4, variants, or analogs thereof.

A. *In vitro* transcription and translation constructs:

pCRII: To generate 151P3D4 sense and anti-sense RNA probes for RNA *in situ* investigations, pCRII constructs (Invitrogen, Carlsbad CA) are generated encoding either all or fragments of the 151P3D4 cDNA. The pCRII vector has Sp6 and T7 promoters flanking the insert to drive the transcription of 151P3D4 RNA for use as probes in RNA *in situ* hybridization experiments. These probes are used to analyze the cell and tissue expression of 151P3D4 at the RNA level. Transcribed 151P3D4 RNA representing the cDNA amino acid coding region of the 151P3D4 gene is used in *in vitro* translation systems such as the TnT™ Coupled Reticulolysate System (Promega, Corp., Madison, WI) to synthesize 151P3D4 protein.

B. Bacterial Constructs:

pGEX Constructs: To generate recombinant 151P3D4 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 151P3D4 cDNA protein coding sequence are cloned into the pGEX family of GST-fusion vectors (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 151P3D4 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) at the carboxyl-terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag is generated by adding 6 histidine codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScission™ recognition site in pGEX-6P-1, may be employed such that it permits cleavage of the GST tag from 151P3D4-related protein. The ampicillin resistance gene and pBR322 origin permits selection and maintenance of the pGEX plasmids in *E. coli*.

pMAL Constructs: To generate, in bacteria, recombinant 151P3D4 proteins that are fused to maltose-binding protein (MBP), all or parts of the 151P3D4 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors (New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 151P3D4 protein sequences with MBP fused at the amino-terminus and a 6X His epitope tag at the carboxyl-terminus. The MBP and 6X His tags permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His epitope tag is generated by adding 6 histidine codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 151P3D4. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds.

pET Constructs: To express 151P3D4 in bacterial cells, all or parts of the 151P3D4 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 151P3D4 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His and S-Tag ™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 151P3D4 protein are expressed as amino-terminal fusions to NusA.

C. Yeast Constructs:

pESC Constructs: To express 151P3D4 in the yeast species *Saccharomyces cerevisiae* for generation of recombinant protein and functional studies, all or parts of the 151P3D4 cDNA protein coding sequence are cloned into the pESC family of vectors each of which contain 1 of 4 selectable markers, HIS3, TRP1, LEU2, and URA3 (Stratagene, La Jolla, CA). These vectors allow controlled expression from the same plasmid of up to 2 different genes or cloned sequences containing either Flag™ or Myc epitope tags in the same yeast cell. This system is useful to confirm protein-protein interactions of 151P3D4. In addition, expression in yeast yields similar post-translational modifications, such as glycosylations and phosphorylations, that are found when expressed in eukaryotic cells.

pESP Constructs: To express 151P3D4 in the yeast species *Saccharomyces pombe*, all or parts of the 151P3D4 cDNA protein coding sequence are cloned into the pESP family of vectors. These vectors allow controlled high level of expression of a 151P3D4 protein sequence that is fused at either the amino terminus or at the carboxyl terminus to GST which aids purification of the recombinant protein. A Flag™ epitope tag allows detection of the recombinant protein with anti- Flag™ antibody.

Example 8: Production of Recombinant 151P3D4 in Eukaryotic Systems

A. Mammalian Constructs:

To express recombinant 151P3D4 in eukaryotic cells, the full or partial length 151P3D4 cDNA sequences can be cloned into any one of a variety of expression vectors known in the art. One or more of the following regions of 151P3D4 are expressed in these constructs, amino acids 1 to 354 of 151P3D4 v.1, amino acids 1 to 721 of 151P3D4 v.2, or any 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50 or more contiguous amino acids from 151P3D4, variants, or analogs thereof. In certain embodiments a region of a specific variant of 151P3D4 is expressed that encodes an amino acid at a specific position which differs from the amino acid of any other variant found at that position. In other embodiments, a region of a variant of 151P3D4 is expressed that lies partly or entirely within a sequence that is unique to that variant.

The constructs can be transfected into any one of a wide variety of mammalian cells such as 293T cells. Transfected 293T cell lysates can be probed with the anti-151P3D4 polyclonal serum, described herein.

pcDNA4/HisMax Constructs: To express 151P3D4 in mammalian cells, a 151P3D4 ORF, or portions thereof, of 151P3D4 are cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has Xpress™ and six histidine (6X His) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

pcDNA3.1/MycHis Constructs: To express 151P3D4 in mammalian cells, a 151P3D4 ORF, or portions thereof, of 151P3D4 with a consensus Kozak translation initiation site was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant protein has the myc epitope and 6X His epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene was used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*. Results of expression from 151P3D4.pcDNA3.1/MycHis construct are shown in Figure 20.

pcDNA3.1/CT-GFP-TOPO Construct: To express 151P3D4 in mammalian cells and to allow detection of the recombinant proteins using fluorescence, a 151P3D4 ORF, or portions thereof, with a consensus Kozak translation initiation site are cloned into pcDNA3.1/CT-GFP-TOPO (Invitrogen, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the Green Fluorescent Protein (GFP) fused to the carboxyl-terminus facilitating non-invasive, *in vivo* detection and cell biology studies. The pcDNA3.1CT-GFP-TOPO vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene allows for selection of mammalian cells that express the protein, and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*. Additional constructs with an amino-terminal GFP fusion are made in pcDNA3.1/NT-GFP-TOPO spanning the entire length of a 151P3D4 protein.

PAPtag: A 151P3D4 ORF, or portions thereof, is cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of a 151P3D4 protein while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of a 151P3D4 protein. The resulting recombinant 151P3D4 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with 151P3D4 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

ptag5: A 151P3D4 ORF, or portions thereof, is cloned into pTag-5. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generates 151P3D4 protein with an amino-terminal IgGκ signal sequence and myc and 6X His epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 151P3D4 protein is optimized for secretion into the media of transfected mammalian cells, and is used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 151P3D4 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

PsecFc: A 151P3D4 ORF, or portions thereof, is also cloned into psecFc. The psecFc vector was assembled by cloning the human immunoglobulin G1 (IgG) Fc (hinge, CH2, CH3 regions) into pSecTag2 (Invitrogen, California). This construct generates an IgG1 Fc fusion at the carboxyl-terminus of the 151P3D4 proteins, while fusing the IgGK signal sequence to N-terminus. 151P3D4 fusions utilizing the murine IgG1 Fc region are also used. The resulting recombinant 151P3D4 proteins are optimized for secretion into the media of transfected mammalian cells, and can be used as immunogens or to identify proteins such as ligands or receptors that interact with 151P3D4 protein. Protein expression is driven from the CMV promoter. The

hygromycin resistance gene present in the vector allows for selection of mammalian cells that express the recombinant protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli.*

pSRα Constructs: To generate mammalian cell lines that express 151P3D4 constitutively, 151P3D4 ORF, or portions thereof, of 151P3D4 are cloned into pSRα constructs. Amphotropic and ecotropic retroviruses are generated by transfection of pSRα constructs into the 293T-10A1 packaging line or co-transfection of pSRα and a helper plasmid (containing deleted packaging sequences) into the 293 cells, respectively. The retrovirus is used to infect a variety of mammalian cell lines, resulting in the integration of the cloned gene, 151P3D4, into the host cell-lines. Protein expression is driven from a long terminal repeat (LTR). The Neomycin resistance gene present in the vector allows for selection of mammalian cells that express the protein, and the ampicillin resistance gene and ColE1 origin permit selection and maintenance of the plasmid in *E. coli.* The retroviral vectors can thereafter be used for infection and generation of various cell lines using, for example, PC3, NIH 3T3, TsuPr1, 293 or rat-1 cells.

Additional pSRα constructs are made that fuse an epitope tag such as the FLAG™ tag to the carboxyl-terminus of 151P3D4 sequences to allow detection using anti-Flag antibodies. For example, the FLAG™ sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO:__) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His fusion proteins of the full-length 151P3D4 proteins.

Additional Viral Vectors: Additional constructs are made for viral-mediated delivery and expression of 151P3D4. High virus titer leading to high level expression of 151P3D4 is achieved in viral delivery systems such as adenoviral vectors and herpes amplicon vectors. A 151P3D4 coding sequences or fragments thereof are amplified by PCR and subcloned into the AdEasy shuttle vector (Stratagene). Recombination and virus packaging are performed according to the manufacturer's instructions to generate adenoviral vectors. Alternatively, 151P3D4 coding sequences or fragments thereof are cloned into the HSV-1 vector (Imgenex) to generate herpes viral vectors. The viral vectors are thereafter used for infection of various cell lines such as PC3, NIH 3T3, 293 or rat-1 cells.

Regulated Expression Systems: To control expression of 151P3D4 in mammalian cells, coding sequences of 151P3D4, or portions thereof, are cloned into regulated mammalian expression systems such as the T-Rex System (Invitrogen), the GeneSwitch System (Invitrogen) and the tightly-regulated Ecdysone System (Sratagene). These systems allow the study of the temporal and concentration dependent effects of recombinant 151P3D4. These vectors are thereafter used to control expression of 151P3D4 in various cell lines such as PC3, NIH 3T3, 293 or rat-1 cells.

B. Baculovirus Expression Systems

To generate recombinant 151P3D4 proteins in a baculovirus expression system, 151P3D4 ORF, or portions thereof, are cloned into the baculovirus transfer vector pBlueBac 4.5 (Invitrogen), which provides a His-tag at the N-terminus. Specifically, pBlueBac-151P3D4 is co-transfected with helper plasmid pBac-N-Blue (Invitrogen) into SF9 (*Spodoptera frugiperda*) insect cells to generate recombinant baculovirus (see Invitrogen instruction manual for details). Baculovirus is then collected from cell supernatant and purified by plaque assay.

Recombinant 151P3D4 protein is then generated by infection of HighFive insect cells (Invitrogen) with purified baculovirus. Recombinant 151P3D4 protein can be detected using anti-151P3D4 or anti-His-tag antibody. 151P3D4 protein can be purified and used in various cell-based assays or as immunogen to generate polyclonal and monoclonal antibodies specific for 151P3D4.

Example 9: Antigenicity Profiles and Secondary Structure

Figure 5(A & B), Figure 6(A & B), Figure 7(A & B), Figure 8(A & B), and Figure 9(A & B) depict graphically five amino acid profiles of 151P3D4 variants 1 and 2, each assessment available by accessing the ProtScale website (URL www.expasy.ch/cgi-bin/protscale.pl) on the ExPasy molecular biology server.

These profiles: Figure 5, Hydrophilicity, (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828); Figure 6, Hydropathicity, (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132); Figure 7, Percentage Accessible Residues (Janin J., 1979 Nature 277:491-492); Figure 8, Average Flexibility, (Bhaskaran R., and Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255); Figure 9, Beta-turn (Deleage, G., Roux B. 1987 Protein Engineering 1:289-294); and optionally others available in the art, such as on the ProtScale website, were used to identify antigenic regions of the 151P3D4 protein. Each of the above amino acid profiles of 151P3D4 were generated using the following ProtScale parameters for analysis: 1) A window size of 9; 2) 100% weight of the window edges compared to the window center; and, 3) amino acid profile values normalized to lie between 0 and 1.

Hydrophilicity (Figure 5), Hydropathicity (Figure 6) and Percentage Accessible Residues (Figure 7) profiles were used to determine stretches of hydrophilic amino acids (i.e., values greater than 0.5 on the Hydrophilicity and Percentage Accessible Residues profile, and values less than 0.5 on the Hydropathicity profile). Such regions are likely to be exposed to the aqueous environment, be present on the surface of the protein, and thus available for immune recognition, such as by antibodies.

Average Flexibility (Figure 8) and Beta-turn (Figure 9) profiles determine stretches of amino acids (i.e., values greater than 0.5 on the Beta-turn profile and the Average Flexibility profile) that are not constrained in secondary structures such as beta sheets and alpha helices. Such regions are also more likely to be exposed on the protein and thus accessible to immune recognition, such as by antibodies.

Antigenic sequences of the 151P3D4 variant proteins indicated, e.g., by the profiles set forth in Figure 5(A & B), Figure 6(A & B), Figure 7(A & B), Figure 8(A & B), and/or Figure 9(A & B) are used to prepare immunogens, either peptides or nucleic acids that encode them, to generate therapeutic and diagnostic anti-151P3D4 antibodies. The immunogen can be any 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50 or more than 50 contiguous amino acids, or the corresponding nucleic acids that encode them, from the 151P3D4 protein variants 1 and 2 listed in Figures 2 and 3. In particular, peptide immunogens of the invention can comprise, a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Hydrophilicity profiles of Figure 5; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value less than 0.5 in the Hydropathicity profile of Figures 6 ; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Percent

Accessible Residues profiles of Figure 7; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Average Flexibility profiles on Figure 8 ; and, a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figures 9 . Peptide immunogens of the invention can also comprise nucleic acids that encode any of the forgoing.

All immunogens of the invention, peptide or nucleic acid, can be embodied in human unit dose form, or comprised by a composition that includes a pharmaceutical excipient compatible with human physiology.

The secondary structure of 151P3D4 protein variants 1 and 2, namely the predicted presence and location of alpha helices, extended strands, and random coils, is predicted from the primary amino acid sequence using the HNN - Hierarchical Neural Network method (Guermeur, 1997, http://pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_nn.html), accessed from the ExPasy molecular biology server (http://www.expasy.ch/tools/). The analysis indicates that 151P3D4 variant 1 is composed of 25.71% alpha helix, 21.47% extended strand, and 52.82% random coil (Figure 13A). Variant 2 is composed of 25.80% alpha helix, 16.64% extended strand, and 57.56% random coil (Figure 13B).

Analysis for the potential presence of transmembrane domains in the 151P3D4 variant proteins was carried out using a variety of transmembrane prediction algorithms accessed from the ExPasy molecular biology server (http://www.expasy.ch/tools/). The programs do not predict the presence of transmembrane domains in the 151P3D4 protein variants, suggesting that they are soluble proteins.

Example 10: Generation of 151P3D4 Polyclonal Antibodies

Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. In addition to immunizing with a full length 151P3D4 protein variant, computer algorithms are employed in design of immunogens that, based on amino acid sequence analysis contain characteristics of being antigenic and available for recognition by the immune system of the immunized host (see the Example entitled "Antigenicity Profiles"). Such regions would be predicted to be hydrophilic, flexible, in beta-turn conformations, and be exposed on the surface of the protein (see, e.g., Figure 5(A & B), Figure 6(A & B), Figure 7(A & B), Figure 8(A & B), or Figure 9(A & B) for amino acid profiles that indicate such regions of 151P3D4 protein variants).

For example, recombinant bacterial fusion proteins or peptides containing hydrophilic, flexible, beta-turn regions of 151P3D4 protein variants are used as antigens to generate polyclonal antibodies in New Zealand White rabbits. For example, in 151P3D4 variant 1, such regions include, but are not limited to, amino acids 99-151, amino acids 218-249, and amino acids 311-332. In sequence specific for variant 2, such regions include, but are not limited to, amino acids 16-38, amino acids 76-90, amino acids 182-230, and amino acids 383-400. It is useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include, but are not limited to, keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. In one embodiment, a peptide encoding amino acids 311-332 of 151P3D4 variant 1 is conjugated to KLH and used to immunize the rabbit. Alternatively the immunizing agent may include all or portions of the 151P3D4

variant proteins, analogs or fusion proteins thereof. For example, the 151P3D4 variant 1 amino acid sequence can be fused using recombinant DNA techniques to any one of a variety of fusion protein partners that are well known in the art, such as glutathione-S-transferase (GST) and HIS tagged fusion proteins. Such fusion proteins are purified from induced bacteria using the appropriate affinity matrix.

In one embodiment, a GST-fusion protein encoding the N-terminal region of 151P3D4 variant 1, amino acids 16-150, minus the first 15 amino acids that likely encodes a cleavable signal peptide, is produced and purified and used as immunogen. Other recombinant bacterial fusion proteins that may be employed include maltose binding protein, LacZ, thioredoxin, NusA, or an immunoglobulin constant region (see the section entitled "Production of 151P3D4 in Prokaryotic Systems" and Current Protocols In Molecular Biology, Volume 2, Unit 16, Frederick M. Ausubul et al. eds., 1995; Linsley, P.S., Brady, W., Urnes, M., Grosmaire, L., Damle, N., and Ledbetter, L.(1991) J.Exp. Med. 174, 561-566).

In addition to bacterial derived fusion proteins, mammalian expressed protein antigens are also used. These antigens are expressed from mammalian expression vectors such as the Tag5 and Fc-fusion vectors (see the section entitled "Production of Recombinant 151P3D4 in Eukaryotic Systems"), and retain post-translational modifications such as glycosylations found in native protein. In one embodiment, amino acids 16-354 of variant 1, minus the endogenous signal peptide, is cloned into the Tag5 mammalian secretion vector. The recombinant protein is purified by metal chelate chromatography from tissue culture supernatants of 293T cells stably expressing the recombinant vector. The purified Tag5 151P3D4 protein is then used as immunogen.

During the immunization protocol, it is useful to mix or emulsify the antigen in adjuvants that enhance the immune response of the host animal. Examples of adjuvants include, but are not limited to, complete Freund's adjuvant (CFA) and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

In a typical protocol, rabbits are initially immunized subcutaneously with up to 200 μg, typically 100-200 μg, of fusion protein or peptide conjugated to KLH mixed in complete Freund's adjuvant (CFA). Rabbits are then injected subcutaneously every two weeks with up to 200 μg, typically 100-200 μg, of the immunogen in incomplete Freund's adjuvant (IFA). Test bleeds are taken approximately 7-10 days following each immunization and used to monitor the titer of the antiserum by ELISA.

To test reactivity and specificity of immune serum, such as the rabbit serum derived from immunization with the Tag5 -151P3D4 variant 1 protein, the full-length 151P3D4 variant 1 cDNA is cloned into pCDNA 3.1 myc-his expression vector (Invitrogen, see the Example entitled "Production of Recombinant 151P3D4 in Eukaryotic Systems"). After transfection of the constructs into 293T cells, cell lysates are probed with the anti-151P3D4 serum and with anti-His antibody (Santa Cruz Biotechnologies, Santa Cruz, CA) to determine specific reactivity to denatured 151P3D4 protein using the Western blot technique (Figure 20) shows expression of Myc His epitope tagged 151P3D4 variant 1 protein in 293T cells as detected by an anti-His antibody. In addition, the immune serum is tested by fluorescence microscopy, flow cytometry and immunoprecipitation against 293T and other recombinant 151P3D4-expressing cells to determine specific recognition of native protein. Western blot, immunoprecipitation, fluorescent microscopy,

and flow cytometric techniques using cells that endogenously express 151P3D4 are also carried out to test reactivity and specificity.

Anti-serum from rabbits immunized with 151P3D4 variant fusion proteins, such as GST and MBP fusion proteins, are purified by depletion of antibodies reactive to the fusion partner sequence by passage over an affinity column containing the fusion partner either alone or in the context of an irrelevant fusion protein. For example, antiserum derived from a GST-151P3D4 variant 1 fusion protein encoding amino acids 16-150 is first purified by passage over a column of GST protein covalently coupled to AffiGel matrix (BioRad, Hercules, Calif.). The antiserum is then affinity purified by passage over a column composed of a MBP-fusion protein also encoding amino acids 16-150 covalently coupled to Affigel matrix. The serum is then further purified by protein G affinity chromatography to isolate the IgG fraction. Sera from other His-tagged antigens and peptide immunized rabbits as well as fusion partner depleted sera are affinity purified by passage over a column matrix composed of the original protein immunogen or free peptide.

Example 11: Generation of 151P3D4 Monoclonal Antibodies (mAbs)

In one embodiment, therapeutic mAbs to 151P3D4 variants comprise those that react with epitopes specific for each variant protein or specific to sequences in common between the variants that would disrupt or modulate the biological function of the 151P3D4 variants, for example those that would disrupt the interaction with ligands and binding partners. Immunogens for generation of such mAbs include those designed to encode or contain the entire 151P3D4 protein variant sequence, regions of the 151P3D4 protein variants predicted to be antigenic from computer analysis of the amino acid sequence (see, e.g., Figure 5(A & B), Figure 6(A & B), Figure 7(A & B), Figure 8(A & B), or Figure 9(A & B); and the Example entitled "Antigenicity Profiles"). Immunogens include peptides, recombinant bacterial proteins, and mammalian expressed Tag 5 proteins and human and murine IgG FC fusion proteins. In addition, cells engineered to express high levels of a respective 151P3D4 variant, such as 293T-151P3D4 variant 1 or 300.19-151P3D4 variant 1murine Pre-B cells, are used to immunize mice.

To generate mAbs to a 151P3D4 variant, mice are first immunized intraperitoneally (IP) with, typically, 10-50 μg of protein immunogen or 10^7 151P3D4-expressing cells mixed in complete Freund's adjuvant. Mice are then subsequently immunized IP every 2-4 weeks with, typically, 10-50 μg of protein immunogen or 10^7 cells mixed in incomplete Freund's adjuvant. Alternatively, MPL-TDM adjuvant is used in immunizations. In addition to the above protein and cell-based immunization strategies, a DNA-based immunization protocol is employed in which a mammalian expression vector encoding a 151P3D4 variant sequence is used to immunize mice by direct injection of the plasmid DNA. For example, amino acids 16-354 is cloned into the Tag5 mammalian secretion vector and the recombinant vector is used as immunogen. In another example the same amino acids are cloned into an Fc-fusion secretion vector in which the 151P3D4 variant 1 sequence is fused at the amino-terminus to an IgK leader sequence and at the carboxyl-terminus to the coding sequence of the human or murine IgG Fc region. This recombinant vector is then used as immunogen. The plasmid immunization protocols are used in combination with purified proteins expressed from the same vector and with cells expressing the respective 151P3D4 variant.

During the immunization protocol, test bleeds are taken 7-10 days following an injection to monitor titer and specificity of the immune response. Once appropriate reactivity and specificity is obtained as determined by ELISA, Western blotting, immunoprecipitation, fluorescence microscopy, and flow cytometric analyses, fusion and hybridoma generation is then carried out with established procedures well known in the art (see, e.g., Harlow and Lane, 1988).

In one embodiment for generating 151P3D4 monoclonal antibodies, a Tag5-151P3D4 variant 1 antigen encoding amino acids 16-354, is expressed and purified from stably transfected 293T cells. Balb C mice are initially immunized intraperitoneally with 25 μg of the Tag5-151P3D4 variant 1 protein mixed in complete Freund's adjuvant. Mice are subsequently immunized every two weeks with 25 μg of the antigen mixed in incomplete Freund's adjuvant for a total of three immunizations. ELISA using the Tag5 antigen determines the titer of serum from immunized mice. Reactivity and specificity of serum to full length 151P3D4 variant 1 protein is monitored by Western blotting, immunoprecipitation and flow cytometry using 293T cells transfected with an expression vector encoding the 151P3D4 variant 1 cDNA (see e.g., the Example entitled "Production of Recombinant 151P3D4 in Eukaryotic Systems" and Figure 20. Other recombinant 151P3D4 variant 1-expressing cells or cells endogenously expressing 151P3D4 variant 1 are also used. Mice showing the strongest reactivity are rested and given a final injection of Tag5 antigen in PBS and then sacrificed four days later. The spleens of the sacrificed mice are harvested and fused to SPO/2 myeloma cells using standard procedures (Harlow and Lane, 1988). Supernatants from HAT selected growth wells are screened by ELISA, Western blot, immunoprecipitation, fluorescent microscopy, and flow cytometry to identify 151P3D4 specific antibody-producing clones.

In another embodiment, a Tag5 antigen encoding amino acids 1-400 of variant 2 is produced, purified and used as immunogen to derive monoclonal antibodies specific to 151P3D4 variant 2. Hybridoma supernatants are then screened on both 151P3D4 variant 2- and 151P3D4 variant 1-expressing cells to identify specific anti-151P3D4 variant 2 monoclonal antibodies.

The binding affinity of a 151P3D4 monoclonal antibody is determined using standard technologies. Affinity measurements quantify the strength of antibody to epitope binding and are used to help define which 151P3D4 monoclonal antibodies preferred for diagnostic or therapeutic use, as appreciated by one of skill in the art. The BIAcore system (Uppsala, Sweden) is a preferred method for determining binding affinity. The BIAcore system uses surface plasmon resonance (SPR, Welford K. 1991, Opt. Quant. Elect. 23:1; Morton and Myszka, 1998, Methods in Enzymology 295: 268) to monitor biomolecular interactions in real time. BIAcore analysis conveniently generates association rate constants, dissociation rate constants, equilibrium dissociation constants, and affinity constants.

Example 12: HLA Class I and Class II Binding Assays

HLA class I and class II binding assays using purified HLA molecules are performed in accordance with disclosed protocols (*e.g.*, PCT publications WO 94/20127 and WO 94/03205; Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)). Briefly, purified MHC molecules (5 to 500 nM) are incubated with various unlabeled peptide inhibitors and 1-10 nM ^{125}I-radiolabeled probe peptides as described. Following

incubation, MHC-peptide complexes are separated from free peptide by gel filtration and the fraction of peptide bound is determined. Typically, in preliminary experiments, each MHC preparation is titered in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays are performed using these HLA concentrations.

Since under these conditions [label]<[HLA] and $IC_{50}\geq$[HLA], the measured IC_{50} values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 µg/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC_{50} of a positive control for inhibition by the IC_{50} for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For database purposes, and inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC_{50} nM values by dividing the IC_{50} nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation is accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

Binding assays as outlined above may be used to analyze HLA supermotif and/or HLA motif-bearing peptides (see Table IV).

Example 13: Identification of HLA Supermotif- and Motif-Bearing CTL Candidate Epitopes

HLA vaccine compositions of the invention can include multiple epitopes. The multiple epitopes can comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification and confirmation of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage is performed using the strategy described below.

Computer searches and algorithms for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in the Example entitled "Antigenicity Profiles" and Tables V-XVIII and XXII-LI employ the protein sequence data from the gene product of 151P3D4 set forth in Figures 2 and 3.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs are performed as follows. All translated 151P3D4 protein sequences are analyzed using a text string search software program to identify potential peptide sequences containing appropriate HLA binding motifs; such programs are readily produced in accordance with information in the art in view of known motif/supermotif disclosures. Furthermore, such calculations can be made mentally.

Identified A2-, A3-, and DR-supermotif sequences are scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms account for the impact of different amino acids at different positions, and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$\text{"}\Delta G\text{"} = a_{1i} \times a_{2i} \times a_{3i} \ldots\ldots \times a_{ni}$$

where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue j occurs at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide.

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i. For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

<u>Selection of HLA-A2 supertype cross-reactive peptides</u>

Protein sequences from 151P3D4 are scanned utilizing motif identification software, to identify 8-, 9- 10- and 11-mer sequences containing the HLA-A2-supermotif main anchor specificity. Typically, these sequences are then scored using the protocol described above and the peptides corresponding to the positive-scoring sequences are synthesized and tested for their capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a prototype A2 supertype molecule).

These peptides are then tested for the capacity to bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). Peptides that bind to at least three of the five A2-supertype alleles tested are typically deemed A2-supertype cross-reactive binders. Preferred peptides bind at an affinity equal to or less than 500 nM to three or more HLA-A2 supertype molecules.

<u>Selection of HLA-A3 supermotif-bearing epitopes</u>

The 151P3D4 protein sequence(s) scanned above is also examined for the presence of peptides with the HLA-A3-supermotif primary anchors. Peptides corresponding to the HLA A3 supermotif-bearing sequences are then synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the molecules encoded by the two most prevalent A3-supertype alleles. The peptides that bind at least one of the two alleles with binding affinities of ≤500 nM, often ≤ 200 nM, are then tested for binding cross-reactivity to the other common A3-supertype alleles (e.g., A*3101, A*3301, and A*6801) to identify those that can bind at least three of the five HLA-A3-supertype molecules tested.

<u>Selection of HLA-B7 supermotif bearing epitopes</u>

The 151P3D4 protein(s) scanned above is also analyzed for the presence of 8-, 9- 10-, or 11-mer peptides with the HLA-B7-supermotif. Corresponding peptides are synthesized and tested for binding to HLA-B*0702, the molecule encoded by the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Peptides binding B*0702 with IC_{50} of ≤500 nM are identified using standard methods. These peptides are then tested for binding to other common B7-supertype molecules (e.g., B*3501, B*5101,

B*5301, and B*5401). Peptides capable of binding to three or more of the five B7-supertype alleles tested are thereby identified.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into vaccine compositions. An analysis of the 151P3D4 protein can also be performed to identify HLA-A1- and A24-motif-containing sequences.

High affinity and/or cross-reactive binding epitopes that bear other motif and/or supermotifs are identified using analogous methodology.

Example 14: Confirmation of Immunogenicity

Cross-reactive candidate CTL A2-supermotif-bearing peptides that are identified as described herein are selected to confirm *in vitro* immunogenicity. Confirmation is performed using the following methodology:

Target Cell Lines for Cellular Screening:

The .221A2.1 cell line, produced by transferring the HLA-A2.1 gene into the HLA-A, -B, -C null mutant human B-lymphoblastoid cell line 721.221, is used as the peptide-loaded target to measure activity of HLA-A2.1-restricted CTL. This cell line is grown in RPMI-1640 medium supplemented with antibiotics, sodium pyruvate, nonessential amino acids and 10% (v/v) heat inactivated FCS. Cells that express an antigen of interest, or transfectants comprising the gene encoding the antigen of interest, can be used as target cells to confirm the ability of peptide-specific CTLs to recognize endogenous antigen.

Primary CTL Induction Cultures:

Generation of Dendritic Cells (DC): PBMCs are thawed in RPMI with 30 μg/ml DNAse, washed twice and resuspended in complete medium (RPMI-1640 plus 5% AB human serum, non-essential amino acids, sodium pyruvate, L-glutamine and penicillin/streptomycin). The monocytes are purified by plating 10 x 10^6 PBMC/well in a 6-well plate. After 2 hours at 37°C, the non-adherent cells are removed by gently shaking the plates and aspirating the supernatants. The wells are washed a total of three times with 3 ml RPMI to remove most of the non-adherent and loosely adherent cells. Three ml of complete medium containing 50 ng/ml of GM-CSF and 1,000 U/ml of IL-4 are then added to each well. TNFα is added to the DCs on day 6 at 75 ng/ml and the cells are used for CTL induction cultures on day 7.

Induction of CTL with DC and Peptide: CD8+ T-cells are isolated by positive selection with Dynal immunomagnetic beads (Dynabeads® M-450) and the detacha-bead® reagent. Typically about 200-250x10^6 PBMC are processed to obtain 24x10^6 $CD8^+$ T-cells (enough for a 48-well plate culture). Briefly, the PBMCs are thawed in RPMI with 30μg/ml DNAse, washed once with PBS containing 1% human AB serum and resuspended in PBS/1% AB serum at a concentration of 20x10^6cells/ml. The magnetic beads are washed 3 times with PBS/AB serum, added to the cells (140μl beads/20x10^6 cells) and incubated for 1 hour at 4°C with continuous mixing. The beads and cells are washed 4x with PBS/AB serum to remove the nonadherent cells and resuspended at 100x10^6 cells/ml (based on the original cell number) in PBS/AB serum containing 100μl/ml detacha-bead® reagent and 30 μg/ml DNAse. The mixture is incubated for 1 hour at room

temperature with continuous mixing. The beads are washed again with PBS/AB/DNAse to collect the CD8+ T-cells. The DC are collected and centrifuged at 1300 rpm for 5-7 minutes, washed once with PBS with 1% BSA, counted and pulsed with 40μg/ml of peptide at a cell concentration of 1-2x10^6/ml in the presence of 3μg/ml β_2- microglobulin for 4 hours at 20°C. The DC are then irradiated (4,200 rads), washed 1 time with medium and counted again.

Setting up induction cultures: 0.25 ml cytokine-generated DC (at 1x10^5 cells/ml) are co-cultured with 0.25ml of CD8+ T-cells (at 2x10^6 cell/ml) in each well of a 48-well plate in the presence of 10 ng/ml of IL-7. Recombinant human IL-10 is added the next day at a final concentration of 10 ng/ml and rhuman IL-2 is added 48 hours later at 10 IU/ml.

Restimulation of the induction cultures with peptide-pulsed adherent cells: Seven and fourteen days after the primary induction, the cells are restimulated with peptide-pulsed adherent cells. The PBMCs are thawed and washed twice with RPMI and DNAse. The cells are resuspended at 5x10^6 cells/ml and irradiated at ~4200 rads. The PBMCs are plated at 2x10^6 in 0.5 ml complete medium per well and incubated for 2 hours at 37°C. The plates are washed twice with RPMI by tapping the plate gently to remove the nonadherent cells and the adherent cells pulsed with 10μg/ml of peptide in the presence of 3 μg/ml β_2 microglobulin in 0.25ml RPMI/5%AB per well for 2 hours at 37°C. Peptide solution from each well is aspirated and the wells are washed once with RPMI. Most of the media is aspirated from the induction cultures (CD8+ cells) and brought to 0.5 ml with fresh media. The cells are then transferred to the wells containing the peptide-pulsed adherent cells. Twenty four hours later recombinant human IL-10 is added at a final concentration of 10 ng/ml and recombinant human IL2 is added the next day and again 2-3 days later at 50IU/ml (Tsai *et al.*, *Critical Reviews in Immunology* 18(1-2):65-75, 1998). Seven days later, the cultures are assayed for CTL activity in a ^{51}Cr release assay. In some experiments the cultures are assayed for peptide-specific recognition in the *in situ* IFNγ ELISA at the time of the second restimulation followed by assay of endogenous recognition 7 days later. After expansion, activity is measured in both assays for a side-by-side comparison.

<u>Measurement of CTL lytic activity by ^{51}Cr release</u>.

Seven days after the second restimulation, cytotoxicity is determined in a standard (5 hr) ^{51}Cr release assay by assaying individual wells at a single E:T. Peptide-pulsed targets are prepared by incubating the cells with 10μg/ml peptide overnight at 37°C.

Adherent target cells are removed from culture flasks with trypsin-EDTA. Target cells are labeled with 200μCi of ^{51}Cr sodium chromate (Dupont, Wilmington, DE) for 1 hour at 37°C. Labeled target cells are resuspended at 10^6 per ml and diluted 1:10 with K562 cells at a concentration of 3.3x10^6/ml (an NK-sensitive erythroblastoma cell line used to reduce non-specific lysis). Target cells (100 μl) and effectors (100μl) are plated in 96 well round-bottom plates and incubated for 5 hours at 37°C. At that time, 100 μl of supernatant are collected from each well and percent lysis is determined according to the formula:

[(cpm of the test sample- cpm of the spontaneous ^{51}Cr release sample)/(cpm of the maximal ^{51}Cr release sample- cpm of the spontaneous ^{51}Cr release sample)] x 100.

Maximum and spontaneous release are determined by incubating the labeled targets with 1% Triton X-100 and media alone, respectively. A positive culture is defined as one in which the specific lysis (sample-

background) is 10% or higher in the case of individual wells and is 15% or more at the two highest E:T ratios when expanded cultures are assayed.

In situ Measurement of Human IFNγ Production as an Indicator of Peptide-specific and Endogenous Recognition

Immulon 2 plates are coated with mouse anti-human IFNγ monoclonal antibody (4 μg/ml 0.1M $NaHCO_3$, pH8.2) overnight at 4°C. The plates are washed with Ca^{2+}, Mg^{2+}-free PBS/0.05% Tween 20 and blocked with PBS/10% FCS for two hours, after which the CTLs (100 μl/well) and targets (100 μl/well) are added to each well, leaving empty wells for the standards and blanks (which received media only). The target cells, either peptide-pulsed or endogenous targets, are used at a concentration of $1x10^6$ cells/ml. The plates are incubated for 48 hours at 37°C with 5% CO_2.

Recombinant human IFN-gamma is added to the standard wells starting at 400 pg or 1200pg/100 microliter/well and the plate incubated for two hours at 37°C. The plates are washed and 100 μl of biotinylated mouse anti-human IFN-gamma monoclonal antibody (2 microgram/ml in PBS/3%FCS/0.05% Tween 20) are added and incubated for 2 hours at room temperature. After washing again, 100 microliter HRP-streptavidin (1:4000) are added and the plates incubated for one hour at room temperature. The plates are then washed 6x with wash buffer, 100 microliter/well developing solution (TMB 1:1) are added, and the plates allowed to develop for 5-15 minutes. The reaction is stopped with 50 microliter/well 1M H_3PO_4 and read at OD450. A culture is considered positive if it measured at least 50 pg of IFN-gamma/well above background and is twice the background level of expression.

CTL Expansion.

Those cultures that demonstrate specific lytic activity against peptide-pulsed targets and/or tumor targets are expanded over a two week period with anti-CD3. Briefly, $5x10^4$ CD8+ cells are added to a T25 flask containing the following: $1x10^6$ irradiated (4,200 rad) PBMC (autologous or allogeneic) per ml, $2x10^5$ irradiated (8,000 rad) EBV- transformed cells per ml, and OKT3 (anti-CD3) at 30ng per ml in RPMI-1640 containing 10% (v/v) human AB serum, non-essential amino acids, sodium pyruvate, 25μM 2-mercaptoethanol, L-glutamine and penicillin/streptomycin. Recombinant human IL2 is added 24 hours later at a final concentration of 200IU/ml and every three days thereafter with fresh media at 50IU/ml. The cells are split if the cell concentration exceeds $1x10^6$/ml and the cultures are assayed between days 13 and 15 at E:T ratios of 30, 10, 3 and 1:1 in the ^{51}Cr release assay or at $1x10^6$/ml in the *in situ* IFNγ assay using the same targets as before the expansion.

Cultures are expanded in the absence of anti-$CD3^+$ as follows. Those cultures that demonstrate specific lytic activity against peptide and endogenous targets are selected and $5x10^4$ $CD8^+$ cells are added to a T25 flask containing the following: $1x10^6$ autologous PBMC per ml which have been peptide-pulsed with 10 μg/ml peptide for two hours at 37°C and irradiated (4,200 rad); $2x10^5$ irradiated (8,000 rad) EBV-transformed cells per ml RPMI-1640 containing 10%(v/v) human AB serum, non-essential AA, sodium pyruvate, 25mM 2-ME, L-glutamine and gentamicin.

Immunogenicity of A2 supermotif-bearing peptides

A2-supermotif cross-reactive binding peptides are tested in the cellular assay for the ability to induce peptide-specific CTL in normal individuals. In this analysis, a peptide is typically considered to be an epitope

if it induces peptide-specific CTLs in at least individuals, and preferably, also recognizes the endogenously expressed peptide.

Immunogenicity can also be confirmed using PBMCs isolated from patients bearing a tumor that expresses 151P3D4. Briefly, PBMCs are isolated from patients, re-stimulated with peptide-pulsed monocytes and assayed for the ability to recognize peptide-pulsed target cells as well as transfected cells endogenously expressing the antigen.

Evaluation of A*03/A11 immunogenicity

HLA-A3 supermotif-bearing cross-reactive binding peptides are also evaluated for immunogenicity using methodology analogous for that used to evaluate the immunogenicity of the HLA-A2 supermotif peptides.

Evaluation of B7 immunogenicity

Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified as set forth herein are confirmed in a manner analogous to the confirmation of A2-and A3-supermotif-bearing peptides.

Peptides bearing other supermotifs/motifs, *e.g.*, HLA-A1, HLA-A24 *etc.* are also confirmed using similar methodology

Example 15: Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analoged to confer upon the peptide certain characteristics, *e.g.* greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analoging peptides to exhibit modulated binding affinity are set forth in this example.

Analoging at Primary Anchor Residues

Peptide engineering strategies are implemented to further increase the cross-reactivity of the epitopes. For example, the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

To analyze the cross-reactivity of the analog peptides, each engineered analog is initially tested for binding to the prototype A2 supertype allele A*0201, then, if A*0201 binding capacity is maintained, for A2-supertype cross-reactivity.

Alternatively, a peptide is confirmed as binding one or all supertype members and then analoged to modulate binding affinity to any one (or more) of the supertype members to add population coverage.

The selection of analogs for immunogenicity in a cellular screening analysis is typically further restricted by the capacity of the parent wild type (WT) peptide to bind at least weakly, *i.e.*, bind at an IC_{50} of 5000nM or less, to three of more A2 supertype alleles. The rationale for this requirement is that the WT peptides must be present endogenously in sufficient quantity to be biologically relevant. Analoged peptides

have been shown to have increased immunogenicity and cross-reactivity by T cells specific for the parent epitope (*see, e.g.*, Parkhurst *et al., J. Immunol.* 157:2539, 1996; and Pogue *et al., Proc. Natl. Acad. Sci. USA* 92:8166, 1995).

In the cellular screening of these peptide analogs, it is important to confirm that analog-specific CTLs are also able to recognize the wild-type peptide and, when possible, target cells that endogenously express the epitope.

<u>Analoging of HLA-A3 and B7-supermotif-bearing peptides</u>

Analogs of HLA-A3 supermotif-bearing epitopes are generated using strategies similar to those employed in analoging HLA-A2 supermotif-bearing peptides. For example, peptides binding to 3/5 of the A3-supertype molecules are engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2.

The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Those peptides that demonstrate ≤ 500 nM binding capacity are then confirmed as having A3-supertype cross-reactivity.

Similarly to the A2- and A3- motif bearing peptides, peptides binding 3 or more B7-supertype alleles can be improved, where possible, to achieve increased cross-reactive binding or greater binding affinity or binding half life. B7 supermotif-bearing peptides are, for example, engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996).

Analoging at primary anchor residues of other motif and/or supermotif-bearing epitopes is performed in a like manner.

The analog peptides are then be confirmed for immunogenicity, typically in a cellular screening assay. Again, it is generally important to demonstrate that analog-specific CTLs are also able to recognize the wild-type peptide and, when possible, targets that endogenously express the epitope.

<u>Analoging at Secondary Anchor Residues</u>

Moreover, HLA supermotifs are of value in engineering highly cross-reactive peptides and/or peptides that bind HLA molecules with increased affinity by identifying particular residues at secondary anchor positions that are associated with such properties. For example, the binding capacity of a B7 supermotif-bearing peptide with an F residue at position 1 is analyzed. The peptide is then analoged to, for example, substitute L for F at position 1. The analoged peptide is evaluated for increased binding affinity, binding half life and/or increased cross-reactivity. Such a procedure identifies analoged peptides with enhanced properties.

Engineered analogs with sufficiently improved binding capacity or cross-reactivity can also be tested for immunogenicity in HLA-B7-transgenic mice, following for example, IFA immunization or lipopeptide immunization. Analoged peptides are additionally tested for the ability to stimulate a recall response using PBMC from patients with 151P3D4-expressing tumors.

Other analoging strategies

Another form of peptide analoging, unrelated to anchor positions, involves the substitution of a cysteine with α-amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substitution of α-amino butyric acid for cysteine not only alleviates this problem, but has been shown to improve binding and crossbinding capabilities in some instances (*see, e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999).

Thus, by the use of single amino acid substitutions, the binding properties and/or cross-reactivity of peptide ligands for HLA supertype molecules can be modulated.

Example 16: Identification and confirmation of 151P3D4-derived sequences with HLA-DR binding motifs

Peptide epitopes bearing an HLA class II supermotif or motif are identified and confirmed as outlined below using methodology similar to that described for HLA Class I peptides.

Selection of HLA-DR-supermotif-bearing epitopes.

To identify 151P3D4-derived, HLA class II HTL epitopes, a 151P3D4 antigen is analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences are selected comprising a DR-supermotif, comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (i.e., at position 1 and position 6) within a 9-mer core, but additionally evaluates sequences for the presence of secondary anchors. Using allele-specific selection tables (see, *e.g.*, Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule. Additionally, it has been found that performing these protocols in tandem, specifically those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

The 151P3D4-derived peptides identified above are tested for their binding capacity for various common HLA-DR molecules. All peptides are initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least two of these three DR molecules are then tested for binding to DR2w2 β1, DR2w2 β2, DR6w19, and DR9 molecules in secondary assays. Finally, peptides binding at least two of the four secondary panel DR molecules, and thus cumulatively at least four of seven different DR molecules, are screened for binding to DR4w15, DR5w11, and DR8w2 molecules in tertiary assays. Peptides binding at least seven of the ten DR molecules comprising the primary, secondary, and tertiary screening assays are considered cross-reactive DR binders. 151P3D4-derived peptides found to bind common HLA-DR alleles are of particular interest.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic populations, DR3 binding capacity is a relevant criterion in the selection of HTL epitopes. Thus, peptides shown to be

candidates may also be assayed for their DR3 binding capacity. However, in view of the binding specificity of the DR3 motif, peptides binding only to DR3 can also be considered as candidates for inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, target 151P3D4 antigens are analyzed for sequences carrying one of the two DR3-specific binding motifs reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides are then synthesized and confirmed as having the ability to bind DR3 with an affinity of 1μM or better, i.e., less than 1 μM. Peptides are found that meet this binding criterion and qualify as HLA class II high affinity binders.

DR3 binding epitopes identified in this manner are included in vaccine compositions with DR supermotif-bearing peptide epitopes.

Similarly to the case of HLA class I motif-bearing peptides, the class II motif-bearing peptides are analoged to improve affinity or cross-reactivity. For example, aspartic acid at position 4 of the 9-mer core sequence is an optimal residue for DR3 binding, and substitution for that residue often improves DR 3 binding.

Example 17: Immunogenicity of 151P3D4-derived HTL epitopes

This example determines immunogenic DR supermotif- and DR3 motif-bearing epitopes among those identified using the methodology set forth herein.

Immunogenicity of HTL epitopes are confirmed in a manner analogous to the determination of immunogenicity of CTL epitopes, by assessing the ability to stimulate HTL responses and/or by using appropriate transgenic mouse models. Immunogenicity is determined by screening for: 1.) *in vitro* primary induction using normal PBMC or 2.) recall responses from patients who have 151P3D4-expressing tumors.

Example 18: Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

In order to analyze population coverage, gene frequencies of HLA alleles are determined. Gene frequencies for each HLA allele are calculated from antigen or allele frequencies utilizing the binomial distribution formulae gf=1-(SQRT(1-af)) (see, *e.g.*, Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic frequencies, cumulative gene frequencies are calculated, and the cumulative antigen frequencies derived by the use of the inverse formula [$af=1-(1-Cgf)^2$].

Where frequency data is not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies is assumed. To obtain total potential supertype population coverage no linkage disequilibrium is assumed, and only alleles confirmed to belong to each of the supertypes are included (minimal estimates). Estimates of total potential coverage achieved by inter-loci combinations are made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (e.g., total=A+B*(1-A)). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include A34,

A66, and A*7401, these alleles were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-supertypes is approximately 86% in five major ethnic groups. Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%. An analogous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Immunogenicity studies in humans (*e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503, 1997; Doolan *et al.*, *Immunity* 7:97, 1997; and Threlkeld *et al.*, *J. Immunol.* 159:1648, 1997) have shown that highly cross-reactive binding peptides are almost always recognized as epitopes. The use of highly cross-reactive binding peptides is an important selection criterion in identifying candidate epitopes for inclusion in a vaccine that is immunogenic in a diverse population.

With a sufficient number of epitopes (as disclosed herein and from the art), an average population coverage is predicted to be greater than 95% in each of five major ethnic populations. The game theory Monte Carlo simulation analysis, which is known in the art (see *e.g.*, Osborne, M.J. and Rubinstein, A. "A course in game theory" MIT Press, 1994), can be used to estimate what percentage of the individuals in a population comprised of the Caucasian, North American Black, Japanese, Chinese, and Hispanic ethnic groups would recognize the vaccine epitopes described herein. A preferred percentage is 90%. A more preferred percentage is 95%.

Example 19: CTL Recognition Of Endogenously Processed Antigens After Priming

This example confirms that CTL induced by native or analoged peptide epitopes identified and selected as described herein recognize endogenously synthesized, *i.e.*, native antigens.

Effector cells isolated from transgenic mice that are immunized with peptide epitopes, for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ^{51}Cr labeled Jurkat-A2.1/K^{b} target cells in the absence or presence of peptide, and also tested on ^{51}Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with 151P3D4 expression vectors.

The results demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized 151P3D4 antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that are being evaluated. In addition to HLA-A*0201/K^{b} transgenic

mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

<u>Example 20: Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice</u>

This example illustrates the induction of CTLs and HTLs in transgenic mice, by use of a 151P3D4-derived CTL and HTL peptide vaccine compositions. The vaccine composition used herein comprise peptides to be administered to a patient with a 151P3D4-expressing tumor. The peptide composition can comprise multiple CTL and/or HTL epitopes. The epitopes are identified using methodology as described herein. This example also illustrates that enhanced immunogenicity can be achieved by inclusion of one or more HTL epitopes in a CTL vaccine composition; such a peptide composition can comprise an HTL epitope conjugated to a CTL epitope. The CTL epitope can be one that binds to multiple HLA family members at an affinity of 500 nM or less, or analogs of that epitope. The peptides may be lipidated, if desired.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are used to confirm the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-bearing epitopes, and are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline, or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.

Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (*e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991)

<u>In vitro</u> CTL activation: One week after priming, spleen cells ($30x10^6$ cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts ($10x10^6$ cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

Assay for cytotoxic activity: Target cells (1.0 to $1.5x10^6$) are incubated at 37°C in the presence of 200 µl of ^{51}Cr. After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1 µg/ml. For the assay, 10^4 ^{51}Cr-labeled target cells are added to different concentrations of effector cells (final volume of 200 µl) in U-bottom 96-well plates. After a six hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = 100 x (experimental release - spontaneous release)/(maximum release - spontaneous release). To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a six hour ^{51}Cr release assay. To obtain specific lytic units/10^6, the lytic units/10^6 obtained in the absence of peptide is subtracted from the lytic units/10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E):

target (T) ratio of 50:1 (i.e., 5×10^5 effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., 5×10^4 effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000)-(1/500,000)] \times 10^6 = 18$ LU.

The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using, for example, CTL epitopes as outlined above in the Example entitled "Confirmation of Immunogenicity." Analyses similar to this may be performed to confirm the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures, it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

Example 21: Selection of CTL and HTL epitopes for inclusion in a 151P3D4-specific vaccine.

This example illustrates a procedure for selecting peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or can be single and/or polyepitopic peptides.

The following principles are utilized when selecting a plurality of epitopes for inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

Epitopes are selected which, upon administration, mimic immune responses that are correlated with 151P3D4 clearance. The number of epitopes used depends on observations of patients who spontaneously clear 151P3D4. For example, if it has been observed that patients who spontaneously clear 151P3D4-expressing cells generate an immune response to at least three (3) epitopes from 151P3D4 antigen, then at least three epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

Epitopes are often selected that have a binding affinity of an IC_{50} of 500 nM or less for an HLA class I molecule, or for class II, an IC_{50} of 1000 nM or less; or HLA Class I peptides with high binding scores from the BIMAS web site, at URL bimas.dcrt.nih.gov/.

In order to achieve broad coverage of the vaccine through out a diverse population, sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. In one embodiment, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.

When creating polyepitopic compositions, or a minigene that encodes same, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as those employed when selecting a peptide comprising nested epitopes. For example, a protein sequence for the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. Epitopes may be nested or overlapping (*i.e.*, frame shifted relative to one another). For example, with overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. A multi-epitopic, peptide can be

generated synthetically, recombinantly, or via cleavage from the native source. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes. This embodiment provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent the creating of any analogs) directs the immune response to multiple peptide sequences that are actually present in 151P3D4, thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions. Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude to an immune response that controls or clears cells that bear or overexpress 151P3D4.

<u>Example 22: Construction of "Minigene" Multi-Epitope DNA Plasmids</u>

This example discusses the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of B cell, CTL and/or HTL epitopes or epitope analogs as described herein.

A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes. HLA class I supermotif or motif-bearing peptide epitopes derived 151P3D4, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from 151P3D4 to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more HTL epitopes as described in the art, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

The minigene DNA plasmid of this example contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance

with principles disclosed herein. The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

Overlapping oligonucleotides that can, for example, average about 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated Tm of each primer pair) for 30 sec, and 72°C for 1 min.

For example, a minigene is prepared as follows. For a first PCR reaction, 5 μg of each of two oligonucleotides are annealed and extended: In an example using eight oligonucleotides, i.e., four pairs of primers, oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 μl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM $(NH4)_2SO_4$, 20 mM Tris-chloride, pH 8.75, 2 mM $MgSO_4$, 0.1% Triton X-100, 100 μg/ml BSA), 0.25 mM each dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

<u>Example 23: The Plasmid Construct and the Degree to Which It Induces Immunogenicity</u>.

The degree to which a plasmid construct, for example a plasmid constructed in accordance with the previous Example, is able to induce immunogenicity is confirmed *in vitro* by determining epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines "antigenicity" and allows the use of human APC. The assay determines the ability of the epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.*, Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated by measuring the amount of lysis or lymphokine release induced by diseased or transfected target cells, and then determining the concentration of peptide necessary to obtain equivalent levels of lysis or lymphokine release (*see, e.g.*, Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).

Alternatively, immunogenicity is confirmed through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analyzed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.*, in Alexander *et al.*, *Immunity* 1:751-761, 1994.

For example, to confirm the capacity of a DNA minigene construct containing at least one HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 μg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA

immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ^{51}Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine.

It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes, whereby it is also found that the minigene elicits appropriate immune responses directed toward the provided epitopes.

To confirm the capacity of a class II epitope-encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitopes that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 μg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4+ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ^{3}H-thymidine incorporation proliferation assay, (*see, e.g.*, Alexander *et al.* Immunity 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in the previous Example, can also be confirmed as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.*, Hanke *et al.*, *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 μg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10^7 pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 μg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an alpha, beta and/or gamma IFN ELISA.

It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes. The use of prime boost protocols in humans is described below in the Example entitled "Induction of CTL Responses Using a Prime Boost Protocol."

Example 24: Peptide Compositions for Prophylactic Uses

Vaccine compositions of the present invention can be used to prevent 151P3D4 expression in persons who are at risk for tumors that bear this antigen. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in the above Examples, which are also selected to target greater than 80% of the population, is administered to individuals at risk for a 151P3D4-associated tumor.

For example, a peptide-based composition is provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freunds Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 µg, generally 100-5,000 µg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against 151P3D4-associated disease.

Alternatively, a composition typically comprising transfecting agents is used for the administration of a nucleic acid-based vaccine in accordance with methodologies known in the art and disclosed herein.

Example 25: Polyepitopic Vaccine Compositions Derived from Native 151P3D4 Sequences

A native 151P3D4 polyprotein sequence is analyzed, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify "relatively short" regions of the polyprotein that comprise multiple epitopes. The "relatively short" regions are preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct or overlapping, "nested" epitopes can be used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The "relatively short" peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping (*i.e.*, frame shifted relative to one another). For example, with overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

The vaccine composition will include, for example, multiple CTL epitopes from 151P3D4 antigen and at least one HTL epitope. This polyepitopic native sequence is administered either as a peptide or as a

nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally, such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup(s) that is presently unknown. Furthermore, this embodiment (excluding an analoged embodiment) directs the immune response to multiple peptide sequences that are actually present in native 151P3D4, thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing peptide or nucleic acid vaccine compositions.

Related to this embodiment, computer programs are available in the art which can be used to identify in a target sequence, the greatest number of epitopes per sequence length.

<u>Example 26: Polyepitopic Vaccine Compositions From Multiple Antigens</u>

The 151P3D4 peptide epitopes of the present invention are used in conjunction with epitopes from other target tumor-associated antigens, to create a vaccine composition that is useful for the prevention or treatment of cancer that expresses 151P3D4 and such other antigens. For example, a vaccine composition can be provided as a single polypeptide that incorporates multiple epitopes from 151P3D4 as well as tumor-associated antigens that are often expressed with a target cancer associated with 151P3D4 expression, or can be administered as a composition comprising a cocktail of one or more discrete epitopes. Alternatively, the vaccine can be administered as a minigene construct or as dendritic cells which have been loaded with the peptide epitopes *in vitro*.

<u>Example 27: Use of peptides to evaluate an immune response</u>

Peptides of the invention may be used to analyze an immune response for the presence of specific antibodies, CTL or HTL directed to 151P3D4. Such an analysis can be performed in a manner described by Ogg *et al., Science* 279:2103-2106, 1998. In this Example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, 151P3D4 HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of disease or following immunization comprising a 151P3D4 peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al., N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5' triphosphate and magnesium. Streptavidin-

phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300g for 5 minutes and resuspended in 50 μl of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive non-diseased donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the 151P3D4 epitope, and thus the status of exposure to 151P3D4, or exposure to a vaccine that elicits a protective or therapeutic response.

Example 28: Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from 151P3D4-associated disease or who have been vaccinated with a 151P3D4 vaccine.

For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any 151P3D4 vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 μg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 μg/ml to each well and HBV core 128-140 epitope is added at 1 μg/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4 x 10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 μl/well of complete RPMI. On days 3 and 10, 100 μl of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with non-diseased control subjects as previously described (Rehermann, *et al., Nature Med.* 2:1104,1108, 1996; Rehermann *et al., J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al. J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al. J. Virol.* 66:2670-2678, 1992).

Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 μM, and labeled with 100 μCi of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

Cytolytic activity is determined in a standard 4-h, split well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: 100 x [(experimental release-spontaneous release)/maximum release-spontaneous release)]. Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to 151P3D4 or a 151P3D4 vaccine.

Similarly, Class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of $1.5x10^5$ cells/well and are stimulated with 10 μg/ml synthetic peptide of the invention, whole 151P3D4 antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 μCi ^{3}H-thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for ^{3}H-thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^{3}H-thymidine incorporation in the presence of antigen divided by the ^{3}H-thymidine incorporation in the absence of antigen.

Example 29: Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

A total of about 27 individuals are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μg of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the

intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

The vaccine is found to be both safe and efficacious.

Example 30: Phase II Trials In Patients Expressing 151P3D4

Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to patients having cancer that expresses 151P3D4. The main objectives of the trial are to determine an effective dose and regimen for inducing CTLs in cancer patients that express 151P3D4, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of these patients, as manifested, e.g., by the reduction and/or shrinking of lesions. Such a study is designed, for example, as follows:

The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65 and represent diverse ethnic backgrounds. All of them have a tumor that expresses 151P3D4.

Clinical manifestations or antigen-specific T-cell responses are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of 151P3D4-associated disease.

Example 31: Induction of CTL Responses Using a Prime Boost Protocol

A prime boost protocol similar in its underlying principle to that used to confirm the efficacy of a DNA vaccine in transgenic mice, such as described above in the Example entitled "The Plasmid Construct and the Degree to Which It Induces Immunogenicity," can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

For example, the initial immunization may be performed using an expression vector, such as that constructed in the Example entitled "Construction of "Minigene" Multi-Epitope DNA Plasmids" in the form

of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be recombinant fowlpox virus administered at a dose of $5\text{-}10^7$ to $5\text{x}10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Analysis of the results indicates that a magnitude of response sufficient to achieve a therapeutic or protective immunity against 151P3D4 is generated.

<u>Example 32: Administration of Vaccine Compositions Using Dendritic Cells (DC)</u>

Vaccines comprising peptide epitopes of the invention can be administered using APCs, or "professional" APCs such as DC. In this example, peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction, respectively, of the target cells that bear the 151P3D4 protein from which the epitopes in the vaccine are derived.

For example, a cocktail of epitope-comprising peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides, and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (*see, e.g., Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although 2-50 x 10^6 DC per patient are typically administered, larger number of DC, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% DC.

In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC generated after treatment with an agent such as Progenipoietin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10}. Generally, the cell doses injected into patients is based on the percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoietin™ mobilizes 2% DC in the peripheral blood of a given patient, and that patient is to receive 5 x 10^6 DC, then the patient will be injected with a total of 2.5 x 10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoietin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

Ex vivo activation of CTL/HTL responses

Alternatively, *ex vivo* CTL or HTL responses to 151P3D4 antigens can be induced by incubating, in tissue culture, the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and immunogenic peptides. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cells, *i.e.*, tumor cells.

Example 33: An Alternative Method of Identifying and Confirming Motif-Bearing Peptides

Another method of identifying and confirming motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing have been extensively characterized to determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can be transfected with nucleic acids that express the antigen of interest, *e.g.* 151P3D4. Peptides produced by endogenous antigen processing of peptides produced as a result of transfection will then bind to HLA molecules within the cell and be transported and displayed on the cell's surface. Peptides are then eluted from the HLA molecules by exposure to mild acid conditions and their amino acid sequence determined, *e.g.*, by mass spectral analysis (*e.g.*, Kubo *et al.*, *J. Immunol.* 152:3913, 1994). Because the majority of peptides that bind a particular HLA molecule are motif-bearing, this is an alternative modality for obtaining the motif-bearing peptides correlated with the particular HLA molecule expressed on the cell.

Alternatively, cell lines that do not express endogenous HLA molecules can be transfected with an expression construct encoding a single HLA allele. These cells can then be used as described, *i.e.*, they can then be transfected with nucleic acids that encode 151P3D4 to isolate peptides corresponding to 151P3D4 that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

Example 34: Complementary Polynucleotides

Sequences complementary to the 151P3D4-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring 151P3D4. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using, e.g., OLIGO 4.06 software (National Biosciences) and the coding sequence of 151P3D4. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to a 151P3D4-encoding transcript.

Example 35: Purification of Naturally-occurring or Recombinant 151P3D4 Using 151P3D4-Specific Antibodies

Naturally occurring or recombinant 151P3D4 is substantially purified by immunoaffinity chromatography using antibodies specific for 151P3D4. An immunoaffinity column is constructed by covalently coupling anti-151P3D4 antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing 151P3D4 are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of 151P3D4 (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/151P3D4 binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and GCR.P is collected.

Example 36: Identification of Molecules Which Interact with 151P3D4

151P3D4, or biologically active fragments thereof, are labeled with 121 1 Bolton-Hunter reagent. (See, e.g., Bolton *et al.* (1973) Biochem. J. 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled 151P3D4, washed, and any wells with labeled 151P3D4 complex are assayed. Data obtained using different concentrations of 151P3D4 are used to calculate values for the number, affinity, and association of 151P3D4 with the candidate molecules.

Example 37: *In Vivo* Assay for 151P3D4 Tumor Growth Promotion

The effect of the 151P3D4 protein on tumor cell growth is evaluated *in vivo* by evaluating tumor development and growth of cells expressing or lacking 151P3D4. For example, SCID mice are injected subcutaneously on each flank with 1×10^6 of either 3T3, bladder, kidney or ovary cancer cell lines (e.g. SCABER, J82, PA-1, CaOv3, A498 or 769P cells) containing tkNeo empty vector or 151P3D4. At least two strategies may be used: (1) Constitutive 151P3D4 expression under regulation of a promoter such as a constitutive promoter obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), or from heterologous mammalian promoters, *e.g.*, the actin promoter or an immunoglobulin promoter, provided such promoters are compatible with the host cell systems, and (2) Regulated expression under control of an inducible vector system, such as ecdysone, tetracycline, etc., provided such promoters are compatible with the host cell systems. Tumor volume is then monitored by caliper measurement at the appearance of palpable tumors and followed over time to determine if 151P3D4-expressing cells grow at a faster rate and whether tumors produced by 151P3D4-expressing cells demonstrate characteristics of altered aggressiveness (e.g. enhanced metastasis, vascularization, reduced responsiveness to chemotherapeutic drugs).

Additionally, mice can be implanted with 1×10^5 of the same cells orthotopically to determine if 151P3D4 has an effect on local growth in the bladder, kidney or ovary, and whether 151P3D4 affects the

ability of the cells to metastasize, specifically to lymph nodes, adrenal, liver and bone (Miki T et al, Oncol Res. 2001;12:209; Fu X et al, Int J Cancer. 1991, 49:938; Kiguchi Ket al, Clin Exp Metastasis. 1998, 16:751).

The assay is also useful to determine the 151P3D4 inhibitory effect of candidate therapeutic compositions, such as for example, 151P3D4 intrabodies, 151P3D4 antisense molecules and ribozymes.

<u>**Example 38: 151P3D4 Monoclonal Antibody-mediated Inhibition of Bladder, Kidney and Ovarian Tumors *In Vivo***</u>

The significant expression of 151P3D4 in cancer tissues, together with its restrictive expression in normal tissues makes 151P3D4 a good target for antibody therapy. Similarly, 151P3D4 is a target for T cell-based immunotherapy. Thus, the therapeutic efficacy of anti-151P3D4 mAbs in human bladder cancer xenograft mouse models is evaluated by using recombinant cell lines such as SCABER-151P3D4, J82-151P3D4, and 3T3-151P3D4 (see, e.g., Kaighn, M.E., *et al.*, Invest Urol, 1979. **17**(1): p. 16-23). Similarly, anti-151P3D4 mAbs are evaluated in human kidney and ovarian cancer xenograft models using recombinant cell lines such as A498-151P3D4 and PA1-151P3D4.

Antibody efficacy on tumor growth and metastasis formation is studied, e.g., in a mouse orthotopic bladder cancer xenograft model, a mouse kidney cancer xenograft model and a mouse ovarian cancer xenograft model. The antibodies can be unconjugated, as discussed in this Example, or can be conjugated to a therapeutic modality, as appreciated in the art. Anti-151P3D4 mAbs inhibit formation of kidney, ovarian and bladder xenografts. Anti-151P3D4 mAbs also retard the growth of established orthotopic tumors and prolonged survival of tumor-bearing mice. These results indicate the utility of anti-151P3D4 mAbs in the treatment of local and advanced stages of ovarian, kidney and bladder cancer. (See, e.g., Saffran, D., et al., PNAS 10:1073-1078 or www.pnas.org/cgi/doi/10.1073/pnas.051624698).

Administration of the anti-151P3D4 mAbs led to retardation of established orthotopic tumor growth and inhibition of metastasis to distant sites, resulting in a significant prolongation in the survival of tumor-bearing mice. These studies indicate that 151P3D4 as an attractive target for immunotherapy and demonstrate the therapeutic potential of anti-151P3D4 mAbs for the treatment of local and metastatic cancer. This example demonstrates that unconjugated 151P3D4 monoclonal antibodies are effective to inhibit the growth of human bladder, kidney and ovarian tumor xenografts grown in SCID mice; accordingly a combination of such efficacious monoclonal antibodies is also effective.

Tumor inhibition using multiple unconjugated 151P3D4 mAbs

Materials and Methods

<u>151P3D4 Monoclonal Antibodies:</u>

Monoclonal antibodies are raised against 151P3D4 as described in the Example entitled "Generation of 151P3D4 Monoclonal Antibodies (mAbs)." The antibodies are characterized by ELISA, Western blot, FACS, and immunoprecipitation for their capacity to bind 151P3D4. Epitope mapping data for the anti-151P3D4 mAbs, as determined by ELISA and Western analysis, recognize epitopes on the 151P3D4 protein. Immunohistochemical analysis of prostate cancer tissues and cells with these antibodies is performed.

The monoclonal antibodies are purified from ascites or hybridoma tissue culture supernatants by Protein-G Sepharose chromatography, dialyzed against PBS, filter sterilized, and stored at -20°C. Protein determinations are performed by a Bradford assay (Bio-Rad, Hercules, CA). A therapeutic monoclonal antibody or a cocktail comprising a mixture of individual monoclonal antibodies is prepared and used for the treatment of mice receiving subcutaneous or orthotopic injections of SCABER, J82, A498, 769P, CaOv1 or PA1 tumor xenografts.

Cell Lines

The bladder, kidney and ovary carcinoma cell lines, SCABER, J82, A498, 769P, CaOv1 and PA1 as well as the fibroblast line NIH 3T3 (American Type Culture Collection) are maintained in DMEM supplemented with L-glutamine and 10% FBS.

A SCABER-151P3D4, J82-151P3D4, A498-151P3D4, 769P-151P3D4, CaOv1-151P3D4, PA1-151P3D4 and 3T3-151P3D4 cell populations are generated by retroviral gene transfer as described in Hubert, R.S., et al., Proc Natl Acad Sci U S A, 1999. 96(25): 14523.

Xenograft Mouse Models.

Subcutaneous (s.c.) tumors are generated by injection of 1 x 10^6 cancer cells mixed at a 1:1 dilution with Matrigel (Collaborative Research) in the right flank of male SCID mice. To test antibody efficacy on tumor formation, i.p. antibody injections are started on the same day as tumor-cell injections. As a control, mice are injected with either purified mouse IgG (ICN) or PBS; or a purified monoclonal antibody that recognizes an irrelevant antigen not expressed in human cells. Tumor sizes are determined by caliper measurements, and the tumor volume is calculated as: Length x Width x Height. Mice with s.c. tumors greater than 1.5 cm in diameter are sacrificed.

Orthotopic injections are performed under anesthesia by using ketamine/xylazine. For bladder orthotopic studies, an incision is made through the abdomen to expose the bladder, and tumor cells (5 x 10^5) mixed with Matrigel are injected into the bladder wall in a 10-µl volume. To monitor tumor growth, mice are palpated and blood is collected on a weekly basis to measure BTA levels. For kidney and ovary orthopotic models, an incision is made through the abdominal muscles to expose the kidney or the ovary. Tumor cells mixed with Matrigel are injected under the kidney capsule or into the ovary in a 10-µl volume (Yoshida Y et al, Anticancer Res. 1998, 18:327; Ahn et al, Tumour Biol. 2001, 22:146). To monitor tumor growth, blood is collected on a weekly basis measuring G250 and SM047 levels. The mice are segregated into groups for the appropriate treatments, with anti-151P3D4 or control mAbs being injected i.p.

Anti-151P3D4 mAbs Inhibit Growth of 151P3D4-Expressing Xenograft-Cancer Tumors

The effect of anti-151P3D4 mAbs on tumor formation is tested on the growth and progression of bladder, kidney and ovarian cancer xenografts using UC3-151P3D4, J82-151P3D4, A498-151P3D4, 769P-151P3D4, CaOv1-151P3D4 and PA1-151P3D4 orthotopic models. As compared with the s.c. tumor model, the orthotopic model, which requires injection of tumor cells directly in the mouse bladder, kidney and ovary, respectively, results in a local tumor growth, development of metastasis in distal sites, deterioration of mouse health, and subsequent death (Saffran, D., et al., PNAS supra; Fu, X., et al., Int J Cancer, 1992. 52(6): p. 987-90; Kubota, T., J Cell Biochem, 1994. 56(1): p. 4-8). The features make the orthotopic model more

representative of human disease progression and allowed us to follow the therapeutic effect of mAbs on clinically relevant end points.

Accordingly, tumor cells are injected into the mouse bladder, kidney or ovary, and 2 days later, the mice are segregated into two groups and treated with either: a) 200-500μg, of anti-151P3D4 Ab, or b) PBS three times per week for two to five weeks.

A major advantage of the orthotopic cancer models is the ability to study the development of metastases. Formation of metastasis in mice bearing established orthotopic tumors is studies by IHC analysis on lung sections using an antibody against a tumor-specific cell-surface protein such as anti-CK20 for bladder cancer, anti-G250 for kidney cancer and SM047 antibody for ovarian cancer models (Lin S et al, Cancer Detect Prev. 2001;25:202; McCluggage W et al, Histopathol 2001, 38:542).

Mice bearing established orthotopic tumors are administered 1000μg injections of either anti-151P3D4 mAb or PBS over a 4-week period. Mice in both groups are allowed to establish a high tumor burden, to ensure a high frequency of metastasis formation in mouse lungs. Mice then are killed and their bladders, livers, bone and lungs are analyzed for the presence of tumor cells by IHC analysis.

These studies demonstrate a broad anti-tumor efficacy of anti-151P3D4 antibodies on initiation and progression of prostate and kidney cancer in xenograft mouse models. Anti-151P3D4 antibodies inhibit tumor formation of tumors as well as retarding the growth of already established tumors and prolong the survival of treated mice. Moreover, anti-151P3D4 mAbs demonstrate a dramatic inhibitory effect on the spread of local bladder, kidney and ovarian tumor to distal sites, even in the presence of a large tumor burden. Thus, anti-151P3D4 mAbs are efficacious on major clinically relevant end points (tumor growth), prolongation of survival, and health.

Example 39: Therapeutic and Diagnostic use of Anti-151P3D4 Antibodies in Humans.

Anti-151P3D4 monoclonal antibodies are safely and effectively used for diagnostic, prophylactic, prognostic and/or therapeutic purposes in humans. Western blot and immunohistochemical analysis of cancer tissues and cancer xenografts with anti-151P3D4 mAb show strong extensive staining in carcinoma but significantly lower or undetectable levels in normal tissues. Detection of 151P3D4 in carcinoma and in metastatic disease demonstrates the usefulness of the mAb as a diagnostic and/or prognostic indicator. Anti-151P3D4 antibodies are therefore used in diagnostic applications such as immunohistochemistry of kidney biopsy specimens to detect cancer from suspect patients.

As determined by flow cytometry, anti-151P3D4 mAb specifically binds to carcinoma cells. Thus, anti-151P3D4 antibodies are used in diagnostic whole body imaging applications, such as radioimmunoscintigraphy and radioimmunotherapy, (see, e.g., Potamianos S., et. al. Anticancer Res 20(2A):925-948 (2000)) for the detection of localized and metastatic cancers that exhibit expression of 151P3D4. Shedding or release of an extracellular domain of 151P3D4 into the extracellular milieu, such as that seen for alkaline phosphodiesterase B10 (Meerson, N. R., Hepatology 27:563-568 (1998)), allows diagnostic detection of 151P3D4 by anti-151P3D4 antibodies in serum and/or urine samples from suspect patients.

Anti-151P3D4 antibodies that specifically bind 151P3D4 are used in therapeutic applications for the treatment of cancers that express 151P3D4. Anti-151P3D4 antibodies are used as an unconjugated modality and as conjugated form in which the antibodies are attached to one of various therapeutic or imaging modalities well known in the art, such as a prodrugs, enzymes or radioisotopes. In preclinical studies, unconjugated and conjugated anti-151P3D4 antibodies are tested for efficacy of tumor prevention and growth inhibition in the SCID mouse cancer xenograft models, e.g., kidney cancer models AGS-K3 and AGS-K6, (see, e.g., the Example entitled "151P3D4 Monoclonal Antibody-mediated Inhibition of Bladder and Lung Tumors *In Vivo*"). Conjugated and unconjugated anti-151P3D4 antibodies are used as a therapeutic modality in human clinical trials either alone or in combination with other treatments as described in following Examples.

Example 40: Human Clinical Trials for the Treatment and Diagnosis of Human Carcinomas through use of Human Anti-151P3D4 Antibodies *In vivo*

Antibodies are used in accordance with the present invention which recognize an epitope on 151P3D4, and are used in the treatment of certain tumors such as those listed in Table I. Based upon a number of factors, including 151P3D4 expression levels, tumors such as those listed in Table I are presently preferred indications. In connection with each of these indications, three clinical approaches are successfully pursued.

I.) Adjunctive therapy: In adjunctive therapy, patients are treated with anti-151P3D4 antibodies in combination with a chemotherapeutic or antineoplastic agent and/or radiation therapy. Primary cancer targets, such as those listed in Table I, are treated under standard protocols by the addition anti-151P3D4 antibodies to standard first and second line therapy. Protocol designs address effectiveness as assessed by reduction in tumor mass as well as the ability to reduce usual doses of standard chemotherapy. These dosage reductions allow additional and/or prolonged therapy by reducing dose-related toxicity of the chemotherapeutic agent. Anti-151P3D4 antibodies are utilized in several adjunctive clinical trials in combination with the chemotherapeutic or antineoplastic agents adriamycin (advanced prostrate carcinoma), cisplatin (advanced head and neck and lung carcinomas), taxol (breast cancer), and doxorubicin (preclinical).

II.) Monotherapy: In connection with the use of the anti-151P3D4 antibodies in monotherapy of tumors, the antibodies are administered to patients without a chemotherapeutic or antineoplastic agent. In one embodiment, monotherapy is conducted clinically in end stage cancer patients with extensive metastatic disease. Patients show some disease stabilization. Trials demonstrate an effect in refractory patients with cancerous tumors.

III.) Imaging Agent: Through binding a radionuclide (e.g., iodine or yttrium (I^{131}, Y^{90}) to anti-151P3D4 antibodies, the radiolabeled antibodies are utilized as a diagnostic and/or imaging agent. In such a role, the labeled antibodies localize to both solid tumors, as well as, metastatic lesions of cells expressing 151P3D4. In connection with the use of the anti-151P3D4 antibodies as imaging agents, the antibodies are used as an adjunct to surgical treatment of solid tumors, as both a pre-surgical screen as well as a post-operative follow-up to determine what tumor remains and/or returns. In one embodiment, a (^{111}In)-151P3D4 antibody is used as an imaging agent in a Phase I human clinical trial in patients having a carcinoma that

expresses 151P3D4 (by analogy see, *e.g.*, Divgi *et al. J. Natl. Cancer Inst.* 83:97-104 (1991)). Patients are followed with standard anterior and posterior gamma camera. The results indicate that primary lesions and metastatic lesions are identified

Dose and Route of Administration

As appreciated by those of ordinary skill in the art, dosing considerations can be determined through comparison with the analogous products that are in the clinic. Thus, anti-151P3D4 antibodies can be administered with doses in the range of 5 to 400 mg/m^2, with the lower doses used, e.g., in connection with safety studies. The affinity of anti-151P3D4 antibodies relative to the affinity of a known antibody for its target is one parameter used by those of skill in the art for determining analogous dose regimens. Further, anti-151P3D4 antibodies that are fully human antibodies, as compared to the chimeric antibody, have slower clearance; accordingly, dosing in patients with such fully human anti-151P3D4 antibodies can be lower, perhaps in the range of 50 to 300 mg/m^2, and still remain efficacious. Dosing in mg/m^2, as opposed to the conventional measurement of dose in mg/kg, is a measurement based on surface area and is a convenient dosing measurement that is designed to include patients of all sizes from infants to adults.

Three distinct delivery approaches are useful for delivery of anti-151P3D4 antibodies. Conventional intravenous delivery is one standard delivery technique for many tumors. However, in connection with tumors in the peritoneal cavity, such as tumors of the ovaries, biliary duct, other ducts, and the like, intraperitoneal administration may prove favorable for obtaining high dose of antibody at the tumor and to also minimize antibody clearance. In a similar manner, certain solid tumors possess vasculature that is appropriate for regional perfusion. Regional perfusion allows for a high dose of antibody at the site of a tumor and minimizes short term clearance of the antibody.

Clinical Development Plan (CDP)

Overview: The CDP follows and develops treatments of anti-151P3D4 antibodies in connection with adjunctive therapy, monotherapy, and as an imaging agent. Trials initially demonstrate safety and thereafter confirm efficacy in repeat doses. Trails are open label comparing standard chemotherapy with standard therapy plus anti-151P3D4 antibodies. As will be appreciated, one criteria that can be utilized in connection with enrollment of patients is 151P3D4 expression levels in their tumors as determined by biopsy.

As with any protein or antibody infusion-based therapeutic, safety concerns are related primarily to (i) cytokine release syndrome, i.e., hypotension, fever, shaking, chills; (ii) the development of an immunogenic response to the material (i.e., development of human antibodies by the patient to the antibody therapeutic, or HAHA response); and, (iii) toxicity to normal cells that express 151P3D4. Standard tests and follow-up are utilized to monitor each of these safety concerns. Anti-151P3D4 antibodies are found to be safe upon human administration.

Example 41: Human Clinical Trial Adjunctive Therapy with Human Anti-151P3D4 Antibody and Chemotherapeutic Agent

A phase I human clinical trial is initiated to assess the safety of six intravenous doses of a human anti-151P3D4 antibody in connection with the treatment of a solid tumor, e.g., a cancer of a tissue listed in

Table I. In the study, the safety of single doses of anti-151P3D4 antibodies when utilized as an adjunctive therapy to an antineoplastic or chemotherapeutic agent, such as cisplatin, topotecan, doxorubicin, adriamycin, taxol, or the like, is assessed. The trial design includes delivery of six single doses of an anti-151P3D4 antibody with dosage of antibody escalating from approximately about 25 mg/m ^{2} to about 275 mg/m ^{2} over the course of the treatment in accordance with the following schedule:

	Day 0	Day 7	Day 14	Day 21	Day 28	Day 35
mAb Dose	25 mg/m ^{2}	75 mg/m ^{2}	125 mg/m ^{2}	175 mg/m ^{2}	225 mg/m ^{2}	275 mg/m ^{2}
Chemotherapy (standard dose)	+	+	+	+	+	+

Patients are closely followed for one-week following each administration of antibody and chemotherapy. In particular, patients are assessed for the safety concerns mentioned above: (i) cytokine release syndrome, i.e., hypotension, fever, shaking, chills; (ii) the development of an immunogenic response to the material (i.e., development of human antibodies by the patient to the human antibody therapeutic, or HAHA response); and, (iii) toxicity to normal cells that express 151P3D4. Standard tests and follow-up are utilized to monitor each of these safety concerns. Patients are also assessed for clinical outcome, and particularly reduction in tumor mass as evidenced by MRI or other imaging.

The anti-151P3D4 antibodies are demonstrated to be safe and efficacious, Phase II trials confirm the efficacy and refine optimum dosing.

Example 42: Human Clinical Trial: Monotherapy with Human Anti-151P3D4 Antibody

Anti-151P3D4 antibodies are safe in connection with the above-discussed adjunctive trial, a Phase II human clinical trial confirms the efficacy and optimum dosing for monotherapy. Such trial is accomplished, and entails the same safety and outcome analyses, to the above-described adjunctive trial with the exception being that patients do not receive chemotherapy concurrently with the receipt of doses of anti-151P3D4 antibodies.

Example 43: Human Clinical Trial: Diagnostic Imaging with Anti-151P3D4 Antibody

Once again, as the adjunctive therapy discussed above is safe within the safety criteria discussed above, a human clinical trial is conducted concerning the use of anti-151P3D4 antibodies as a diagnostic imaging agent. The protocol is designed in a substantially similar manner to those described in the art, such as in Divgi *et al. J. Natl. Cancer Inst.* 83:97-104 (1991). The antibodies are found to be both safe and efficacious when used as a diagnostic modality.

Example 44: Homology Comparison of 151P3D4 to Known Sequences

Two variants of 151P3D4 have been identified, 151P3D4 v.1 and v 2. The 151P3D4 v.1 gene exhibits strong homology to a previously cloned gene, namely the human cartilage linking protein 1 (gi 4503053), and shows 100% identity to that gene over the entire length of the protein (Figure 4B). In addition, the 151P3D4 v.1 protein shows homology to the bovine and rat homologs of the human cartilage linking protein (gi 1709660 and gi 9506519) (Figures 4F and 4G). 151P3D4 v.1 is a 354 aa protein which localizes primarily to the extracellular compartment (see Table XXI). The second variant, 151P3D4 v.2, is a 721 aa protein, that shares identity with 151P3D4 v.1 over 200 amino acids (Table LV and Figure 4D). The 151P3D4 v.2 gene also exhibits homology to the human cartilage link protein-1 (gi 4503053), showing 99% identity and 99% homology to that protein (Figure 4H). However, this homology between variant 2 and cartilage link protein does not extend over the entire length of variant 2, but is limited to the last 400 aa of that protein. The first 400 aa of 151P3D4 v.2 show homology to human ribosomal protein L13a of the 60S subunit (gi. 18574549) (see Table XXI). Besides the addition of 400 aa at its N-terminus, 151P3D4 v.2 also differs from variant 1 in its localization profile. 151P3D4 v.2 localizes to the cytosol, with potential localization to the nucleus (see Table XXI). Motif analysis revealed the presence of link motif as well as immunoglobulin domain in both 151P3D4 variants (see Table XXI).

Cartilage link protein-1, a protein with a known link motif, has been shown to regulate tissue remodeling, bone resorption and protein interaction (Chen Q et al. Dev Biol. 1995, 172:293). The importance of cartilage link protein 1 is illustrated in engineered mice lacking cartilage link protein (Watanabe H, Yamada Y. Nat Genet. 1999, 21:225). These mutant mice demonstrate defects in cartilage and bone development. The cartilage link protein, via its link motif, mediates cell adhesion of fibroblasts and other cells to extracellular matrix (Yang B et al, Matrix Biol. 1998, 16:541). The link motif is a binding domain for hyaluronic acid (Kohda D et al, Cell. 1996, 86:767), with a structure very similar to type C-lectin. It plays a role in the assembly of extracellular matrix, cell adhesion, and migration (Kohda D et al, Cell. 1996, 86:767). The immunoglobulin domain is a 100 aa long motif which includes a conserved intra-domain disulfide bond. Immunoglobulin-like domains participate in protein interactions (Wang J, Springer TA. Immunol Rev. 1998, 163:197).

The presence of an immunoglobulin motif and a link motif indicate that 151P3D4 regulates protein interactions and participates in the process of cell adhesion, cell migration, tumor formation and progression. By way of its protein interaction domain, 151P3D4 functions in regulating signal transduction in mammalian cells, thereby regulating gene expression and cellular outcomes, including cell proliferation, survival, invasion, motility, etc, all of which have a direct effect on tumor growth and progression.

Accordingly, when 151P3D4 functions as a regulator of protein interactions, cell adhesion, tumor formation, invasion or cell signaling, 151P3D4 is used for therapeutic, diagnostic, prognostic and/or preventative purposes. In addition, when a variant of 151P3D4 is expressed in cancerous tissues, such as those listed in Table I, they are used for therapeutic, diagnostic, prognostic and/or preventative purposes.

Example 45: Regulation of Transcription

The localization of 151P3D4 coupled to the presence of protein interaction domains within its sequence, indicate that 151P3D4 modulates the transcriptional regulation of eukaryotic genes. Regulation of gene expression is confirmed, e.g., by studying gene expression in cells expressing or lacking 151P3D4. For this purpose, two types of experiments are performed.

In the first set of experiments, RNA from parental and 151P3D4-expressing cells are extracted and hybridized to commercially available gene arrays (Clontech) (Smid-Koopman E et al. Br J Cancer. 2000. 83:246). Resting cells as well as cells treated with FBS, androgen or growth factors are compared. Differentially expressed genes are identified in accordance with procedures known in the art. The differentially expressed genes are then mapped to biological pathways (Chen K et al. Thyroid. 2001. 11:41.).

In the second set of experiments, specific transcriptional pathway activation is evaluated using commercially available (Stratagene) luciferase reporter constructs including: NFkB-luc, SRE-luc, ELK1-luc, ARE-luc, p53-luc, and CRE-luc. These transcriptional reporters contain consensus binding sites for known transcription factors that lie downstream of well-characterized signal transduction pathways, and represent a good tool to ascertain pathway activation and screen for positive and negative modulators of pathway activation.

Thus, 151P3D4 plays a role in gene regulation, and it is used as a target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 46: Identification and Confirmation of Potential Signal Transduction Pathways

Many mammalian proteins have been reported to interact with signaling molecules and to participate in regulating signaling pathways. (J Neurochem. 2001; 76:217-223). In particular, protein interaction motifs have been instrumental in inducing kinase activation, recruitment of proteins and complex formation (Samelson L. Annu Rev Immunol. 2002;20:371). Based on the presence of a protein interacton motif, 151P3D4 regulates signaling pathways important for cell growth and invasion. In addition, the 151P3D4 protein contains several phosphorylation sites (see Table XX) indicating an association with specific signaling cascades. Using immunoprecipitation and Western blotting techniques, proteins are identified that associate with 151P3D4 and mediate signaling events. Several pathways known to play a role in cancer biology can be regulated by 151P3D4, including phospholipid pathways such as PI3K, AKT, etc, adhesion and migration pathways, including FAK, Rho, Rac-1, β–catenin, etc, as well as mitogenic/survival cascades such as ERK, p38, etc (Cell Growth Differ. 2000,11:279; J Biol Chem. 1999, 274:801; Oncogene. 2000, 19:3003, J. Cell Biol. 1997, 138:913.).

To confirm that 151P3D4 directly or indirectly activates known signal transduction pathways in cells, luciferase (luc) based transcriptional reporter assays are carried out in cells expressing individual genes. These transcriptional reporters contain consensus-binding sites for known transcription factors that lie downstream of well-characterized signal transduction pathways. The reporters and examples of these associated transcription factors, signal transduction pathways, and activation stimuli are listed below.

1. NFkB-luc, NFkB/Rel; Ik-kinase/SAPK; growth/apoptosis/stress
2. SRE-luc, SRF/TCF/ELK1; MAPK/SAPK; growth/differentiation
3. AP-1-luc, FOS/JUN; MAPK/SAPK/PKC; growth/apoptosis/stress
4. ARE-luc, androgen receptor; steroids/MAPK; growth/differentiation/apoptosis
5. p53-luc, p53; SAPK; growth/differentiation/apoptosis
6. CRE-luc, CREB/ATF2; PKA/p38; growth/apoptosis/stress
7. TCF-luc, TCF/Lef; β-catenin, Adhesion/invasion

Gene-mediated effects can be assayed in cells showing mRNA expression. Luciferase reporter plasmids can be introduced by lipid-mediated transfection (TFX-50, Promega). Luciferase activity, an indicator of relative transcriptional activity, is measured by incubation of cell extracts with luciferin substrate and luminescence of the reaction is monitored in a luminometer.

Signaling pathways activated by 151P3D4 are mapped and used for the identification and validation of therapeutic targets. When 151P3D4 is involved in cell signaling, it is used as target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 47: Involvement in Tumor Progression

Based on the role of link motif in cell adhesion, cell migration and tumor formation, the 151P3D4 gene can contribute to tumor initiation and progression. The role of 151P3D4 in tumor growth is confirmed in a variety of primary and transfected cell lines including bladder, kidney and ovary cell lines, as well as NIH 3T3 cells engineered to stably express 151P3D4. Parental cells lacking 151P3D4 and cells expressing 151P3D4 are evaluated for cell growth using a well-documented proliferation assay (Fraser SP, Grimes JA, Djamgoz MB. Prostate. 2000;44:61, Johnson DE, Ochieng J, Evans SL. Anticancer Drugs. 1996, 7:288).

To confirm the role of 151P3D4 in the transformation process, its effect in colony forming assays is investigated. Parental NIH-3T3 cells lacking 151P3D4 are compared to NIH-3T3 cells expressing 151P3D4, using a soft agar assay under stringent and more permissive conditions (Song Z. et al. Cancer Res. 2000;60:6730).

To confirm the role of 151P3D4 in invasion and metastasis of cancer cells, a well-established assay is used, e.g., a Transwell Insert System assay (Becton Dickinson) (Cancer Res. 1999; 59:6010). Control cells, including bladder, ovary and kidney cell lines lacking 151P3D4 are compared to cells expressing 151P3D4. Cells are loaded with the fluorescent dye, calcein, and plated in the top well of the Transwell insert coated with a basement membrane analog. Invasion is determined by fluorescence of cells in the lower chamber relative to the fluorescence of the entire cell population.

151P3D4 can also play a role in cell cycle and apoptosis. Parental cells and cells expressing 151P3D4 are compared for differences in cell cycle regulation using a well-established BrdU assay (Abdel-Malek ZA. J Cell Physiol. 1988, 136:247). In short, cells are grown under both optimal (full serum) and limiting (low serum) conditions are labeled with BrdU and stained with anti-BrdU Ab and propidium iodide. Cells are analyzed for entry into the G1, S, and G2M phases of the cell cycle. Alternatively, the effect of stress on apoptosis is evaluated in control parental cells and cells expressing 151P3D4, including normal and

tumor bladder, kidney and ovary cells. Engineered and parental cells are treated with various chemotherapeutic agents, such as etoposide, taxol, etc, and protein synthesis inhibitors, such as cycloheximide. Cells are stained with annexin V-FITC and cell death is measured by FACS analysis. The modulation of cell death by 151P3D4 can play a critical role in regulating tumor progression and tumor load.

When 151P3D4 plays a role in cell growth, transformation, invasion or apoptosis, it is used as a target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 48: Involvement in Angiogenesis

Angiogenesis or new capillary blood vessel formation is necessary for tumor growth (Hanahan D, Folkman J. Cell. 1996, 86:353; Folkman J. Endocrinology. 1998 139:441). Based on the effect of phsophodieseterase inhibitors on endothelial cells, 151P3D4 plays a role in angiogenesis (DeFouw L et al, Microvasc Res 2001, 62:263). Several assays have been developed to measure angiogenesis *in vitro* and *in vivo*, such as the tissue culture assays endothelial cell tube formation and endothelial cell proliferation. Using these assays as well as *in vitro* neo-vascularization, the role of 151P3D4 in angiogenesis, enhancement or inhibition, is confirmed.

For example, endothelial cells engineered to express 151P3D4 are evaluated using tube formation and proliferation assays. The effect of 151P3D4 is also confirmed in animal models *in vivo*. For example, cells either expressing or lacking 151P3D4 are implanted subcutaneously in immunocompromised mice. Endothelial cell migration and angiogenesis are evaluated 5-15 days later using immunohistochemistry techniques. 151P3D4 affects angiogenesis, and it is used as a target for diagnostic, prognostic, preventative and/or therapeutic purposes

Example 49: Involvement in Protein-Protein Interactions

Link as well as imunoglobulin motifs have been shown to mediate interaction with other proteins, resulting in the formation of a multi-protein complex (). Using immunoprecipitation techniques as well as two yeast hybrid systems, proteins are identified that associate with 151P3D4. Immunoprecipitates from cells expressing 151P3D4 and cells lacking 151P3D4 are compared for specific protein-protein associations.

Studies are performed to confirm the extent of association of 151P3D4 with effector molecules, such as nuclear proteins, transcription factors, kinases, phsophates etc. Studies comparing 151P3D4 positive and 151P3D4 negative cells as well as studies comparing unstimulated/resting cells and cells treated with epithelial cell activators, such as cytokines, growth factors and anti-integrin Ab reveal unique interactions.

In addition, protein-protein interactions are confirmed using two yeast hybrid methodology (Curr Opin Chem Biol. 1999, 3:64). A vector carrying a library of proteins fused to the activation domain of a transcription factor is introduced into yeast expressing a 151P3D4-DNA-binding domain fusion protein and a reporter construct. Protein-protein interaction is detected by colorimetric reporter activity. Specific association with effector molecules and transcription factors directs one of skill to the mode of action of 151P3D4, and thus identifies therapeutic, prognostic, preventative and/or diagnostic targets for cancer. This and similar assays are also used to identify and screen for small molecules that interact with 151P3D4.

Thus it is found that 151P3D4 associates with proteins and small molecules. Accordingly, 151P3D4 and these proteins and small molecules are used for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 50: Involvement in Adhesion

Cell adhesion plays a critical role in tissue colonization and metastasis. The presence of link motif in 151P3D4 is indicative of its role in cell adhesion. To confirm that 151P3D4 plays a role in cell adhesion, control cells lacking 151P3D4 are compared to cells expressing 151P3D4, using techniques previously described (see, e.g., Haier et al, Br. J. Cancer. 1999, 80:1867; Lehr and Pienta, J. Natl. Cancer Inst. 1998, 90:118). Briefly, in one embodiment, cells labeled with a fluorescent indicator, such as calcein, are incubated on tissue culture wells coated with media alone or with matrix proteins. Adherent cells are detected by fluorimetric analysis and percent adhesion is calculated. This experimental system can be used to identify proteins, antibodies and/or small molecules that modulate cell adhesion to extracellular matrix and cell-cell interaction. Since cell adhesion plays a critical role in tumor growth, progression, and, colonization, the gene involved in this process can serves as a diagnostic, preventative and therapeutic modality.

Throughout this application, various website data content, publications, patent applications and patents are referenced. (Websites are referenced by their Uniform Resource Locator, or URL, addresses on the World Wide Web.) The disclosures of each of these references are hereby incorporated by reference herein in their entireties.

The present invention is not to be limited in scope by the embodiments disclosed herein, which are intended as single illustrations of individual aspects of the invention, and any that are functionally equivalent are within the scope of the invention. Various modifications to the models and methods of the invention, in addition to those described herein, will become apparent to those skilled in the art from the foregoing description and teachings, and are similarly intended to fall within the scope of the invention. Such modifications or other embodiments can be practiced without departing from the true scope and spirit of the invention.

TABLE I: Tissues that Express 151P3D4 When Malignant

- Bladder
- Kidney
- Colon
- Lung
- Ovary
- Breast
- Stomach
- Uterus

TABLE II: Amino Acid Abbreviations

SINGLE LETTER	THREE LETTER	FULL NAME
F	Phe	phenylalanine
L	Leu	leucine
S	Ser	serine
Y	Tyr	tyrosine
C	Cys	cysteine
W	Trp	tryptophan
P	Pro	proline
H	His	histidine
Q	Gln	glutamine
R	Arg	arginine
I	Ile	isoleucine
M	Met	methionine
T	Thr	threonine
N	Asn	asparagine
K	Lys	lysine
V	Val	valine
A	Ala	alanine
D	Asp	aspartic acid
E	Glu	glutamic acid
G	Gly	glycine

TABLE III: Amino Acid Substitution Matrix

Adapted from the GCG Software 9.0 BLOSUM62 amino acid substitution matrix (block substitution matrix). The higher the value, the more likely a substitution is found in related, natural proteins. (See URL www.ikp.unibe.ch/manual/blosum62.html)

A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	.
4	0	-2	-1	-2	0	-2	-1	-1	-1	-1	-2	-1	-1	-1	1	0	0	-3	-2	A
	9	-3	-4	-2	-3	-3	-1	-3	-1	-1	-3	-3	-3	-3	-1	-1	-1	-2	-2	C
		6	2	-3	-1	-1	-3	-1	-4	-3	1	-1	0	-2	0	-1	-3	-4	-3	D
			5	-3	-2	0	-3	1	-3	-2	0	-1	2	0	0	-1	-2	-3	-2	E
				6	-3	-1	0	-3	0	0	-3	-4	-3	-3	-2	-2	-1	1	3	F
					6	-2	-4	-2	-4	-3	0	-2	-2	-2	0	-2	-3	-2	-3	G
						8	-3	-1	-3	-2	1	-2	0	0	-1	-2	-3	-2	2	H
							4	-3	2	1	-3	-3	-3	-3	-2	-1	3	-3	-1	I
								5	-2	-1	0	-1	1	2	0	-1	-2	-3	-2	K
									4	2	-3	-3	-2	-2	-2	-1	1	-2	-1	L
										5	-2	-2	0	-1	-1	-1	1	-1	-1	M
											6	-2	0	0	1	0	-3	-4	-2	N
												7	-1	-2	-1	-1	-2	-4	-3	P
													5	1	0	-1	-2	-2	-1	Q
														5	-1	-1	-3	-3	-2	R
															4	1	-2	-3	-2	S
																5	0	-2	-2	T
																	4	-3	-1	V
																		11	2	W
																			7	Y

TABLE IV
HLA Class I/II Motifs/Supermotifs

TABLE IV (A): HLA Class I Supermotifs/Motifs

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	**TI***LVMS*		**FWY**
A2	**LIVM***ATQ*		**IV***MATL*
A3	**VSMA***TLI*		**RK**
A24	**YF***WIVLMT*		**FI***YWLM*
B7	**P**		**VILF***MWYA*
B27	**RHK**		**FYL***WMIVA*
B44	**E***D*		**FWYLIMVA**
B58	**ATS**		**FWY***LIVMA*
B62	**QL***IVMP*		**FWYMIVLA**
MOTIFS			
A1	**TSM**		**Y**
A1		**DE***AS*	**Y**
A2.1	**LM***VQIAT*		**V***LIMAT*
A3	**LMVISATF***CGD*		**KYR***HFA*
A11	**VTMLISAGN***CDF*		**K***RYH*
A24	**YFW***M*		**FLIW**
A*3101	**MVT***ALIS*		**R***K*
A*3301	**MVALF***IST*		**RK**
A*6801	**AVT***MSLI*		**RK**
B*0702	**P**		**LMF***WYAIV*
B*3501	**P**		**LMFWY***IVA*
B51	**P**		**LIVF***WYAM*
B*5301	**P**		**IMFWY***ALV*
B*5401	**P**		**ATIV***LMFWY*

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE IV (B): HLA Class II Supermotif

1	**6**	**9**
W, F, Y, V, .I, L	A, V, I, L, P, C, S, T	A, V, I, L, C, S, T, M, Y

TABLE IV (C): HLA Class II Motifs

MOTIFS		1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4	preferred	FMY*LIVW*	M	T		I	VST*CPALIM*	MH		MH
	deleterious				W			R		WDE
DR1	preferred	MF*LIVWY*			PAMQ		VMAT*SPLIC*	M		AVM
	deleterious		C	CH	FD	CWD		GDE	D	
DR7	preferred	MF*LIVWY*	M	W	A		IVMSA*CTPL*	M		IV
	deleterious		C		G			GRD	N	G
<u>DR3</u>	<u>MOTIFS</u>	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6			
motif a preferred		LIVMFY			D					
motif b preferred		LIVMFAY			DNQEST		KRH			
DR Supermotif		MF*LIVWY*					VMSTA*CPLI*			

Italicized residues indicate less preferred or "tolerated" residues

Docket No. 511582006940

TABLE IV (D): HLA Class I Supermotifs

SUPER-MOTIFS	POSITION:	1	2	3	4	5	6	7	8	C-terminus
A1			1° Anchor TIL*VMS*							1° Anchor FWY
A2			1° Anchor LIVM*AT* *Q*							1° Anchor LIVMAT
A3	preferred		1° Anchor VSMA*TL* *I*	YFW (4/5)			YFW (3/5)	YFW (4/5)	P (4/5)	1° Anchor RK
	deleterious	DE (3/5); P (5/5)		DE (4/5)						
A24			1° Anchor YF*WIVL* *MT*							1° Anchor FIY*WLM*
B7	preferred	FWY (5/5) LIVM (3/5)	1° Anchor P	FWY (4/5)					FWY (3/5)	1°Anchor VILF*MWYA*
	deleterious	DE (3/5); P(5/5); G(4/5); A(3/5); QN(3/5)				DE (3/5)	G (4/5)	QN (4/5)	DE (4/5)	
B27			1° Anchor RHK							1°Anchor FYL*WMIVA*
B44			1° Anchor E*D*							1° Anchor FWYLIMV A
B58			1° Anchor ATS							1° Anchor FWY*LIVMA*
B62			1° Anchor QL*IVMP*							1° Anchor FWY*MIVLA*

Italicized residues indicate less preferred or "tolerated" residues

TABLE IV (E): HLA Class I Motifs

	POSITION:	1	2	3	4	5	6	7	8	9	C-terminus
A1 9-mer	preferred	GFYW	1°Anchor STM	DEA	YFW		P	DEQN	YFW	or C-terminus 1°Anchor Y	
	deleterious	DE		RHKLIVMP	A	G	A				
A1 9-mer	preferred	GRHK	ASTCLIVM	1°Anchor DE*AS*	GSTC		ASTC	LIVM	DE	1°Anchor Y	
	deleterious	A	RHKDEPY FW		DE	PQN	RHK	PG	GP		
A1 10-mer	preferred	YFW	1°Anchor STM	DEAQN	A	YFWQN		PASTC	GDE	P	1°Anchor Y
	deleterious	GP		RHKGLIVM	DE	RHK	QNA	RHKYFW	RHK	A	
A1 10-mer	preferred	YFW	STCLIVM	1°Anchor DE*AS*	A	YFW		PG	G	YFW	1°Anchor Y
	deleterious	RHK	RHKDEPY FW			P	G		PRHK	QN	
A2.1 9-mer	preferred	YFW	1°Anchor L*MIVQAT*	YFW	STC	YFW		A	P	1°Anchor V*LIMAT*	
	deleterious	DEP		DERKH			RKH	DERKH			

Italicized residues indicate less preferred or "tolerated" residues

Docket No. 511582006940

TABLE IV (E): HLA Class I Motifs, continued

	POSITION:	1	2	3	4	5	*6*	7	8	9	C-Terminus
A2.1 10-mer	preferred	AYFW	1°Anchor LM*IVQAT*	LVIM	G		*G*		FYWL VIM		1°Anchor V*LIMAT*
	deleterious	DEP		DE	RKHA	P		RKH	DERKH	RKH	
A3	preferred	RHK	1°Anchor LMVISATFCGD	YFW	PRHKYFW	A	YFW		P	1°Anchor KYR*HFA*	
	deleterious	DEP		DE							
A11	preferred	A	1°Anchor VTLMISAGN*CDF*	YFW	YFW	A	YFW	YFW	P	1°Anchor K*RYH*	
	deleterious	DEP						A	G		
A24 9-mer	preferred	YFWRHK	1°Anchor YFW*M*		STC			YFW	YFW	1°Anchor FLIW	
	deleterious	DEG		DE	G	QNP	DERHK	G	AQN		
A24 10-mer	preferred		1°Anchor YFW*M*		P	YFWP		P			1°Anchor FLIW
	deleterious			GDE	QN	RHK	DE	A	QN	DEA	
A3101	preferred	RHK	1°Anchor MVT*ALIS*	YFW	P		YFW	YFW	AP	1°Anchor *RK*	
	deleterious	DEP		DE		ADE	DE	DE	DE		
A3301	preferred		1°Anchor MVALF*IST*	YFW				AYFW		1°Anchor RK	
	deleterious	GP		DE							

Italicized residues indicate less preferred or "tolerated" residues

TABLE IV (E): HLA Class I Motifs, continued

	POSITION:	1	2	3	4	5	6	7	8	9	C-Terminus
A6801	preferred	YFWSTC	1°Anchor AVT*MSLI*			YFWL IVM		YFW	P	1°Anchor RK	
	deleterious	GP		DEG		RHK			A		
B0702	preferred	RHKFWY	1°Anchor P	RHK		RHK	RHK	RHK	PA	1°Anchor LMF*WYAI* *V*	
	deleterious	DEQNP		DEP	DE	DE	GDE	QN	DE		
B3501	preferred	FWYLIV M	1°Anchor P	FWY				FWY		1°Anchor LMFWY*IV* *A*	
	deleterious	AGP				G	G				
B51	preferred	LIVMFW Y	1°Anchor P	FWY	STC	FWY		G	FWY	1°Anchor LIVF*WYA* *M*	
	deleterious	AGPDER HKSTC				DE	G	DEQN	GDE		
B5301	preferred	LIVMFW Y	1°Anchor P	FWY	STC	FWY		LIVM FWY	FWY	1°Anchor IMFWY*AL* *V*	
	deleterious	AGPQN					G	RHKQ N	DE		
B5401	preferred	FWY	1°Anchor P	FWY LIVM		LIVM		ALIV M	FWYAP	1°Anchor ATIV*LMF* *WY*	
	deleterious	GPQNDE		GDE STC		RHKD E	DE	QNDG E	DE		

Italicized residues indicate less preferred or "tolerated" residues. The information in this Table is specific for 9-mers unless otherwise specified.

FFTable V: v.1-A1-9mers: 151P3D4			
Pos	123456789	Score	SeqID
126	ITDLTLEDY	62.500	
264	LIHPTKLTY	25.000	
14	WADHLSDNY	25.000	
130	TLEDYGRYK	18.000	
57	VTLPCKFYR	12.500	
280	LNDGAQIAK	12.500	
230	NTVPGVRNY	12.500	
153	ALDLQGVVF	10.000	
18	LSDNYTLDH	3.750	
293	FAAWKILGY	2.500	
155	DLQGVVFPY	2.500	
144	GLEDDTVVV	1.800	
43	EAEQAKVFS	1.800	
41	LVEAEQAKV	1.800	
213	GSVQYPITK	1.500	
183	DQDAVIASF	1.500	
119	DSDASLVIT	1.500	
64	YRDPTAFGS	1.250	
129	LTLEDYGRY	1.250	
201	GLDWCNAGW	1.000	
181	CLDQDAVIA	1.000	
23	TLDHDRAIH	1.000	
209	WLSDGSVQY	1.000	
308	WLADGSVRY	1.000	
68	TAFGSGIHK	1.000	
33	QAENGPHLL	0.900	
141	VIEGLEDDT	0.900	
254	TSNFNGRFY	0.750	
117	GSDSDASLV	0.750	
255	SNFNGRFYY	0.625	
337	FPDKKHKLY	0.625	
56	NVTLPCKFY	0.500	
335	VGFPDKKHK	0.500	
187	VIASFDQLY	0.500	
158	GVVFPYFPR	0.500	
91	EVDVFVSMG	0.500	
325	CSPTEAAVR	0.300	
253	FTSNFNGRF	0.250	
103	KTYGGYQGR	0.250	
303	RCDAGWLAD	0.250	
97	SMGYHKKTY	0.250	
327	PTEAAVRFV	0.225	
89	LKEVDVFVS	0.225	
159	VVFPYFPRL	0.200	
95	FVSMGYHKK	0.200	
128	DLTLEDYGR	0.200	
324	RCSPTEAAV	0.200	
40	LLVEAEQAK	0.200	
329	EAAVRFVGF	0.200	
215	VQYPITKPR	0.150	

Table V: v.1-A1-9mers: 151P3D4			
Pos	123456789	Score	SeqID
240	FWDKDKSRY	0.125	
92	VDVFVSMGY	0.125	
161	FPYFPRLGR	0.125	
247	RYDVFCFTS	0.125	
148	DTVVVALDL	0.125	
345	YGVYCFRAY	0.125	
343	KLYGVYCFR	0.100	
54	GGNVTLPCK	0.100	
249	DVFCFTSNF	0.100	
289	VGQIFAAWK	0.100	
272	YDEAVQACL	0.090	
174	FHEAQQACL	0.090	
138	KCEVIEGLE	0.090	
312	GSVRYPISR	0.075	
245	KSRYDVFCF	0.075	
210	LSDGSVQYP	0.075	
71	GSGIHKIRI	0.075	
85	TSDYLKEVD	0.075	
314	VRYPISRPR	0.050	
219	ITKPREPCG	0.050	
4	LLLLVLISI	0.050	
309	LADGSVRYP	0.050	
185	DAVIASFDQ	0.050	
176	EAQQACLDQ	0.050	
146	EDDTVVVAL	0.050	
270	LTYDEAVQA	0.050	
166	RLGRYNLNF	0.050	
150	VVVALDLQG	0.050	
107	GYQGRVFLK	0.050	
6	LLVLISICW	0.050	
3	SLLLLVLIS	0.050	
326	SPTEAAVRF	0.050	
72	SGIHKIRIK	0.050	
123	SLVITDLTL	0.050	
145	LEDDTVVVA	0.050	
251	FCFTSNFNG	0.050	
232	VPGVRNYGF	0.050	
131	LEDYGRYKC	0.050	
222	PREPCGGQN	0.045	
156	LQGVVFPYF	0.030	
189	ASFDQLYDA	0.030	
2	KSLLLLVLI	0.030	
162	PYFPRLGRY	0.025	
316	YPISRPRRR	0.025	
55	GNVTLPCKF	0.025	
190	SFDQLYDAW	0.025	
105	YGGYQGRVF	0.025	
70	FGSGIHKIR	0.025	
271	TYDEAVQAC	0.025	
194	LYDAWRGGL	0.025	

Table V: v.2-A1-9mers: 151P3D4			
Pos	123456789	Score	SeqID
34	KVDLLVPTK	20.000	
385	SLEEGLGGK	18.000	
183	TLEEKRKEK	18.000	
123	NTNPSRRPY	12.500	
1	MLEHTTKTF	9.000	
97	SCEGINISG	4.500	
59	FVGSYKLAY	2.500	
367	PADLAGSGY	2.500	
220	YTESPGGGS	2.250	
238	TIAPLAATR	2.000	
208	QAEKNMKKK	1.800	
157	ASEAYKKVC	1.350	
354	KSENNSWYV	1.350	
226	GGSPRGLGF	1.250	
302	STYDSLSPY	1.250	
188	RKEKAEIHY	1.125	
400	KAENGPHLL	0.900	
191	KAEIHYRKN	0.900	
17	VVESIRDHS	0.900	
382	AIESLEEGL	0.900	
51	AKDFGHVQF	0.500	
7	KTFPLRALH	0.500	
134	QVPSRIFWR	0.500	
296	SCPTSSSTY	0.500	
70	DGEHWTVYQ	0.450	
105	GSFCRNKLK	0.300	
103	ISGSFCRNK	0.300	
373	SGYCGALWK	0.250	
180	VTATLEEKR	0.250	
37	LLVPTKVTG	0.200	
389	GLGGKQKDK	0.200	
168	GAPHEVGWK	0.200	
181	TATLEEKRK	0.200	
179	AVTATLEEK	0.200	
56	HVQFVGSYK	0.200	
306	SLSPYGPRN	0.200	
361	YVENGRPAD	0.180	
323	PSGGGGLKK	0.150	
207	KQAEKNMKK	0.150	
222	ESPGGGSPR	0.150	
295	SSCPTSSST	0.150	
305	DSLSPYGPR	0.150	
83	RKDKVLLGR	0.125	
68	SNDGEHWTV	0.125	
101	INISGSFCR	0.125	
169	APHEVGWKY	0.125	
46	IITQGAKDF	0.100	
150	SCCPQGHAS	0.100	
154	QGHASEAYK	0.100	
75	TVYQDEKQR	0.100	

Table V: v.2-A1-9mers: 151P3D4			
Pos	123456789	Score	SeqID
78	QDEKQRKDK	0.090	
384	ESLEEGLGG	0.075	
133	FQVPSRIFW	0.075	
279	ASPAAWLPL	0.075	
4	HTTKTFPLR	0.050	
145	KADGGSCCP	0.050	
95	VVSCEGINI	0.050	
280	SPAAWLPLR	0.050	
346	RGKPQRKPK	0.050	
265	HRPPALSAR	0.050	
377	GALWKAIES	0.050	
44	TGIITQGAK	0.050	
326	GGGLKKPAR	0.050	
288	RTPWTRPSS	0.050	
322	SPSGGGGLK	0.050	
237	KTIAPLAAT	0.050	
167	SGAPHEVGW	0.050	
112	LKYLAFLHK	0.050	
121	RMNTNPSRR	0.050	
303	TYDSLSPYG	0.050	
199	NKQLMRLQK	0.050	
386	LEEGLGGKQ	0.045	
372	GSGYCGALW	0.030	
261	GSSAHRPPA	0.030	
262	SSAHRPPAL	0.030	
69	NDGEHWTVY	0.025	
74	WTVYQDEKQ	0.025	
21	IRDHSGQKM	0.025	
314	NPLPNPRHS	0.025	
291	WTRPSSCPT	0.025	
99	EGINISGSF	0.025	
43	VTGIITQGA	0.025	
316	LPNPRHSPS	0.025	
47	ITQGAKDFG	0.025	
55	GHVQFVGSY	0.025	
274	APVPAASPA	0.025	
211	KNMKKKIDK	0.025	
284	WLPLRTPWT	0.020	
241	PLAATRATR	0.020	
190	EKAEIHYRK	0.020	
344	LARGKPQRK	0.020	
20	SIRDHSGQK	0.020	
163	KVCLSGAPH	0.020	
155	GHASEAYKK	0.020	
369	DLAGSGYCG	0.020	
87	VLLGRKAVV	0.020	
343	VLARGKPQR	0.020	
12	RALHIVVES	0.020	
203	MRLQKQAEK	0.020	
358	NSWYVENGR	0.015	

Table VI: v.1-A1-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
91	EVDVFVSMGY	125.000	
41	LVEAEQAKVF	9.000	
33	QAENGPHLLV	4.500	
43	EAEQAKVFSH	4.500	
254	TSNFNGRFYY	3.750	
117	GSDSDASLVI	3.750	
181	CLDQDAVIAS	2.500	
23	TLDHDRAIHI	2.500	
263	YLIHPTKLTY	2.500	
324	RCSPTEAAVR	2.000	
130	TLEDYGRYKC	1.800	
144	GLEDDTVVVA	1.800	
85	TSDYLKEVDV	1.500	
210	LSDGSVQYPI	1.500	
126	ITDLTLEDYG	1.250	
253	FTSNFNGRFY	1.250	
327	PTEAAVRFVG	1.125	
303	RCDAGWLADG	1.000	
279	CLNDGAQIAK	1.000	
309	LADGSVRYPI	1.000	
141	VIEGLEDDTV	0.900	
96	VSMGYHKKTY	0.750	
190	SFDQLYDAWR	0.500	
125	VITDLTLEDY	0.500	
201	GLDWCNAGWL	0.500	
56	NVTLPCKFYR	0.500	
128	DLTLEDYGRY	0.500	
14	WADHLSDNYT	0.500	
129	LTLEDYGRYK	0.500	
186	AVIASFDQLY	0.500	
138	KCEVIEGLED	0.450	
93	DVFVSMGYHK	0.400	
288	KVGQIFAAWK	0.400	
119	DSDASLVITD	0.375	
71	GSGIHKIRIK	0.300	
325	CSPTEAAVRF	0.300	
106	GGYQGRVFLK	0.250	
64	YRDPTAFGSG	0.250	
67	PTAFGSGIHK	0.250	
280	LNDGAQIAKV	0.250	
230	NTVPGVRNYG	0.250	
212	DGSVQYPITK	0.250	
39	HLLVEAEQAK	0.200	
155	DLQGVVFPYF	0.200	
334	FVGFPDKKHK	0.200	
231	TVPGVRNYGF	0.200	
152	VALDLQGVVF	0.200	
154	LDLQGVVFPY	0.125	
292	IFAAWKILGY	0.125	
161	FPYFPRLGRY	0.125	

Table VI: v.1-A1-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
55	GNVTLPCKFY	0.125	
157	QGVVFPYFPR	0.125	
229	QNTVPGVRNY	0.125	
311	DGSVRYPISR	0.125	
81	WTKLTSDYLK	0.100	
53	RGGNVTLPCK	0.100	
314	VRYPISRPRR	0.100	
214	SVQYPITKPR	0.100	
251	FCFTSNFNGR	0.100	
159	VVFPYFPRLG	0.100	
153	ALDLQGVVFP	0.100	
89	LKEVDVFVSM	0.090	
18	LSDNYTLDHD	0.075	
2	KSLLLLVLIS	0.075	
122	ASLVITDLTL	0.075	
337	FPDKKHKLYG	0.062	
291	QIFAAWKILG	0.050	
22	YTLDHDRAIH	0.050	
236	RNYGFWDKDK	0.050	
145	LEDDTVVVAL	0.050	
149	TVVVALDLQG	0.050	
35	ENGPHLLVEA	0.050	
57	VTLPCKFYRD	0.050	
343	KLYGVYCFRA	0.050	
208	GWLSDGSVQY	0.050	
3	SLLLLVLISI	0.050	
17	HLSDNYTLDH	0.050	
271	TYDEAVQACL	0.050	
307	GWLADGSVRY	0.050	
5	LLLVLISICW	0.050	
222	PREPCGGQNT	0.045	
272	YDEAVQACLN	0.045	
331	AVRFVGFPDK	0.040	
247	RYDVFCFTSN	0.025	
13	CWADHLSDNY	0.025	
242	DKDKSRYDVF	0.025	
219	ITKPREPCGG	0.025	
160	VFPYFPRLGR	0.025	
238	YGFWDKDKSR	0.025	
103	KTYGGYQGRV	0.025	
344	LYGVYCFRAY	0.025	
335	VGFPDKKHKL	0.025	
270	LTYDEAVQAC	0.025	
54	GGNVTLPCKF	0.025	
148	DTVVVALDLQ	0.025	
336	GFPDKKHKLY	0.025	
227	GGQNTVPGVR	0.025	
31	HIQAENGPHL	0.020	
40	LLVEAEQAKV	0.020	
269	KLTYDEAVQA	0.020	

Table VI: v.2-A1-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
191	KAEIHYRKNK	18.000	
295	SSCPTSSSTY	7.500	
68	SNDGEHWTVY	6.250	
400	KAENGPHLLV	4.500	
105	GSFCRNKLKY	3.750	
157	ASEAYKKVCL	2.700	
361	YVENGRPADL	1.800	
77	YQDEKQRKDK	1.500	
372	GSGYCGALWK	1.500	
7	KTFPLRALHI	1.250	
382	AIESLEEGLG	0.900	
385	SLEEGLGGKQ	0.900	
386	LEEGLGGKQK	0.900	
183	TLEEKRKEKA	0.900	
17	VVESIRDHSG	0.900	
97	SCEGINISGS	0.900	
133	FQVPSRIFWR	0.750	
301	SSTYDSLSPY	0.750	
145	KADGGSCCPQ	0.500	
123	NTNPSRRPYH	0.500	
182	ATLEEKRKEK	0.500	
43	VTGIITQGAK	0.500	
168	GAPHEVGWKY	0.500	
34	KVDLLVPTKV	0.500	
278	AASPAAWLPL	0.500	
100	GINISGSFCR	0.500	
237	KTIAPLAATR	0.500	
167	SGAPHEVGWK	0.500	
21	IRDHSGQKMK	0.500	
180	VTATLEEKRK	0.500	
24	HSGQKMKQDK	0.300	
321	HSPSGGGGLK	0.300	
384	ESLEEGLGGK	0.300	
279	ASPAAWLPLR	0.300	
354	KSENNSWYVE	0.270	
74	WTVYQDEKQR	0.250	
322	SPSGGGGLKK	0.250	
250	IGHPGGRTPR	0.250	
220	YTESPGGGSP	0.225	
102	NISGSFCRNK	0.200	
75	TVYQDEKQRK	0.200	
342	NVLARGKPQR	0.200	
178	QAVTATLEEK	0.200	
47	ITQGAKDFGH	0.125	
152	CPQGHASEAY	0.125	
122	MNTNPSRRPY	0.125	
58	QFVGSYKLAY	0.125	
366	RPADLAGSGY	0.125	
225	GGGSPRGLGF	0.125	
54	FGHVQFVGSY	0.125	

Table VI: v.2-A1-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
238	TIAPLAATRA	0.100	
154	QGHASEAYKK	0.100	
284	WLPLRTPWTR	0.100	
45	GIITQGAKDF	0.100	
13	ALHIVVESIR	0.100	
179	AVTATLEEKR	0.100	
37	LLVPTKVTGI	0.100	
111	KLKYLAFLHK	0.100	
1	MLEHTTKTFP	0.090	
208	QAEKNMKKKI	0.090	
227	GSPRGLGFIF	0.075	
96	VSCEGINISG	0.075	
240	APLAATRATR	0.050	
115	LAFLHKRMNT	0.050	
104	SGSFCRNKLK	0.050	
367	PADLAGSGYC	0.050	
206	QKQAEKNMKK	0.050	
302	STYDSLSPYG	0.050	
221	TESPGGGSPR	0.050	
129	RPYHFQVPSR	0.050	
94	VVVSCEGINI	0.050	
291	WTRPSSCPTS	0.050	
83	RKDKVLLGRK	0.050	
274	APVPAASPAA	0.050	
216	KIDKYTESPG	0.050	
388	EGLGGKQKDK	0.050	
325	GGGGLKKPAR	0.050	
124	TNPSRRPYHF	0.050	
316	LPNPRHSPSG	0.050	
210	EKNMKKKIDK	0.050	
70	DGEHWTVYQD	0.045	
188	RKEKAEIHYR	0.045	
30	KQDKKVDLLV	0.037	
19	ESIRDHSGQK	0.030	
305	DSLSPYGPRN	0.030	
261	GSSAHRPPAL	0.030	
262	SSAHRPPALS	0.030	
222	ESPGGGSPRG	0.030	
207	KQAEKNMKKK	0.030	
166	LSGAPHEVGW	0.030	
288	RTPWTRPSSC	0.025	
198	KNKQLMRLQK	0.025	
228	SPRGLGFIFK	0.025	
357	NNSWYVENGR	0.025	
226	GGSPRGLGFI	0.025	
51	AKDFGHVQFV	0.025	
247	ATRIGHPGGR	0.025	
202	LMRLQKQAEK	0.020	
59	FVGSYKLAYS	0.020	
33	KKVDLLVPTK	0.020	

Table VII: v.1-A2-9mers: 151P3D4			
Pos	123456789	Score	SeqID
88	YLKEVDVFV	252.512	
4	LLLVLISI	150.931	
7	LVLISICWA	34.588	
263	YLIHPTKLT	34.279	
5	LLLVLISIC	29.468	
151	VVALDLQGV	23.795	
159	VVFPYFPRL	22.339	
123	SLVITDLTL	21.362	
84	LTSDYLKEV	15.486	
32	IQAENGPHL	15.096	
298	ILGYDRCDA	8.446	
279	CLNDGAQIA	8.351	
290	GQIFAAWKI	7.933	
291	QIFAAWKIL	7.575	
144	GLEDDTVVV	7.483	
90	KEVDVFVSM	2.634	
106	GGYQGRVFL	2.454	
2	KSLLLLVLI	2.028	
22	YTLDHDRAI	2.022	
257	FNGRFYYLI	1.786	
186	AVIASFDQL	1.740	
270	LTYDEAVQA	1.539	
209	WLSDGSVQY	1.405	
308	WLADGSVRY	1.405	
343	KLYGVYCFR	1.377	
34	AENGPHLLV	1.352	
76	KIRIKWTKL	1.328	
152	VALDLQGVV	1.328	
189	ASFDQLYDA	1.132	
142	IEGLEDDTV	1.127	
227	GGQNTVPGV	1.044	
181	CLDQDAVIA	0.815	
41	LVEAEQAKV	0.662	
137	YKCEVIEGL	0.631	
116	GGSDSDASL	0.572	
178	QQACLDQDA	0.504	
306	AGWLADGSV	0.490	
207	AGWLSDGSV	0.490	
179	QACLDQDAV	0.473	
324	RCSPTEAAV	0.454	
346	GVYCFRAYN	0.436	
180	ACLDQDAVI	0.424	
276	VQACLNDGA	0.420	
193	QLYDAWRGG	0.332	
284	AQIAKVGQI	0.316	
86	SDYLKEVDV	0.309	
39	HLLVEAEQA	0.306	
96	VSMGYHKKT	0.306	
202	LDWCNAGWL	0.299	
3	SLLLLVLIS	0.260	

Table VII: v.1-A2-9mers: 151P3D4			
Pos	123456789	Score	SeqID
145	LEDDTVVVA	0.254	
278	ACLNDGAQI	0.252	
281	NDGAQIAKV	0.222	
143	EGLEDDTVV	0.212	
172	LNFHEAQQA	0.204	
8	VLISICWAD	0.190	
117	GSDSDASLV	0.182	
268	TKLTYDEAV	0.175	
256	NFNGRFYYL	0.155	
223	REPCGGQNT	0.145	
246	SRYDVFCFT	0.142	
156	LQGVVFPYF	0.134	
81	WTKLTSDYL	0.129	
6	LLVLISICW	0.127	
10	ISICWADHL	0.116	
40	LLVEAEQAK	0.104	
24	LDHDRAIHI	0.101	
287	AKVGQIFAA	0.092	
50	FSHRGGNVT	0.092	
122	ASLVITDLT	0.088	
83	KLTSDYLKE	0.078	
36	NGPHLLVEA	0.075	
155	DLQGVVFPY	0.075	
166	RLGRYNLNF	0.075	
71	GSGIHKIRI	0.068	
187	VIASFDQLY	0.066	
108	YQGRVFLKG	0.066	
131	LEDYGRYKC	0.066	
336	GFPDKKHKL	0.061	
255	SNFNGRFYY	0.057	
15	ADHLSDNYT	0.057	
199	RGGLDWCNA	0.055	
141	VIEGLEDDT	0.055	
97	SMGYHKKTY	0.054	
121	DASLVITDL	0.051	
262	YYLIHPTKL	0.050	
164	FPRLGRYNL	0.049	
251	FCFTSNFNG	0.048	
1	MKSLLLLVL	0.048	
288	KVGQIFAAW	0.043	
57	VTLPCKFYR	0.042	
260	RFYYLIHPT	0.038	
56	NVTLPCKFY	0.036	
231	TVPGVRNYG	0.036	
224	EPCGGQNTV	0.034	
53	RGGNVTLPC	0.032	
334	FVGFPDKKH	0.030	
201	GLDWCNAGW	0.030	
9	LISICWADH	0.030	
58	TLPCKFYRD	0.028	

Table VII: v.2-A2-9mers: 151P3D4			
Pos	123456789	Score	SeqID
378	ALWKAIESL	199.826	
284	WLPLRTPWT	188.536	
87	VLLGRKAVV	179.368	
234	FIFKTIAPL	114.985	
86	KVLLGRKAV	78.811	
165	CLSGAPHEV	69.552	
88	LLGRKAVVV	48.478	
114	YLAFLHKRM	22.853	
231	GLGFIFKTI	19.822	
201	QLMRLQKQA	18.382	
52	KDFGHVQFV	15.825	
57	VQFVGSYKL	13.624	
13	ALHIVVESI	11.758	
230	RGLGFIFKT	9.124	
9	FPLRALHIV	7.287	
67	YSNDGEHWT	5.046	
354	KSENNSWYV	4.195	
100	GINISGSFC	3.757	
38	LVPTKVTGI	3.569	
30	KQDKKVDLL	3.417	
95	VVSCEGINI	1.552	
110	NKLKYLAFL	1.389	
68	SNDGEHWTV	1.362	
138	RIFWRQEKA	1.238	
336	CQGQKHNVL	0.888	
36	DLLVPTKVT	0.848	
237	KTIAPLAAT	0.833	
117	FLHKRMNTN	0.788	
362	VENGRPADL	0.706	
172	EVGWKYQAV	0.685	
107	FCRNKLKYL	0.617	
35	VDLLVPTKV	0.608	
81	KQRKDKVLL	0.576	
375	YCGALWKAI	0.533	
93	AVVVSCEGI	0.447	
308	SPYGPRNPL	0.446	
158	SEAYKKVCL	0.415	
27	QKMKQDKKV	0.357	
175	WKYQAVTAT	0.350	
33	KKVDLLVPT	0.342	
232	LGFIFKTIA	0.318	
173	VGWKYQAVT	0.281	
289	TPWTRPSSC	0.269	
242	LAATRATRI	0.246	
279	ASPAAWLPL	0.237	
29	MKQDKKVDL	0.207	
156	HASEAYKKV	0.202	
133	FQVPSRIFW	0.191	
370	LAGSGYCGA	0.176	
262	SSAHRPPAL	0.139	
104	SGSFCRNKL	0.139	
249	RIGHPGGRT	0.133	
37	LLVPTKVTG	0.127	
131	YHFQVPSRI	0.123	
399	RKAENGPHL	0.122	
239	IAPLAATRA	0.117	
43	VTGIITQGA	0.117	
49	QGAKDFGHV	0.112	
227	GSPRGLGFI	0.112	
299	TSSSTYDSL	0.102	
134	QVPSRIFWR	0.096	
382	AIESLEEGL	0.092	
194	IHYRKNKQL	0.081	
268	PALSARAPV	0.079	
306	SLSPYGPRN	0.075	
256	RTPRAGSSA	0.069	
197	RKNKQLMRL	0.068	
400	KAENGPHLL	0.066	
270	LSARAPVPA	0.055	
111	KLKYLAFLH	0.053	
42	KVTGIITQG	0.052	
393	KQKDKERKA	0.051	
295	SSCPTSSST	0.049	
10	PLRALHIVV	0.048	
200	KQLMRLQKQ	0.045	
48	TQGAKDFGH	0.044	
204	RLQKQAEKN	0.037	
291	WTRPSSCPT	0.036	
240	APLAATRAT	0.036	
277	PAASPAAWL	0.036	
328	GLKKPARHC	0.035	
261	GSSAHRPPA	0.032	
337	QGQKHNVLA	0.032	
152	CPQGHASEA	0.032	
325	GGGGLKKPA	0.032	
274	APVPAASPA	0.032	
266	RPPALSARA	0.032	
236	FKTIAPLAA	0.032	
302	STYDSLSPY	0.031	
59	FVGSYKLAY	0.030	
205	LQKQAEKNM	0.030	
64	KLAYSNDGE	0.026	
343	VLARGKPQR	0.025	
163	KVCLSGAPH	0.023	
207	KQAEKNMKK	0.022	
16	IVVESIRDH	0.021	
102	NISGSFCRN	0.019	
116	AFLHKRMNT	0.019	
368	ADLAGSGYC	0.018	
371	AGSGYCGAL	0.018	

Table VIII: v.1-A2-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
83	KLTSDYLKEV	559.894	
40	LLVEAEQAKV	484.777	
343	KLYGVYCFRA	322.721	
6	LLVLISICWA	106.837	
3	SLLLLVLISI	88.783	
193	QLYDAWRGGL	36.436	
4	LLLLVLISIC	29.468	
150	VVVALDLQGV	23.795	
269	KLTYDEAVQA	17.388	
32	IQAENGPHLL	15.096	
73	GIHKIRIKWT	12.962	
48	KVFSHRGGNV	10.245	
297	KILGYDRCDA	8.846	
201	GLDWCNAGWL	6.110	
255	SNFNGRFYYL	5.392	
171	NLNFHEAQQA	4.968	
326	SPTEAAVRFV	4.710	
23	TLDHDRAIHI	4.173	
285	QIAKVGQIFA	3.757	
209	WLSDGSVQYP	3.556	
158	GVVFPYFPRL	3.551	
270	LTYDEAVQAC	3.540	
105	YGGYQGRVFL	3.528	
178	QQACLDQDAV	3.455	
95	FVSMGYHKKT	2.999	
145	LEDDTVVVAL	2.664	
9	LISICWADHL	2.447	
116	GGSDSDASLV	1.861	
290	GQIFAAWKIL	1.510	
103	KTYGGYQGRV	1.406	
223	REPCGGQNTV	1.352	
130	TLEDYGRYKC	1.304	
68	TAFGSGIHKI	1.233	
144	GLEDDTVVVA	1.229	
14	WADHLSDNYT	1.047	
226	CGGQNTVPGV	1.044	
166	RLGRYNLNFH	0.943	
142	IEGLEDDTVV	0.943	
335	VGFPDKKHKL	0.877	
289	VGQIFAAWKI	0.868	
113	FLKGGSDSDA	0.800	
308	WLADGSVRYP	0.711	
280	LNDGAQIAKV	0.710	
50	FSHRGGNVTL	0.641	
151	VVALDLQGVV	0.551	
122	ASLVITDLTL	0.516	
141	VIEGLEDDTV	0.510	
177	AQQACLDQDA	0.504	
115	KGGSDSDASL	0.488	
5	LLLVLISICW	0.469	

Table VIII: v.1-A2-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
263	YLIHPTKLTY	0.343	
70	FGSGIHKIRI	0.313	
108	YQGRVFLKGG	0.304	
97	SMGYHKKTYG	0.296	
76	KIRIKWTKLT	0.273	
188	IASFDQLYDA	0.270	
88	YLKEVDVFVS	0.269	
196	DAWRGGLDWC	0.266	
8	VLISICWADH	0.215	
275	AVQACLNDGA	0.213	
143	EGLEDDTVVV	0.212	
172	LNFHEAQQAC	0.204	
180	ACLDQDAVIA	0.202	
90	KEVDVFVSMG	0.182	
85	TSDYLKEVDV	0.182	
277	QACLNDGAQI	0.145	
245	KSRYDVFCFT	0.135	
340	KKHKLYGVYC	0.133	
206	NAGWLSDGSV	0.126	
31	HIQAENGPHL	0.100	
309	LADGSVRYPI	0.099	
140	EVIEGLEDDT	0.098	
288	KVGQIFAAWK	0.095	
125	VITDLTLEDY	0.080	
153	ALDLQGVVFP	0.075	
217	YPITKPREPC	0.073	
181	CLDQDAVIAS	0.069	
120	SDASLVITDL	0.068	
163	YFPRLGRYNL	0.068	
241	WDKDKSRYDV	0.064	
298	ILGYDRCDAG	0.062	
33	QAENGPHLLV	0.062	
7	LVLISICWAD	0.062	
279	CLNDGAQIAK	0.061	
173	NFHEAQQACL	0.061	
179	QACLDQDAVI	0.059	
155	DLQGVVFPYF	0.058	
1	MKSLLLLVLI	0.057	
42	VEAEQAKVFS	0.056	
65	RDPTAFGSGI	0.055	
286	IAKVGQIFAA	0.055	
156	LQGVVFPYFP	0.054	
278	ACLNDGAQIA	0.049	
345	YGVYCFRAYN	0.047	
210	LSDGSVQYPI	0.046	
264	LIHPTKLTYD	0.044	
261	FYYLIHPTKL	0.044	
283	GAQIAKVGQI	0.043	
56	NVTLPCKFYR	0.042	
256	NFNGRFYYLI	0.041	

Table VIII: v.2-A2-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
87	VLLGRKAVVV	179.368	
67	YSNDGEHWTV	64.221	
37	LLVPTKVTGI	40.792	
86	KVLLGRKAVV	32.313	
234	FIFKTIAPLA	11.626	
30	KQDKKVDLLV	9.873	
34	KVDLLVPTKV	8.520	
231	GLGFIFKTIA	7.740	
200	KQLMRLQKQA	6.523	
204	RLQKQAEKNM	4.968	
269	ALSARAPVPA	4.968	
57	VQFVGSYKLA	4.752	
2	LEHTTKTFPL	4.096	
9	FPLRALHIVV	3.168	
164	VCLSGAPHEV	2.856	
381	KAIESLEEGL	2.086	
28	KMKQDKKVDL	1.890	
7	KTFPLRALHI	1.876	
373	SGYCGALWKA	1.790	
48	TQGAKDFGHV	1.742	
94	VVVSCEGINI	1.552	
42	KVTGIITQGA	1.521	
276	VPAASPAAWL	1.304	
377	GALWKAIESL	1.237	
212	NMKKKIDKYT	1.036	
238	TIAPLAATRA	0.683	
115	LAFLHKRMNT	0.651	
183	TLEEKRKEKA	0.639	
12	RALHIVVESI	0.604	
369	DLAGSGYCGA	0.559	
361	YVENGRPADL	0.550	
284	WLPLRTPWTR	0.514	
133	FQVPSRIFWR	0.510	
278	AASPAAWLPL	0.504	
336	CQGQKHNVLA	0.504	
51	AKDFGHVQFV	0.489	
230	RGLGFIFKTI	0.479	
173	VGWKYQAVTA	0.458	
175	WKYQAVTATL	0.437	
59	FVGSYKLAYS	0.379	
353	PKSENNSWYV	0.359	
92	KAVVVSCEGI	0.249	
26	GQKMKQDKKV	0.247	
103	ISGSFCRNKL	0.237	
307	LSPYGPRNPL	0.237	
29	MKQDKKVDLL	0.233	
241	PLAATRATRI	0.230	
193	EIHYRKNKQL	0.220	
400	KAENGPHLLV	0.216	
20	SIRDHSGQKM	0.213	

Table VIII: v.2-A2-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
106	SFCRNKLKYL	0.188	
261	GSSAHRPPAL	0.139	
270	LSARAPVPAA	0.127	
378	ALWKAIESLE	0.124	
399	RKAENGPHLL	0.122	
88	LLGRKAVVVS	0.119	
226	GGSPRGLGFI	0.112	
236	FKTIAPLAAT	0.110	
38	LVPTKVTGII	0.083	
362	VENGRPADLA	0.080	
302	STYDSLSPYG	0.075	
155	GHASEAYKKV	0.072	
273	RAPVPAASPA	0.069	
288	RTPWTRPSSC	0.069	
263	SAHRPPALSA	0.069	
171	HEVGWKYQAV	0.069	
117	FLHKRMNTNP	0.069	
114	YLAFLHKRMN	0.069	
370	LAGSGYCGAL	0.066	
56	HVQFVGSYKL	0.064	
109	RNKLKYLAFL	0.062	
201	QLMRLQKQAE	0.055	
207	KQAEKNMKKK	0.050	
280	SPAAWLPLRT	0.049	
334	RHCQGQKHNV	0.048	
46	IITQGAKDFG	0.047	
8	TFPLRALHIV	0.046	
239	IAPLAATRAT	0.035	
233	GFIFKTIAPL	0.034	
64	KLAYSNDGEH	0.034	
39	VPTKVTGIIT	0.034	
151	CCPQGHASEA	0.032	
260	AGSSAHRPPA	0.032	
324	SGGGGLKKPA	0.032	
274	APVPAASPAA	0.032	
223	SPGGGSPRGL	0.028	
35	VDLLVPTKVT	0.027	
343	VLARGKPQRK	0.025	
327	GGLKKPARHC	0.024	
16	IVVESIRDHS	0.022	
283	AWLPLRTPWT	0.021	
36	DLLVPTKVTG	0.021	
172	EVGWKYQAVT	0.020	
194	IHYRKNKQLM	0.019	
134	QVPSRIFWRQ	0.019	
165	CLSGAPHEVG	0.015	
216	KIDKYTESPG	0.014	
99	EGINISGSFC	0.013	
100	GINISGSFCR	0.012	
77	YQDEKQRKDK	0.011	

Table IX: v.1-A3-9mers: 151P3D4			
Pos	123456789	Score	SeqID
343	KLYGVYCFR	135.000	
40	LLVEAEQAK	45.000	
155	DLQGVVFPY	24.300	
166	RLGRYNLNF	12.000	
158	GVVFPYFPR	8.100	
130	TLEDYGRYK	6.000	
103	KTYGGYQGR	4.500	
159	VVFPYFPRL	4.050	
4	LLLLVLISI	4.050	
308	WLADGSVRY	4.000	
209	WLSDGSVQY	4.000	
128	DLTLEDYGR	3.600	
68	TAFGSGIHK	3.000	
213	GSVQYPITK	2.700	
153	ALDLQGVVF	2.000	
95	FVSMGYHKK	2.000	
97	SMGYHKKTY	2.000	
123	SLVITDLTL	1.800	
57	VTLPCKFYR	1.350	
187	VIASFDQLY	1.200	
264	LIHPTKLTY	1.200	
249	DVFCFTSNF	0.900	
6	LLVLISICW	0.900	
107	GYQGRVFLK	0.810	
215	VQYPITKPR	0.675	
144	GLEDDTVVV	0.600	
201	GLDWCNAGW	0.600	
161	FPYFPRLGR	0.600	
312	GSVRYPISR	0.540	
88	YLKEVDVFV	0.450	
5	LLLVLISIC	0.450	
3	SLLLLVLIS	0.360	
56	NVTLPCKFY	0.300	
39	HLLVEAEQA	0.300	
285	QIAKVGQIF	0.300	
332	VRFVGFPDK	0.300	
126	ITDLTLEDY	0.300	
245	KSRYDVFCF	0.270	
156	LQGVVFPYF	0.270	
186	AVIASFDQL	0.270	
288	KVGQIFAAW	0.270	
290	GQIFAAWKI	0.243	
181	CLDQDAVIA	0.200	
23	TLDHDRAIH	0.200	
279	CLNDGAQIA	0.200	
298	ILGYDRCDA	0.200	
235	VRNYGFWDK	0.180	
76	KIRIKWTKL	0.180	
73	GIHKIRIKW	0.180	
58	TLPCKFYRD	0.180	

Table IX: v.1-A3-9mers: 151P3D4			
Pos	123456789	Score	SeqID
228	GQNTVPGVR	0.162	
45	EQAKVFSHR	0.162	
261	FYYLIHPTK	0.150	
291	QIFAAWKIL	0.150	
230	NTVPGVRNY	0.135	
8	VLISICWAD	0.135	
75	HKIRIKWTK	0.135	
333	RFVGFPDKK	0.135	
129	LTLEDYGRY	0.135	
280	LNDGAQIAK	0.120	
293	FAAWKILGY	0.120	
255	SNFNGRFYY	0.120	
83	KLTSDYLKE	0.120	
263	YLIHPTKLT	0.113	
54	GGNVTLPCK	0.090	
94	VFVSMGYHK	0.090	
82	TKLTSDYLK	0.090	
253	FTSNFNGRF	0.090	
346	GVYCFRAYN	0.090	
335	VGFPDKKHK	0.075	
289	VGQIFAAWK	0.060	
269	KLTYDEAVQ	0.060	
232	VPGVRNYGF	0.060	
234	GVRNYGFWD	0.054	
270	LTYDEAVQA	0.050	
7	LVLISICWA	0.045	
183	DQDAVIASF	0.041	
148	DTVVVALDL	0.041	
14	WADHLSDNY	0.040	
62	KFYRDPTAF	0.030	
239	GFWDKDKSR	0.030	
237	NYGFWDKDK	0.030	
151	VVALDLQGV	0.030	
326	SPTEAAVRF	0.030	
81	WTKLTSDYL	0.030	
113	FLKGGSDSD	0.030	
32	IQAENGPHL	0.027	
342	HKLYGVYCF	0.027	
284	AQIAKVGQI	0.024	
84	LTSDYLKEV	0.022	
189	ASFDQLYDA	0.022	
2	KSLLLLVLI	0.020	
325	CSPTEAAVR	0.020	
9	LISICWADH	0.020	
337	FPDKKHKLY	0.020	
171	NLNFHEAQQ	0.020	
41	LVEAEQAKV	0.020	
17	HLSDNYTLD	0.020	
55	GNVTLPCKF	0.018	
92	VDVFVSMGY	0.018	

Table IX: v.2-A3-9mers: 151P3D4			
Pos	123456789	Score	SeqID
389	GLGGKQKDK	45.000	
34	KVDLLVPTK	18.000	
183	TLEEKRKEK	15.000	
385	SLEEGLGGK	13.500	
212	NMKKKIDKY	6.000	
207	KQAEKNMKK	5.400	
378	ALWKAIESL	4.500	
231	GLGFIFKTI	4.050	
121	RMNTNPSRR	4.000	
343	VLARGKPQR	4.000	
179	AVTATLEEK	3.000	
56	HVQFVGSYK	3.000	
13	ALHIVVESI	2.700	
59	FVGSYKLAY	2.400	
338	GQKHNVLAR	2.160	
26	GQKMKQDKK	1.800	
111	KLKYLAFLH	1.800	
134	QVPSRIFWR	1.800	
302	STYDSLSPY	1.500	
75	TVYQDEKQR	1.000	
1	MLEHTTKTF	1.000	
105	GSFCRNKLK	0.750	
20	SIRDHSGQK	0.600	
112	LKYLAFLHK	0.600	
4	HTTKTFPLR	0.600	
238	TIAPLAATR	0.600	
168	GAPHEVGWK	0.540	
87	VLLGRKAVV	0.450	
234	FIFKTIAPL	0.450	
241	PLAATRATR	0.400	
211	KNMKKKIDK	0.360	
344	LARGKPQRK	0.300	
165	CLSGAPHEV	0.300	
57	VQFVGSYKL	0.270	
169	APHEVGWKY	0.270	
7	KTFPLRALH	0.225	
88	LLGRKAVVV	0.200	
373	SGYCGALWK	0.200	
180	VTATLEEKR	0.200	
155	GHASEAYKK	0.180	
280	SPAAWLPLR	0.180	
285	LPLRTPWTR	0.180	
38	LVPTKVTGI	0.180	
30	KQDKKVDLL	0.162	
208	QAEKNMKKK	0.150	
201	QLMRLQKQA	0.150	
358	NSWYVENGR	0.150	
192	AEIHYRKNK	0.135	
95	VVSCEGINI	0.120	
284	WLPLRTPWT	0.100	

Table IX: v.2-A3-9mers: 151P3D4			
Pos	123456789	Score	SeqID
46	IITQGAKDF	0.100	
138	RIFWRQEKA	0.100	
114	YLAFLHKRM	0.100	
181	TATLEEKRK	0.100	
137	SRIFWRQEK	0.090	
306	SLSPYGPRN	0.090	
228	SPRGLGFIF	0.090	
93	AVVVSCEGI	0.090	
328	GLKKPARHC	0.090	
322	SPSGGGGLK	0.090	
113	KYLAFLHKR	0.081	
308	SPYGPRNPL	0.068	
392	GKQKDKERK	0.060	
73	HWTVYQDEK	0.060	
382	AIESLEEGL	0.060	
64	KLAYSNDGE	0.060	
5	TTKTFPLRA	0.060	
163	KVCLSGAPH	0.060	
125	NPSRRPYHF	0.060	
100	GINISGSFC	0.060	
81	KQRKDKVLL	0.054	
189	KEKAEIHYR	0.054	
237	KTIAPLAAT	0.051	
55	GHVQFVGSY	0.049	
37	LLVPTKVTG	0.045	
86	KVLLGRKAV	0.045	
190	EKAEIHYRK	0.041	
199	NKQLMRLQK	0.040	
296	SCPTSSSTY	0.040	
10	PLRALHIVV	0.040	
101	INISGSFCR	0.036	
36	DLLVPTKVT	0.034	
323	PSGGGGLKK	0.030	
103	ISGSFCRNK	0.030	
203	MRLQKQAEK	0.030	
117	FLHKRMNTN	0.030	
28	KMKQDKKVD	0.030	
123	NTNPSRRPY	0.030	
369	DLAGSGYCG	0.027	
133	FQVPSRIFW	0.027	
84	KDKVLLGRK	0.027	
42	KVTGIITQG	0.020	
204	RLQKQAEKN	0.020	
25	SGQKMKQDK	0.020	
206	QKQAEKNMK	0.020	
244	ATRATRIGH	0.020	
202	LMRLQKQAE	0.020	
154	QGHASEAYK	0.020	
269	ALSARAPVP	0.020	
76	VYQDEKQRK	0.020	

Table X: v.1-A3-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
234	GVRNYGFWDK	54.000	
343	KLYGVYCFRA	40.500	
279	CLNDGAQIAK	40.000	
39	HLLVEAEQAK	30.000	
288	KVGQIFAAWK	18.000	
263	YLIHPTKLTY	12.000	
93	DVFVSMGYHK	9.000	
331	AVRFVGFPDK	6.000	
155	DLQGVVFPYF	4.050	
3	SLLLLVLISI	4.050	
81	WTKLTSDYLK	3.000	
106	GGYQGRVFLK	2.700	
193	QLYDAWRGGL	2.700	
158	GVVFPYFPRL	2.430	
186	AVIASFDQLY	1.800	
144	GLEDDTVVVA	1.800	
83	KLTSDYLKEV	1.350	
23	TLDHDRAIHI	1.200	
17	HLSDNYTLDH	1.200	
56	NVTLPCKFYR	1.200	
334	FVGFPDKKHK	1.000	
5	LLLVLISICW	0.900	
231	TVPGVRNYGF	0.900	
129	LTLEDYGRYK	0.675	
125	VITDLTLEDY	0.600	
130	TLEDYGRYKC	0.600	
294	AAWKILGYDR	0.600	
269	KLTYDEAVQA	0.600	
251	FCFTSNFNGR	0.600	
201	GLDWCNAGWL	0.540	
88	YLKEVDVFVS	0.540	
4	LLLLVLISIC	0.450	
236	RNYGFWDKDK	0.450	
40	LLVEAEQAKV	0.450	
6	LLVLISICWA	0.450	
91	EVDVFVSMGY	0.360	
128	DLTLEDYGRY	0.360	
113	FLKGGSDSDA	0.300	
214	SVQYPITKPR	0.300	
8	VLISICWADH	0.300	
332	VRFVGFPDKK	0.300	
166	RLGRYNLNFH	0.300	
181	CLDQDAVIAS	0.240	
103	KTYGGYQGRV	0.203	
171	NLNFHEAQQA	0.200	
67	PTAFGSGIHK	0.200	
9	LISICWADHL	0.180	
260	RFYYLIHPTK	0.150	
270	LTYDEAVQAC	0.150	
284	AQIAKVGQIF	0.135	

Table X: v.1-A3-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
297	KILGYDRCDA	0.135	
41	LVEAEQAKVF	0.100	
74	IHKIRIKWTK	0.090	
161	FPYFPRLGRY	0.090	
48	KVFSHRGGNV	0.090	
154	LDLQGVVFPY	0.081	
68	TAFGSGIHKI	0.068	
239	GFWDKDKSRY	0.060	
324	RCSPTEAAVR	0.060	
313	SVRYPISRPR	0.060	
153	ALDLQGVVFP	0.060	
291	QIFAAWKILG	0.060	
254	TSNFNGRFYY	0.060	
209	WLSDGSVQYP	0.060	
31	HIQAENGPHL	0.060	
341	KHKLYGVYCF	0.054	
255	SNFNGRFYYL	0.054	
44	AEQAKVFSHR	0.054	
123	SLVITDLTLE	0.045	
71	GSGIHKIRIK	0.045	
150	VVVALDLQGV	0.045	
76	KIRIKWTKLT	0.045	
309	LADGSVRYPI	0.041	
290	GQIFAAWKIL	0.041	
285	QIAKVGQIFA	0.040	
212	DGSVQYPITK	0.036	
53	RGGNVTLPCK	0.030	
94	VFVSMGYHKK	0.030	
314	VRYPISRPRR	0.030	
141	VIEGLEDDTV	0.030	
152	VALDLQGVVF	0.030	
86	SDYLKEVDVF	0.030	
55	GNVTLPCKFY	0.027	
157	QGVVFPYFPR	0.027	
32	IQAENGPHLL	0.027	
73	GIHKIRIKWT	0.022	
96	VSMGYHKKTY	0.022	
57	VTLPCKFYRD	0.020	
210	LSDGSVQYPI	0.020	
298	ILGYDRCDAG	0.020	
111	RVFLKGGSDS	0.020	
97	SMGYHKKTYG	0.020	
275	AVQACLNDGA	0.020	
253	FTSNFNGRFY	0.020	
306	AGWLADGSVR	0.020	
79	IKWTKLTSDY	0.020	
208	GWLSDGSVQY	0.018	
307	GWLADGSVRY	0.018	
127	TDLTLEDYGR	0.018	
328	TEAAVRFVGF	0.018	

Table X: v.2-A3-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
111	KLKYLAFLHK	360.000	
202	LMRLQKQAEK	20.000	
343	VLARGKPQRK	20.000	
284	WLPLRTPWTR	12.000	
75	TVYQDEKQRK	10.000	
13	ALHIVVESIR	6.000	
37	LLVPTKVTGI	4.050	
100	GINISGSFCR	3.600	
207	KQAEKNMKKK	2.025	
228	SPRGLGFIFK	1.800	
28	KMKQDKKVDL	1.800	
231	GLGFIFKTIA	1.800	
7	KTFPLRALHI	1.350	
133	FQVPSRIFWR	1.215	
182	ATLEEKRKEK	1.125	
237	KTIAPLAATR	0.900	
191	KAEIHYRKNK	0.900	
102	NISGSFCRNK	0.900	
189	KEKAEIHYRK	0.810	
372	GSGYCGALWK	0.600	
322	SPSGGGGLKK	0.600	
342	NVLARGKPQR	0.600	
105	GSFCRNKLKY	0.600	
129	RPYHFQVPSR	0.600	
205	LQKQAEKNMK	0.600	
168	GAPHEVGWKY	0.540	
180	VTATLEEKRK	0.500	
178	QAVTATLEEK	0.450	
87	VLLGRKAVVV	0.450	
45	GIITQGAKDF	0.450	
77	YQDEKQRKDK	0.450	
179	AVTATLEEKR	0.400	
183	TLEEKRKEKA	0.300	
43	VTGIITQGAK	0.300	
33	KKVDLLVPTK	0.270	
198	KNKQLMRLQK	0.240	
269	ALSARAPVPA	0.200	
64	KLAYSNDGEH	0.180	
94	VVVSCEGINI	0.180	
56	HVQFVGSYKL	0.180	
331	KPARHCQGQK	0.180	
74	WTVYQDEKQR	0.150	
234	FIFKTIAPLA	0.150	
378	ALWKAIESLE	0.150	
55	GHVQFVGSYK	0.135	
42	KVTGIITQGA	0.135	
352	KPKSENNSWY	0.120	
311	GPRNPLPNPR	0.120	
88	LLGRKAVVVS	0.120	
24	HSGQKMKQDK	0.100	

Table X: v.2-A3-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
204	RLQKQAEKNM	0.100	
279	ASPAAWLPLR	0.090	
34	KVDLLVPTKV	0.090	
369	DLAGSGYCGA	0.090	
112	LKYLAFLHKR	0.090	
86	KVLLGRKAVV	0.090	
389	GLGGKQKDKE	0.090	
227	GSPRGLGFIF	0.090	
72	EHWTVYQDEK	0.090	
212	NMKKKIDKYT	0.075	
391	GGKQKDKERK	0.060	
154	QGHASEAYKK	0.060	
153	PQGHASEAYK	0.060	
50	GAKDFGHVQF	0.060	
152	CPQGHASEAY	0.060	
240	APLAATRATR	0.060	
361	YVENGRPADL	0.060	
241	PLAATRATRI	0.060	
247	ATRIGHPGGR	0.060	
328	GLKKPARHCQ	0.060	
4	HTTKTFPLRA	0.060	
211	KNMKKKIDKY	0.054	
58	QFVGSYKLAY	0.054	
30	KQDKKVDLLV	0.054	
47	ITQGAKDFGH	0.045	
165	CLSGAPHEVG	0.045	
386	LEEGLGGKQK	0.045	
381	KAIESLEEGL	0.041	
377	GALWKAIESL	0.041	
12	RALHIVVESI	0.041	
257	TPRAGSSAHR	0.040	
366	RPADLAGSGY	0.040	
206	QKQAEKNMKK	0.040	
187	KRKEKAEIHY	0.036	
384	ESLEEGLGGK	0.030	
136	PSRIFWRQEK	0.030	
295	SSCPTSSSTY	0.030	
301	SSTYDSLSPY	0.030	
201	QLMRLQKQAE	0.030	
238	TIAPLAATRA	0.030	
321	HSPSGGGGLK	0.030	
38	LVPTKVTGII	0.027	
167	SGAPHEVGWK	0.027	
92	KAVVVSCEGI	0.027	
134	QVPSRIFWRQ	0.027	
337	QGQKHNVLAR	0.024	
1	MLEHTTKTFP	0.020	
117	FLHKRMNTNP	0.020	
20	SIRDHSGQKM	0.020	
25	SGQKMKQDKK	0.020	

Table XI: v.1-A11-9mers: 151P3D4			
Pos	123456789	Score	SeqID
158	GVVFPYFPR	5.400	
107	GYQGRVFLK	3.600	
95	FVSMGYHKK	2.000	
103	KTYGGYQGR	1.200	
57	VTLPCKFYR	0.900	
333	RFVGFPDKK	0.900	
68	TAFGSGIHK	0.800	
261	FYYLIHPTK	0.800	
94	VFVSMGYHK	0.600	
40	LLVEAEQAK	0.600	
343	KLYGVYCFR	0.480	
228	GQNTVPGVR	0.360	
315	RYPISRPRR	0.240	
237	NYGFWDKDK	0.200	
213	GSVQYPITK	0.180	
161	FPYFPRLGR	0.160	
239	GFWDKDKSR	0.120	
215	VQYPITKPR	0.120	
280	LNDGAQIAK	0.080	
75	HKIRIKWTK	0.060	
82	TKLTSDYLK	0.060	
54	GGNVTLPCK	0.060	
288	KVGQIFAAW	0.060	
290	GQIFAAWKI	0.054	
128	DLTLEDYGR	0.048	
130	TLEDYGRYK	0.040	
252	CFTSNFNGR	0.040	
332	VRFVGFPDK	0.040	
235	VRNYGFWDK	0.040	
159	VVFPYFPRL	0.040	
312	GSVRYPISR	0.036	
45	EQAKVFSHR	0.036	
186	AVIASFDQL	0.030	
7	LVLISICWA	0.030	
73	GIHKIRIKW	0.024	
166	RLGRYNLNF	0.024	
270	LTYDEAVQA	0.020	
335	VGFPDKKHK	0.020	
151	VVALDLQGV	0.020	
289	VGQIFAAWK	0.020	
41	LVEAEQAKV	0.020	
307	GWLADGSVR	0.018	
234	GVRNYGFWD	0.018	
129	LTLEDYGRY	0.015	
201	GLDWCNAGW	0.012	
346	GVYCFRAYN	0.012	
169	RYNLNFHEA	0.012	
4	LLLLVLISI	0.012	
249	DVFCFTSNF	0.012	
6	LLVLISICW	0.012	

Table XI: v.1-A11-9mers: 151P3D4			
Pos	123456789	Score	SeqID
144	GLEDDTVVV	0.012	
300	GYDRCDAGW	0.012	
76	KIRIKWTKL	0.012	
48	KVFSHRGGN	0.012	
62	KFYRDPTAF	0.012	
111	RVFLKGGSD	0.012	
123	SLVITDLTL	0.012	
344	LYGVYCFRA	0.012	
93	DVFVSMGYH	0.012	
253	FTSNFNGRF	0.010	
56	NVTLPCKFY	0.010	
334	FVGFPDKKH	0.010	
126	ITDLTLEDY	0.010	
81	WTKLTSDYL	0.010	
148	DTVVVALDL	0.009	
284	AQIAKVGQI	0.009	
264	LIHPTKLTY	0.008	
295	AWKILGYDR	0.008	
316	YPISRPRRR	0.006	
178	QQACLDQDA	0.006	
324	RCSPTEAAV	0.006	
150	VVVALDLQG	0.006	
276	VQACLNDGA	0.006	
32	IQAENGPHL	0.006	
331	AVRFVGFPD	0.006	
262	YYLIHPTKL	0.006	
39	HLLVEAEQA	0.006	
156	LQGVVFPYF	0.006	
336	GFPDKKHKL	0.006	
84	LTSDYLKEV	0.005	
20	DNYTLDHDR	0.005	
9	LISICWADH	0.004	
104	TYGGYQGRV	0.004	
325	CSPTEAAVR	0.004	
293	FAAWKILGY	0.004	
291	QIFAAWKIL	0.004	
256	NFNGRFYYL	0.004	
164	FPRLGRYNL	0.004	
232	VPGVRNYGF	0.004	
298	ILGYDRCDA	0.004	
209	WLSDGSVQY	0.004	
153	ALDLQGVVF	0.004	
279	CLNDGAQIA	0.004	
286	IAKVGQIFA	0.004	
194	LYDAWRGGL	0.004	
191	FDQLYDAWR	0.004	
181	CLDQDAVIA	0.004	
31	HIQAENGPH	0.004	
308	WLADGSVRY	0.004	
88	YLKEVDVFV	0.004	

Table XI: v.2-A11-9mers: 151P3D4			
Pos	123456789	Score	SeqID
34	KVDLLVPTK	6.000	
207	KQAEKNMKK	3.600	
56	HVQFVGSYK	2.000	
179	AVTATLEEK	2.000	
26	GQKMKQDKK	1.800	
134	QVPSRIFWR	1.200	
338	GQKHNVLAR	0.720	
389	GLGGKQKDK	0.600	
168	GAPHEVGWK	0.600	
211	KNMKKKIDK	0.480	
75	TVYQDEKQR	0.400	
385	SLEEGLGGK	0.400	
76	VYQDEKQRK	0.400	
20	SIRDHSGQK	0.400	
113	KYLAFLHKR	0.360	
121	RMNTNPSRR	0.240	
322	SPSGGGGLK	0.200	
344	LARGKPQRK	0.200	
4	HTTKTFPLR	0.200	
183	TLEEKRKEK	0.200	
180	VTATLEEKR	0.200	
155	GHASEAYKK	0.120	
285	LPLRTPWTR	0.120	
208	QAEKNMKKK	0.100	
181	TATLEEKRK	0.100	
238	TIAPLAATR	0.080	
343	VLARGKPQR	0.080	
373	SGYCGALWK	0.080	
112	LKYLAFLHK	0.080	
84	KDKVLLGRK	0.060	
105	GSFCRNKLK	0.060	
392	GKQKDKERK	0.060	
7	KTFPLRALH	0.060	
163	KVCLSGAPH	0.060	
86	KVLLGRKAV	0.045	
192	AEIHYRKNK	0.045	
280	SPAAWLPLR	0.040	
95	VVSCEGINI	0.040	
199	NKQLMRLQK	0.040	
59	FVGSYKLAY	0.040	
101	INISGSFCR	0.036	
111	KLKYLAFLH	0.036	
189	KEKAEIHYR	0.036	
22	RDHSGQKMK	0.030	
346	RGKPQRKPK	0.030	
203	MRLQKQAEK	0.030	
44	TGIITQGAK	0.030	
137	SRIFWRQEK	0.030	
256	RTPRAGSSA	0.030	
93	AVVVSCEGI	0.030	

Table XI: v.2-A11-9mers: 151P3D4			
Pos	123456789	Score	SeqID
83	RKDKVLLGR	0.024	
120	KRMNTNPSR	0.024	
138	RIFWRQEKA	0.024	
57	VQFVGSYKL	0.024	
374	GYCGALWKA	0.024	
5	TTKTFPLRA	0.020	
25	SGQKMKQDK	0.020	
332	PARHCQGQK	0.020	
38	LVPTKVTGI	0.020	
206	QKQAEKNMK	0.020	
244	ATRATRIGH	0.020	
302	STYDSLSPY	0.020	
73	HWTVYQDEK	0.020	
154	QGHASEAYK	0.020	
81	KQRKDKVLL	0.018	
133	FQVPSRIFW	0.018	
48	TQGAKDFGH	0.018	
30	KQDKKVDLL	0.018	
326	GGGLKKPAR	0.012	
251	GHPGGRTPR	0.012	
176	KYQAVTATL	0.012	
190	EKAEIHYRK	0.012	
78	QDEKQRKDK	0.010	
43	VTGIITQGA	0.010	
387	EEGLGGKQK	0.009	
241	PLAATRATR	0.008	
130	PYHFQVPSR	0.008	
378	ALWKAIESL	0.008	
358	NSWYVENGR	0.008	
196	YRKNKQLMR	0.008	
234	FIFKTIAPL	0.008	
14	LHIVVESIR	0.006	
391	GGKQKDKER	0.006	
340	KHNVLARGK	0.006	
248	TRIGHPGGR	0.006	
87	VLLGRKAVV	0.006	
172	EVGWKYQAV	0.006	
400	KAENGPHLL	0.006	
352	KPKSENNSW	0.006	
42	KVTGIITQG	0.006	
228	SPRGLGFIF	0.006	
231	GLGFIFKTI	0.006	
336	CQGQKHNVL	0.006	
266	RPPALSARA	0.006	
237	KTIAPLAAT	0.005	
323	PSGGGGLKK	0.004	
229	PRGLGFIFK	0.004	
169	APHEVGWKY	0.004	
308	SPYGPRNPL	0.004	
106	SFCRNKLKY	0.004	

Table XII: v.1-A11-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
234	GVRNYGFWDK	12.000	
288	KVGQIFAAWK	6.000	
93	DVFVSMGYHK	2.400	
81	WTKLTSDYLK	2.000	
331	AVRFVGFPDK	2.000	
260	RFYYLIHPTK	1.200	
56	NVTLPCKFYR	1.200	
334	FVGFPDKKHK	1.000	
279	CLNDGAQIAK	0.800	
39	HLLVEAEQAK	0.600	
106	GGYQGRVFLK	0.360	
94	VFVSMGYHKK	0.300	
67	PTAFGSGIHK	0.200	
214	SVQYPITKPR	0.200	
294	AAWKILGYDR	0.160	
129	LTLEDYGRYK	0.150	
236	RNYGFWDKDK	0.120	
324	RCSPTEAAVR	0.120	
48	KVFSHRGGNV	0.120	
158	GVVFPYFPRL	0.090	
160	VFPYFPRLGR	0.080	
251	FCFTSNFNGR	0.080	
343	KLYGVYCFRA	0.072	
53	RGGNVTLPCK	0.060	
103	KTYGGYQGRV	0.060	
74	IHKIRIKWTK	0.040	
190	SFDQLYDAWR	0.040	
231	TVPGVRNYGF	0.040	
332	VRFVGFPDKK	0.040	
313	SVRYPISRPR	0.040	
186	AVIASFDQLY	0.030	
150	VVVALDLQGV	0.030	
315	RYPISRPRRR	0.024	
275	AVQACLNDGA	0.020	
69	AFGSGIHKIR	0.020	
151	VVALDLQGVV	0.020	
157	QGVVFPYFPR	0.018	
297	KILGYDRCDA	0.018	
22	YTLDHDRAIH	0.015	
290	GQIFAAWKIL	0.013	
102	KKTYGGYQGR	0.012	
127	TDLTLEDYGR	0.012	
227	GGQNTVPGVR	0.012	
111	RVFLKGGSDS	0.012	
136	RYKCEVIEGL	0.012	
300	GYDRCDAGWL	0.012	
44	AEQAKVFSHR	0.012	
91	EVDVFVSMGY	0.012	
239	GFWDKDKSRY	0.012	
263	YLIHPTKLTY	0.012	

Table XII: v.1-A11-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
144	GLEDDTVVVA	0.012	
212	DGSVQYPITK	0.012	
166	RLGRYNLNFH	0.012	
5	LLLVLISICW	0.012	
3	SLLLLVLISI	0.012	
201	GLDWCNAGWL	0.012	
99	GYHKKTYGGY	0.012	
269	KLTYDEAVQA	0.012	
41	LVEAEQAKVF	0.010	
284	AQIAKVGQIF	0.009	
306	AGWLADGSVR	0.008	
314	VRYPISRPRR	0.008	
23	TLDHDRAIHI	0.008	
17	HLSDNYTLDH	0.008	
261	FYYLIHPTKL	0.008	
285	QIAKVGQIFA	0.008	
193	QLYDAWRGGL	0.008	
71	GSGIHKIRIK	0.006	
342	HKLYGVYCFR	0.006	
7	LVLISICWAD	0.006	
124	LVITDLTLED	0.006	
286	IAKVGQIFAA	0.006	
6	LLVLISICWA	0.006	
149	TVVVALDLQG	0.006	
178	QQACLDQDAV	0.006	
32	IQAENGPHLL	0.006	
8	VLISICWADH	0.006	
40	LLVEAEQAKV	0.006	
283	GAQIAKVGQI	0.006	
177	AQQACLDQDA	0.006	
83	KLTSDYLKEV	0.006	
333	RFVGFPDKKH	0.005	
19	SDNYTLDHDR	0.004	
9	LISICWADHL	0.004	
188	IASFDQLYDA	0.004	
163	YFPRLGRYNL	0.004	
256	NFNGRFYYLI	0.004	
171	NLNFHEAQQA	0.004	
271	TYDEAVQACL	0.004	
125	VITDLTLEDY	0.004	
33	QAENGPHLLV	0.004	
31	HIQAENGPHL	0.004	
292	IFAAWKILGY	0.004	
113	FLKGGSDSDA	0.004	
68	TAFGSGIHKI	0.004	
309	LADGSVRYPI	0.004	
161	FPYFPRLGRY	0.004	
238	YGFWDKDKSR	0.004	
141	VIEGLEDDTV	0.004	
336	GFPDKKHKLY	0.003	

Table XII: v.2-A11-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
75	TVYQDEKQRK	4.000	
111	KLKYLAFLHK	2.400	
43	VTGIITQGAK	1.000	
207	KQAEKNMKKK	0.900	
237	KTIAPLAATR	0.900	
182	ATLEEKRKEK	0.750	
100	GINISGSFCR	0.720	
205	LQKQAEKNMK	0.600	
342	NVLARGKPQR	0.600	
331	KPARHCQGQK	0.600	
133	FQVPSRIFWR	0.540	
180	VTATLEEKRK	0.500	
343	VLARGKPQRK	0.400	
228	SPRGLGFIFK	0.400	
322	SPSGGGGLKK	0.400	
202	LMRLQKQAEK	0.400	
179	AVTATLEEKR	0.400	
189	KEKAEIHYRK	0.360	
178	QAVTATLEEK	0.300	
191	KAEIHYRKNK	0.300	
77	YQDEKQRKDK	0.300	
198	KNKQLMRLQK	0.240	
129	RPYHFQVPSR	0.240	
247	ATRIGHPGGR	0.200	
195	HYRKNKQLMR	0.160	
284	WLPLRTPWTR	0.160	
74	WTVYQDEKQR	0.150	
372	GSGYCGALWK	0.120	
311	GPRNPLPNPR	0.120	
7	KTFPLRALHI	0.120	
55	GHVQFVGSYK	0.090	
33	KKVDLLVPTK	0.090	
86	KVLLGRKAVV	0.090	
13	ALHIVVESIR	0.080	
391	GGKQKDKERK	0.060	
153	PQGHASEAYK	0.060	
83	RKDKVLLGRK	0.060	
94	VVVSCEGINI	0.060	
34	KVDLLVPTKV	0.060	
42	KVTGIITQGA	0.060	
240	APLAATRATR	0.060	
206	QKQAEKNMKK	0.040	
154	QGHASEAYKK	0.040	
102	NISGSFCRNK	0.040	
257	TPRAGSSAHR	0.040	
56	HVQFVGSYKL	0.040	
30	KQDKKVDLLV	0.036	
386	LEEGLGGKQK	0.030	
256	RTPRAGSSAH	0.030	
47	ITQGAKDFGH	0.030	

Table XII: v.2-A11-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
120	KRMNTNPSRR	0.024	
25	SGQKMKQDKK	0.020	
38	LVPTKVTGII	0.020	
167	SGAPHEVGWK	0.020	
321	HSPSGGGGLK	0.020	
4	HTTKTFPLRA	0.020	
24	HSGQKMKQDK	0.020	
361	YVENGRPADL	0.020	
200	KQLMRLQKQA	0.013	
188	RKEKAEIHYR	0.012	
325	GGGGLKKPAR	0.012	
64	KLAYSNDGEH	0.012	
210	EKNMKKKIDK	0.012	
400	KAENGPHLLV	0.012	
72	EHWTVYQDEK	0.012	
231	GLGFIFKTIA	0.012	
28	KMKQDKKVDL	0.012	
221	TESPGGGSPR	0.012	
168	GAPHEVGWKY	0.012	
104	SGSFCRNKLK	0.010	
123	NTNPSRRPYH	0.010	
21	IRDHSGQKMK	0.010	
345	ARGKPQRKPK	0.010	
45	GIITQGAKDF	0.009	
19	ESIRDHSGQK	0.009	
26	GQKMKQDKKV	0.009	
113	KYLAFLHKRM	0.009	
233	GFIFKTIAPL	0.009	
92	KAVVVSCEGI	0.009	
12	RALHIVVESI	0.009	
377	GALWKAIESL	0.009	
384	ESLEEGLGGK	0.009	
381	KAIESLEEGL	0.009	
82	QRKDKVLLGR	0.008	
234	FIFKTIAPLA	0.008	
337	QGQKHNVLAR	0.008	
357	NNSWYVENGR	0.008	
112	LKYLAFLHKR	0.008	
374	GYCGALWKAI	0.006	
163	KVCLSGAPHE	0.006	
9	FPLRALHIVV	0.006	
352	KPKSENNSWY	0.006	
50	GAKDFGHVQF	0.006	
336	CQGQKHNVLA	0.006	
37	LLVPTKVTGI	0.006	
204	RLQKQAEKNM	0.006	
58	QFVGSYKLAY	0.006	
57	VQFVGSYKLA	0.006	
366	RPADLAGSGY	0.006	
273	RAPVPAASPA	0.006	

Table XIII: v.1-A24-9mers: 151P3D4			
Pos	123456789	Score	SeqID
262	YYLIHPTKL	330.000	
194	LYDAWRGGL	200.000	
87	DYLKEVDVF	150.000	
336	GFPDKKHKL	39.600	
256	NFNGRFYYL	36.000	
62	KFYRDPTAF	20.000	
169	RYNLNFHEA	19.800	
247	RYDVFCFTS	10.000	
76	KIRIKWTKL	8.800	
148	DTVVVALDL	8.400	
271	TYDEAVQAC	7.200	
186	AVIASFDQL	7.200	
10	ISICWADHL	6.000	
33	QAENGPHLL	6.000	
123	SLVITDLTL	6.000	
159	VVFPYFPRL	5.760	
121	DASLVITDL	5.600	
133	DYGRYKCEV	5.500	
69	AFGSGIHKI	5.500	
344	LYGVYCFRA	5.000	
300	GYDRCDAGW	5.000	
21	NYTLDHDRA	5.000	
104	TYGGYQGRV	5.000	
32	IQAENGPHL	4.800	
116	GGSDSDASL	4.800	
245	KSRYDVFCF	4.000	
164	FPRLGRYNL	4.000	
166	RLGRYNLNF	4.000	
81	WTKLTSDYL	4.000	
291	QIFAAWKIL	4.000	
106	GGYQGRVFL	4.000	
55	GNVTLPCKF	3.960	
2	KSLLLLVLI	3.600	
156	LQGVVFPYF	3.360	
285	QIAKVGQIF	3.360	
183	DQDAVIASF	2.800	
329	EAAVRFVGF	2.400	
326	SPTEAAVRF	2.400	
4	LLLLVLISI	2.100	
249	DVFCFTSNF	2.000	
232	VPGVRNYGF	2.000	
105	YGGYQGRVF	2.000	
253	FTSNFNGRF	2.000	
153	ALDLQGVVF	2.000	
22	YTLDHDRAI	1.800	
180	ACLDQDAVI	1.800	
290	GQIFAAWKI	1.650	
284	AQIAKVGQI	1.500	
278	ACLNDGAQI	1.500	
315	RYPISRPRR	1.500	

Table XIII: v.1-A24-9mers: 151P3D4			
Pos	123456789	Score	SeqID
260	RFYYLIHPT	1.200	
136	RYKCEVIEG	1.100	
134	YGRYKCEVI	1.000	
71	GSGIHKIRI	1.000	
257	FNGRFYYLI	1.000	
66	DPTAFGSGI	1.000	
163	YFPRLGRYN	0.900	
272	YDEAVQACL	0.840	
112	VFLKGGSDS	0.750	
216	QYPITKPRE	0.750	
107	GYQGRVFLK	0.750	
173	NFHEAQQAC	0.720	
261	FYYLIHPTK	0.700	
137	YKCEVIEGL	0.672	
190	SFDQLYDAW	0.600	
250	VFCFTSNFN	0.600	
162	PYFPRLGRY	0.600	
63	FYRDPTAFG	0.600	
16	DHLSDNYTL	0.600	
174	FHEAQQACL	0.600	
146	EDDTVVVAL	0.560	
99	GYHKKTYGG	0.500	
237	NYGFWDKDK	0.500	
49	VFSHRGGNV	0.500	
1	MKSLLLLVL	0.480	
28	RAIHIQAEN	0.462	
51	SHRGGNVTL	0.400	
243	KDKSRYDVF	0.400	
202	LDWCNAGWL	0.400	
301	YDRCDAGWL	0.400	
288	KVGQIFAAW	0.336	
90	KEVDVFVSM	0.302	
342	HKLYGVYCF	0.300	
53	RGGNVTLPC	0.280	
324	RCSPTEAAV	0.240	
42	VEAEQAKVF	0.240	
80	KWTKLTSDY	0.240	
152	VALDLQGVV	0.216	
279	CLNDGAQIA	0.216	
155	DLQGVVFPY	0.210	
122	ASLVITDLT	0.210	
6	LLVLISICW	0.210	
199	RGGLDWCNA	0.200	
48	KVFSHRGGN	0.200	
320	RPRRRCSPT	0.200	
115	KGGSDSDAS	0.200	
78	RIKWTKLTS	0.200	
36	NGPHLLVEA	0.198	
345	YGVYCFRAY	0.180	
129	LTLEDYGRY	0.180	

Table XIII: v.2-A24-9mers: 151P3D4			
Pos	123456789	Score	SeqID
176	KYQAVTATL	840.000	
195	HYRKNKQLM	30.000	
132	HFQVPSRIF	15.000	
400	KAENGPHLL	12.000	
360	WYVENGRPA	9.000	
81	KQRKDKVLL	8.000	
30	KQDKKVDLL	8.000	
8	TFPLRALHI	7.500	
382	AIESLEEGL	7.200	
279	ASPAAWLPL	6.000	
321	HSPSGGGGL	6.000	
374	GYCGALWKA	5.500	
104	SGSFCRNKL	5.280	
66	AYSNDGEHW	5.000	
336	CQGQKHNVL	4.800	
308	SPYGPRNPL	4.800	
57	VQFVGSYKL	4.400	
99	EGINISGSF	4.200	
107	FCRNKLKYL	4.000	
234	FIFKTIAPL	4.000	
378	ALWKAIESL	4.000	
109	RNKLKYLAF	4.000	
299	TSSSTYDSL	4.000	
371	AGSGYCGAL	4.000	
262	SSAHRPPAL	4.000	
1	MLEHTTKTF	3.000	
226	GGSPRGLGF	2.400	
228	SPRGLGFIF	2.400	
46	IITQGAKDF	2.000	
125	NPSRRPYHF	2.000	
231	GLGFIFKTI	1.680	
113	KYLAFLHKR	1.650	
227	GSPRGLGFI	1.500	
38	LVPTKVTGI	1.500	
93	AVVVSCEGI	1.500	
39	VPTKVTGII	1.400	
13	ALHIVVESI	1.400	
375	YCGALWKAI	1.200	
219	KYTESPGGG	1.200	
197	RKNKQLMRL	1.200	
76	VYQDEKQRK	1.080	
95	VVSCEGINI	1.000	
242	LAATRATRI	1.000	
399	RKAENGPHL	0.960	
58	QFVGSYKLA	0.750	
116	AFLHKRMNT	0.750	
29	MKQDKKVDL	0.720	
160	AYKKVCLSG	0.700	
235	IFKTIAPLA	0.700	
114	YLAFLHKRM	0.600	
362	VENGRPADL	0.600	
110	NKLKYLAFL	0.600	
303	TYDSLSPYG	0.600	
80	EKQRKDKVL	0.600	
106	SFCRNKLKY	0.550	
205	LQKQAEKNM	0.500	
62	SYKLAYSND	0.500	
12	RALHIVVES	0.462	
3	EHTTKTFPL	0.400	
158	SEAYKKVCL	0.400	
277	PAASPAAWL	0.400	
224	PGGGSPRGL	0.400	
194	IHYRKNKQL	0.400	
6	TKTFPLRAL	0.400	
266	RPPALSARA	0.360	
191	KAEIHYRKN	0.330	
204	RLQKQAEKN	0.330	
230	RGLGFIFKT	0.330	
86	KVLLGRKAV	0.300	
354	KSENNSWYV	0.300	
288	RTPWTRPSS	0.300	
142	RQEKADGGS	0.300	
237	KTIAPLAAT	0.300	
256	RTPRAGSSA	0.300	
393	KQKDKERKA	0.264	
352	KPKSENNSW	0.240	
138	RIFWRQEKA	0.220	
283	AWLPLRTPW	0.216	
17	VVESIRDHS	0.210	
293	RPSSCPTSS	0.200	
249	RIGHPGGRT	0.200	
51	AKDFGHVQF	0.200	
129	RPYHFQVPS	0.200	
169	APHEVGWKY	0.185	
316	LPNPRHSPS	0.180	
67	YSNDGEHWT	0.180	
201	QLMRLQKQA	0.180	
133	FQVPSRIFW	0.180	
123	NTNPSRRPY	0.180	
274	APVPAASPA	0.180	
314	NPLPNPRHS	0.180	
43	VTGIITQGA	0.168	
152	CPQGHASEA	0.165	
356	ENNSWYVEN	0.165	
377	GALWKAIES	0.165	
335	HCQGQKHNV	0.150	
94	VVVSCEGIN	0.150	
100	GINISGSFC	0.150	
87	VLLGRKAVV	0.150	
239	IAPLAATRA	0.150	

Table XIV: v.1-A24-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
136	RYKCEVIEGL	560.000	
271	TYDEAVQACL	336.000	
261	FYYLIHPTKL	220.000	
300	GYDRCDAGWL	200.000	
104	TYGGYQGRVF	100.000	
133	DYGRYKCEVI	50.000	
21	NYTLDHDRAI	50.000	
163	YFPRLGRYNL	30.000	
173	NFHEAQQACL	24.000	
247	RYDVFCFTSN	12.000	
87	DYLKEVDVFV	10.500	
252	CFTSNFNGRF	10.000	
115	KGGSDSDASL	8.000	
80	KWTKLTSDYL	8.000	
256	NFNGRFYYLI	7.500	
262	YYLIHPTKLT	7.500	
158	GVVFPYFPRL	7.200	
185	DAVIASFDQL	7.200	
344	LYGVYCFRAY	6.000	
122	ASLVITDLTL	6.000	
63	FYRDPTAFGS	6.000	
31	HIQAENGPHL	6.000	
290	GQIFAAWKIL	6.000	
237	NYGFWDKDKS	5.500	
335	VGFPDKKHKL	5.280	
155	DLQGVVFPYF	5.040	
284	AQIAKVGQIF	5.040	
99	GYHKKTYGGY	5.000	
32	IQAENGPHLL	4.800	
255	SNFNGRFYYL	4.800	
193	QLYDAWRGGL	4.800	
105	YGGYQGRVFL	4.000	
50	FSHRGGNVTL	4.000	
201	GLDWCNAGWL	4.000	
9	LISICWADHL	4.000	
54	GGNVTLPCKF	3.960	
152	VALDLQGVVF	3.600	
41	LVEAEQAKVF	3.000	
231	TVPGVRNYGF	3.000	
325	CSPTEAAVRF	3.000	
3	SLLLLVLISI	2.100	
289	VGQIFAAWKI	1.650	
169	RYNLNFHEAQ	1.500	
283	GAQIAKVGQI	1.500	
315	RYPISRPRRR	1.500	
309	LADGSVRYPI	1.400	
210	LSDGSVQYPI	1.400	
107	GYQGRVFLKG	1.386	
68	TAFGSGIHKI	1.100	
23	TLDHDRAIHI	1.000	

Table XIV: v.1-A24-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
277	QACLNDGAQI	1.000	
117	GSDSDASLVI	1.000	
70	FGSGIHKIRI	1.000	
179	QACLDQDAVI	1.000	
336	GFPDKKHKLY	0.900	
216	QYPITKPREP	0.825	
162	PYFPRLGRYN	0.720	
145	LEDDTVVVAL	0.672	
75	HKIRIKWTKL	0.660	
239	GFWDKDKSRY	0.600	
49	VFSHRGGNVT	0.600	
120	SDASLVITDL	0.560	
147	DDTVVVALDL	0.560	
182	LDQDAVIASF	0.504	
194	LYDAWRGGLD	0.500	
292	IFAAWKILGY	0.500	
15	ADHLSDNYTL	0.400	
341	KHKLYGVYCF	0.400	
2	KSLLLLVLIS	0.360	
245	KSRYDVFCFT	0.336	
65	RDPTAFGSGI	0.300	
297	KILGYDRCDA	0.300	
248	YDVFCFTSNF	0.300	
328	TEAAVRFVGF	0.240	
221	KPREPCGGQN	0.240	
72	SGIHKIRIKW	0.231	
83	KLTSDYLKEV	0.220	
177	AQQACLDQDA	0.216	
140	EVIEGLEDDT	0.216	
5	LLLVLISICW	0.210	
269	KLTYDEAVQA	0.200	
61	CKFYRDPTAF	0.200	
48	KVFSHRGGNV	0.200	
343	KLYGVYCFRA	0.200	
103	KTYGGYQGRV	0.200	
76	KIRIKWTKLT	0.200	
111	RVFLKGGSDS	0.200	
244	DKSRYDVFCF	0.200	
242	DKDKSRYDVF	0.200	
86	SDYLKEVDVF	0.200	
130	TLEDYGRYKC	0.198	
40	LLVEAEQAKV	0.198	
180	ACLDQDAVIA	0.180	
278	ACLNDGAQIA	0.180	
275	AVQACLNDGA	0.180	
4	LLLLVLISIC	0.180	
143	EGLEDDTVVV	0.180	
150	VVVALDLQGV	0.180	
144	GLEDDTVVVA	0.180	
200	GGLDWCNAGW	0.180	

Table XIV: v.2-A24-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
113	KYLAFLHKRM	90.000	
374	GYCGALWKAI	60.000	
233	GFIFKTIAPL	30.000	
106	SFCRNKLKYL	20.000	
381	KAIESLEEGL	17.280	
219	KYTESPGGGS	12.000	
109	RNKLKYLAFL	8.000	
28	KMKQDKKVDL	8.000	
335	HCQGQKHNVL	7.200	
307	LSPYGPRNPL	7.200	
130	PYHFQVPSRI	7.000	
56	HVQFVGSYKL	6.600	
361	YVENGRPADL	6.000	
157	ASEAYKKVCL	6.000	
377	GALWKAIESL	6.000	
103	ISGSFCRNKL	5.280	
230	RGLGFIFKTI	5.040	
160	AYKKVCLSGA	5.000	
66	AYSNDGEHWT	5.000	
278	AASPAAWLPL	4.800	
12	RALHIVVESI	4.200	
276	VPAASPAAWL	4.000	
261	GSSAHRPPAL	4.000	
223	SPGGGSPRGL	4.000	
193	EIHYRKNKQL	4.000	
370	LAGSGYCGAL	4.000	
5	TTKTFPLRAL	4.000	
227	GSPRGLGFIF	3.600	
124	TNPSRRPYHF	3.000	
92	KAVVVSCEGI	3.000	
45	GIITQGAKDF	3.000	
50	GAKDFGHVQF	2.400	
7	KTFPLRALHI	2.400	
38	LVPTKVTGII	2.100	
225	GGGSPRGLGF	2.000	
37	LLVPTKVTGI	1.800	
208	QAEKNMKKKI	1.650	
94	VVVSCEGINI	1.500	
204	RLQKQAEKNM	1.500	
176	KYQAVTATLE	1.500	
226	GGSPRGLGFI	1.200	
76	VYQDEKQRKD	0.990	
320	RHSPSGGGGL	0.960	
399	RKAENGPHLL	0.960	
116	AFLHKRMNTN	0.900	
360	WYVENGRPAD	0.900	
20	SIRDHSGQKM	0.792	
8	TFPLRALHIV	0.750	
132	HFQVPSRIFW	0.750	
58	QFVGSYKLAY	0.750	

Table XIV: v.2-A24-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
29	MKQDKKVDLL	0.720	
80	EKQRKDKVLL	0.600	
53	DFGHVQFVGS	0.600	
309	PYGPRNPLPN	0.600	
62	SYKLAYSNDG	0.600	
175	WKYQAVTATL	0.560	
195	HYRKNKQLMR	0.500	
303	TYDSLSPYGP	0.500	
235	IFKTIAPLAA	0.500	
196	YRKNKQLMRL	0.400	
398	ERKAENGPHL	0.400	
79	DEKQRKDKVL	0.400	
2	LEHTTKTFPL	0.400	
298	PTSSSTYDSL	0.400	
200	KQLMRLQKQA	0.360	
42	KVTGIITQGA	0.336	
211	KNMKKKIDKY	0.330	
348	KPQRKPKSEN	0.330	
34	KVDLLVPTKV	0.308	
273	RAPVPAASPA	0.300	
400	KAENGPHLLV	0.300	
142	RQEKADGGSC	0.300	
313	RNPLPNPRHS	0.300	
86	KVLLGRKAVV	0.300	
288	RTPWTRPSSC	0.300	
108	CRNKLKYLAF	0.300	
98	CEGINISGSF	0.280	
30	KQDKKVDLLV	0.280	
346	RGKPQRKPKS	0.264	
16	IVVESIRDHS	0.252	
366	RPADLAGSGY	0.240	
168	GAPHEVGWKY	0.231	
293	RPSSCPTSSS	0.200	
131	YHFQVPSRIF	0.200	
352	KPKSENNSWY	0.200	
183	TLEEKRKEKA	0.198	
67	YSNDGEHWTV	0.180	
274	APVPAASPAA	0.180	
283	AWLPLRTPWT	0.180	
9	FPLRALHIVV	0.180	
101	INISGSFCRN	0.180	
151	CCPQGHASEA	0.165	
164	VCLSGAPHEV	0.165	
87	VLLGRKAVVV	0.150	
305	DSLSPYGPRN	0.150	
97	SCEGINISGS	0.150	
99	EGINISGSFC	0.150	
152	CPQGHASEAY	0.150	
327	GGLKKPARHC	0.150	
239	IAPLAATRAT	0.150	

Table XV: v.1-B7-9mers: 151P3D4			
Pos	123456789	Score	SeqID
164	FPRLGRYNL	1200.000	
186	AVIASFDQL	60.000	
76	KIRIKWTKL	40.000	
159	VVFPYFPRL	20.000	
320	RPRRRCSPT	20.000	
121	DASLVITDL	12.000	
66	DPTAFGSGI	8.000	
106	GGYQGRVFL	6.000	
148	DTVVVALDL	4.000	
81	WTKLTSDYL	4.000	
51	SHRGGNVTL	4.000	
134	YGRYKCEVI	4.000	
116	GGSDSDASL	4.000	
224	EPCGGQNTV	4.000	
123	SLVITDLTL	4.000	
10	ISICWADHL	4.000	
291	QIFAAWKIL	4.000	
32	IQAENGPHL	4.000	
301	YDRCDAGWL	4.000	
33	QAENGPHLL	3.600	
221	KPREPCGGQ	3.000	
331	AVRFVGFPD	1.500	
180	ACLDQDAVI	1.200	
278	ACLNDGAQI	1.200	
284	AQIAKVGQI	1.200	
151	VVALDLQGV	1.000	
313	SVRYPISRP	0.750	
207	AGWLSDGSV	0.600	
152	VALDLQGVV	0.600	
179	QACLDQDAV	0.600	
306	AGWLADGSV	0.600	
234	GVRNYGFWD	0.500	
7	LVLISICWA	0.500	
161	FPYFPRLGR	0.450	
4	LLLLVLISI	0.400	
22	YTLDHDRAI	0.400	
137	YKCEVIEGL	0.400	
256	NFNGRFYYL	0.400	
202	LDWCNAGWL	0.400	
326	SPTEAAVRF	0.400	
71	GSGIHKIRI	0.400	
16	DHLSDNYTL	0.400	
1	MKSLLLLVL	0.400	
290	GQIFAAWKI	0.400	
336	GFPDKKHKL	0.400	
2	KSLLLLVLI	0.400	
257	FNGRFYYLI	0.400	
262	YYLIHPTKL	0.400	
232	VPGVRNYGF	0.400	
286	IAKVGQIFA	0.300	

Table XV: v.1-B7-9mers: 151P3D4			
Pos	123456789	Score	SeqID
41	LVEAEQAKV	0.300	
122	ASLVITDLT	0.300	
189	ASFDQLYDA	0.300	
318	ISRPRRRCS	0.300	
197	AWRGGLDWC	0.300	
96	VSMGYHKKT	0.300	
324	RCSPTEAAV	0.200	
88	YLKEVDVFV	0.200	
217	YPITKPREP	0.200	
316	YPISRPRRR	0.200	
37	GPHLLVEAE	0.200	
59	LPCKFYRDP	0.200	
245	KSRYDVFCF	0.200	
227	GGQNTVPGV	0.200	
266	HPTKLTYDE	0.200	
84	LTSDYLKEV	0.200	
143	EGLEDDTVV	0.200	
310	ADGSVRYPI	0.180	
194	LYDAWRGGL	0.180	
263	YLIHPTKLT	0.150	
275	AVQACLNDG	0.150	
298	ILGYDRCDA	0.150	
346	GVYCFRAYN	0.150	
56	NVTLPCKFY	0.150	
48	KVFSHRGGN	0.150	
69	AFGSGIHKI	0.120	
337	FPDKKHKLY	0.120	
146	EDDTVVVAL	0.120	
174	FHEAQQACL	0.120	
272	YDEAVQACL	0.120	
249	DVFCFTSNF	0.100	
172	LNFHEAQQA	0.100	
322	RRRCSPTEA	0.100	
90	KEVDVFVSM	0.100	
50	FSHRGGNVT	0.100	
279	CLNDGAQIA	0.100	
26	HDRAIHIQA	0.100	
167	LGRYNLNFH	0.100	
5	LLLVLISIC	0.100	
36	NGPHLLVEA	0.100	
270	LTYDEAVQA	0.100	
178	QQACLDQDA	0.100	
109	QGRVFLKGG	0.100	
199	RGGLDWCNA	0.100	
288	KVGQIFAAW	0.100	
212	DGSVQYPIT	0.100	
258	NGRFYYLIH	0.100	
39	HLLVEAEQA	0.100	
276	VQACLNDGA	0.100	
53	RGGNVTLPC	0.100	

Table XV: v.2-B7-9mers: 151P3D4			
Pos	123456789	Score	SeqID
308	SPYGPRNPL	180.000	
81	KQRKDKVLL	40.000	
107	FCRNKLKYL	40.000	
279	ASPAAWLPL	12.000	
378	ALWKAIESL	12.000	
371	AGSGYCGAL	12.000	
39	VPTKVTGII	8.000	
240	APLAATRAT	6.000	
104	SGSFCRNKL	6.000	
93	AVVVSCEGI	6.000	
274	APVPAASPA	6.000	
271	SARAPVPAA	4.500	
336	CQGQKHNVL	4.000	
299	TSSSTYDSL	4.000	
234	FIFKTIAPL	4.000	
262	SSAHRPPAL	4.000	
228	SPRGLGFIF	4.000	
57	VQFVGSYKL	4.000	
9	FPLRALHIV	4.000	
321	HSPSGGGGL	4.000	
400	KAENGPHLL	3.600	
382	AIESLEEGL	3.600	
311	GPRNPLPNP	3.000	
38	LVPTKVTGI	2.000	
318	NPRHSPSGG	2.000	
95	VVSCEGINI	2.000	
266	RPPALSARA	2.000	
289	TPWTRPSSC	2.000	
257	TPRAGSSAH	2.000	
252	HPGGRTPRA	2.000	
152	CPQGHASEA	2.000	
277	PAASPAAWL	1.800	
86	KVLLGRKAV	1.500	
13	ALHIVVESI	1.200	
169	APHEVGWKY	1.200	
30	KQDKKVDLL	1.200	
242	LAATRATRI	1.200	
291	WTRPSSCPT	1.000	
114	YLAFLHKRM	1.000	
205	LQKQAEKNM	1.000	
195	HYRKNKQLM	1.000	
172	EVGWKYQAV	1.000	
6	TKTFPLRAL	0.600	
156	HASEAYKKV	0.600	
264	AHRPPALSA	0.450	
254	GGRTPRAGS	0.450	
244	ATRATRIGH	0.450	
362	VENGRPADL	0.400	
29	MKQDKKVDL	0.400	
3	EHTTKTFPL	0.400	

Table XV: v.2-B7-9mers: 151P3D4			
Pos	123456789	Score	SeqID
316	LPNPRHSPS	0.400	
129	RPYHFQVPS	0.400	
110	NKLKYLAFL	0.400	
186	EKRKEKAEI	0.400	
125	NPSRRPYHF	0.400	
375	YCGALWKAI	0.400	
176	KYQAVTATL	0.400	
399	RKAENGPHL	0.400	
227	GSPRGLGFI	0.400	
293	RPSSCPTSS	0.400	
276	VPAASPAAW	0.400	
352	KPKSENNSW	0.400	
231	GLGFIFKTI	0.400	
80	EKQRKDKVL	0.400	
224	PGGGSPRGL	0.400	
314	NPLPNPRHS	0.400	
197	RKNKQLMRL	0.400	
194	IHYRKNKQL	0.400	
158	SEAYKKVCL	0.400	
239	IAPLAATRA	0.300	
247	ATRIGHPGG	0.300	
344	LARGKPQRK	0.300	
201	QLMRLQKQA	0.300	
370	LAGSGYCGA	0.300	
297	CPTSSSTYD	0.200	
280	SPAAWLPLR	0.200	
285	LPLRTPWTR	0.200	
335	HCQGQKHNV	0.200	
366	RPADLAGSG	0.200	
49	QGAKDFGHV	0.200	
89	LGRKAVVVS	0.200	
322	SPSGGGGLK	0.200	
127	SRRPYHFQV	0.200	
88	LLGRKAVVV	0.200	
135	VPSRIFWRQ	0.200	
331	KPARHCQGQ	0.200	
10	PLRALHIVV	0.200	
87	VLLGRKAVV	0.200	
348	KPQRKPKSE	0.200	
223	SPGGGSPRG	0.200	
165	CLSGAPHEV	0.200	
363	ENGRPADLA	0.150	
149	GSCCPQGHA	0.150	
179	AVTATLEEK	0.150	
237	KTIAPLAAT	0.150	
249	RIGHPGGRT	0.150	
261	GSSAHRPPA	0.150	
36	DLLVPTKVT	0.150	
328	GLKKPARHC	0.150	
282	AAWLPLRTP	0.135	

Table XVI: v.1-B7-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
158	GVVFPYFPRL	20.000	
185	DAVIASFDQL	12.000	
122	ASLVITDLTL	12.000	
105	YGGYQGRVFL	6.000	
193	QLYDAWRGGL	6.000	
316	YPISRPRRRC	4.500	
217	YPITKPREPC	4.500	
335	VGFPDKKHKL	4.000	
9	LISICWADHL	4.000	
255	SNFNGRFYYL	4.000	
32	IQAENGPHLL	4.000	
221	KPREPCGGQN	4.000	
50	FSHRGGNVTL	4.000	
290	GQIFAAWKIL	4.000	
115	KGGSDSDASL	4.000	
164	FPRLGRYNLN	4.000	
31	HIQAENGPHL	4.000	
326	SPTEAAVRFV	4.000	
59	LPCKFYRDPT	3.000	
320	RPRRRCSPTE	2.000	
266	HPTKLTYDEA	2.000	
331	AVRFVGFPDK	1.500	
275	AVQACLNDGA	1.500	
179	QACLDQDAVI	1.200	
15	ADHLSDNYTL	1.200	
277	QACLNDGAQI	1.200	
283	GAQIAKVGQI	1.200	
201	GLDWCNAGWL	1.200	
68	TAFGSGIHKI	1.200	
48	KVFSHRGGNV	1.000	
151	VVALDLQGVV	1.000	
150	VVVALDLQGV	1.000	
245	KSRYDVFCFT	1.000	
76	KIRIKWTKLT	1.000	
305	DAGWLADGSV	0.600	
206	NAGWLSDGSV	0.600	
163	YFPRLGRYNL	0.600	
309	LADGSVRYPI	0.540	
234	GVRNYGFWDK	0.500	
140	EVIEGLEDDT	0.500	
95	FVSMGYHKKT	0.500	
313	SVRYPISRPR	0.500	
70	FGSGIHKIRI	0.400	
161	FPYFPRLGRY	0.400	
136	RYKCEVIEGL	0.400	
147	DDTVVVALDL	0.400	
173	NFHEAQQACL	0.400	
232	VPGVRNYGFW	0.400	
289	VGQIFAAWKI	0.400	
75	HKIRIKWTKL	0.400	

Table XVI: v.1-B7-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
261	FYYLIHPTKL	0.400	
3	SLLLLVLISI	0.400	
120	SDASLVITDL	0.400	
80	KWTKLTSDYL	0.400	
286	IAKVGQIFAA	0.300	
121	DASLVITDLT	0.300	
186	AVIASFDQLY	0.300	
188	IASFDQLYDA	0.300	
180	ACLDQDAVIA	0.300	
196	DAWRGGLDWC	0.300	
177	AQQACLDQDA	0.300	
278	ACLNDGAQIA	0.300	
33	QAENGPHLLV	0.270	
66	DPTAFGSGIH	0.200	
226	CGGQNTVPGV	0.200	
224	EPCGGQNTVP	0.200	
116	GGSDSDASLV	0.200	
109	QGRVFLKGGS	0.200	
37	GPHLLVEAEQ	0.200	
178	QQACLDQDAV	0.200	
143	EGLEDDTVVV	0.200	
103	KTYGGYQGRV	0.200	
40	LLVEAEQAKV	0.200	
83	KLTSDYLKEV	0.200	
297	KILGYDRCDA	0.150	
318	ISRPRRRCSP	0.150	
322	RRRCSPTEAA	0.150	
271	TYDEAVQACL	0.120	
145	LEDDTVVVAL	0.120	
117	GSDSDASLVI	0.120	
210	LSDGSVQYPI	0.120	
300	GYDRCDAGWL	0.120	
23	TLDHDRAIHI	0.120	
167	LGRYNLNFHE	0.100	
249	DVFCFTSNFN	0.100	
269	KLTYDEAVQA	0.100	
73	GIHKIRIKWT	0.100	
6	LLVLISICWA	0.100	
35	ENGPHLLVEA	0.100	
20	DNYTLDHDRA	0.100	
270	LTYDEAVQAC	0.100	
285	QIAKVGQIFA	0.100	
111	RVFLKGGSDS	0.100	
172	LNFHEAQQAC	0.100	
171	NLNFHEAQQA	0.100	
134	YGRYKCEVIE	0.100	
113	FLKGGSDSDA	0.100	
343	KLYGVYCFRA	0.100	
4	LLLLVLISIC	0.100	
231	TVPGVRNYGF	0.100	

Table XVI: v.2-B7-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
276	VPAASPAAWL	120.000	
223	SPGGGSPRGL	80.000	
278	AASPAAWLPL	36.000	
56	HVQFVGSYKL	20.000	
377	GALWKAIESL	12.000	
370	LAGSGYCGAL	12.000	
381	KAIESLEEGL	12.000	
20	SIRDHSGQKM	10.000	
307	LSPYGPRNPL	9.000	
5	TTKTFPLRAL	6.000	
361	YVENGRPADL	6.000	
103	ISGSFCRNKL	6.000	
274	APVPAASPAA	6.000	
109	RNKLKYLAFL	4.000	
335	HCQGQKHNVL	4.000	
261	GSSAHRPPAL	4.000	
28	KMKQDKKVDL	4.000	
9	FPLRALHIVV	4.000	
193	EIHYRKNKQL	4.000	
157	ASEAYKKVCL	3.600	
318	NPRHSPSGGG	3.000	
39	VPTKVTGIIT	2.000	
94	VVVSCEGINI	2.000	
228	SPRGLGFIFK	2.000	
311	GPRNPLPNPR	2.000	
38	LVPTKVTGII	2.000	
257	TPRAGSSAHR	2.000	
280	SPAAWLPLRT	2.000	
92	KAVVVSCEGI	1.200	
12	RALHIVVESI	1.200	
89	LGRKAVVVSC	1.000	
107	FCRNKLKYLA	1.000	
204	RLQKQAEKNM	1.000	
86	KVLLGRKAVV	1.000	
240	APLAATRATR	0.900	
169	APHEVGWKYQ	0.600	
348	KPQRKPKSEN	0.600	
267	PPALSARAPV	0.600	
293	RPSSCPTSSS	0.600	
271	SARAPVPAAS	0.600	
42	KVTGIITQGA	0.500	
172	EVGWKYQAVT	0.500	
115	LAFLHKRMNT	0.450	
260	AGSSAHRPPA	0.450	
263	SAHRPPALSA	0.450	
344	LARGKPQRKP	0.450	
314	NPLPNPRHSP	0.450	
226	GGSPRGLGFI	0.400	
106	SFCRNKLKYL	0.400	
398	ERKAENGPHL	0.400	

Table XVI: v.2-B7-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
366	RPADLAGSGY	0.400	
2	LEHTTKTFPL	0.400	
175	WKYQAVTATL	0.400	
152	CPQGHASEAY	0.400	
79	DEKQRKDKVL	0.400	
399	RKAENGPHLL	0.400	
320	RHSPSGGGGL	0.400	
297	CPTSSSTYDS	0.400	
298	PTSSSTYDSL	0.400	
233	GFIFKTIAPL	0.400	
196	YRKNKQLMRL	0.400	
230	RGLGFIFKTI	0.400	
7	KTFPLRALHI	0.400	
80	EKQRKDKVLL	0.400	
352	KPKSENNSWY	0.400	
29	MKQDKKVDLL	0.400	
37	LLVPTKVTGI	0.400	
208	QAEKNMKKKI	0.360	
239	IAPLAATRAT	0.300	
34	KVDLLVPTKV	0.300	
289	TPWTRPSSCP	0.300	
125	NPSRRPYHFQ	0.300	
156	HASEAYKKVC	0.300	
247	ATRIGHPGGR	0.300	
244	ATRATRIGHP	0.300	
269	ALSARAPVPA	0.300	
285	LPLRTPWTRP	0.300	
93	AVVVSCEGIN	0.300	
273	RAPVPAASPA	0.300	
282	AAWLPLRTPW	0.270	
400	KAENGPHLLV	0.270	
291	WTRPSSCPTS	0.200	
26	GQKMKQDKKV	0.200	
164	VCLSGAPHEV	0.200	
252	HPGGRTPRAG	0.200	
322	SPSGGGGLKK	0.200	
308	SPYGPRNPLP	0.200	
87	VLLGRKAVVV	0.200	
67	YSNDGEHWTV	0.200	
129	RPYHFQVPSR	0.200	
331	KPARHCQGQK	0.200	
254	GGRTPRAGSS	0.200	
126	PSRRPYHFQV	0.200	
364	NGRPADLAGS	0.200	
266	RPPALSARAP	0.200	
48	TQGAKDFGHV	0.200	
316	LPNPRHSPSG	0.200	
135	VPSRIFWRQE	0.200	
179	AVTATLEEKR	0.150	
327	GGLKKPARHC	0.150	

Table XVII: v.1-B35-9mers: 151P3D4			
Pos	123456789	Score	SeqID
164	FPRLGRYNL	60.000	
245	KSRYDVFCF	45.000	
326	SPTEAAVRF	40.000	
232	VPGVRNYGF	20.000	
320	RPRRRCSPT	12.000	
337	FPDKKHKLY	12.000	
254	TSNFNGRFY	10.000	
66	DPTAFGSGI	8.000	
76	KIRIKWTKL	6.000	
293	FAAWKILGY	6.000	
129	LTLEDYGRY	6.000	
10	ISICWADHL	5.000	
209	WLSDGSVQY	4.000	
308	WLADGSVRY	4.000	
224	EPCGGQNTV	4.000	
2	KSLLLLVLI	4.000	
81	WTKLTSDYL	3.000	
121	DASLVITDL	3.000	
329	EAAVRFVGF	3.000	
221	KPREPCGGQ	2.400	
187	VIASFDQLY	2.000	
230	NTVPGVRNY	2.000	
255	SNFNGRFYY	2.000	
71	GSGIHKIRI	2.000	
345	YGVYCFRAY	2.000	
166	RLGRYNLNF	2.000	
116	GGSDSDASL	2.000	
264	LIHPTKLTY	2.000	
97	SMGYHKKTY	2.000	
56	NVTLPCKFY	2.000	
155	DLQGVVFPY	2.000	
32	IQAENGPHL	2.000	
14	WADHLSDNY	1.800	
196	DAWRGGLDW	1.500	
318	ISRPRRRCS	1.500	
134	YGRYKCEVI	1.200	
88	YLKEVDVFV	1.200	
152	VALDLQGVV	1.200	
106	GGYQGRVFL	1.000	
148	DTVVVALDL	1.000	
189	ASFDQLYDA	1.000	
186	AVIASFDQL	1.000	
253	FTSNFNGRF	1.000	
123	SLVITDLTL	1.000	
55	GNVTLPCKF	1.000	
159	VVFPYFPRL	1.000	
285	QIAKVGQIF	1.000	
156	LQGVVFPYF	1.000	
249	DVFCFTSNF	1.000	
291	QIFAAWKIL	1.000	

Table XVII: v.1-B35-9mers: 151P3D4			
Pos	123456789	Score	SeqID
105	YGGYQGRVF	1.000	
288	KVGQIFAAW	1.000	
179	QACLDQDAV	0.900	
286	IAKVGQIFA	0.900	
33	QAENGPHLL	0.900	
90	KEVDVFVSM	0.800	
22	YTLDHDRAI	0.800	
180	ACLDQDAVI	0.800	
278	ACLNDGAQI	0.600	
243	KDKSRYDVF	0.600	
100	YHKKTYGGY	0.600	
78	RIKWTKLTS	0.600	
143	EGLEDDTVV	0.600	
28	RAIHIQAEN	0.600	
126	ITDLTLEDY	0.600	
96	VSMGYHKKT	0.500	
122	ASLVITDLT	0.500	
6	LLVLISICW	0.500	
50	FSHRGGNVT	0.500	
73	GIHKIRIKW	0.500	
301	YDRCDAGWL	0.450	
117	GSDSDASLV	0.450	
84	LTSDYLKEV	0.400	
80	KWTKLTSDY	0.400	
284	AQIAKVGQI	0.400	
324	RCSPTEAAV	0.400	
257	FNGRFYYLI	0.400	
4	LLLLVLISI	0.400	
290	GQIFAAWKI	0.400	
340	KKHKLYGVY	0.400	
153	ALDLQGVVF	0.300	
305	DAGWLADGS	0.300	
199	RGGLDWCNA	0.300	
115	KGGSDSDAS	0.300	
151	VVALDLQGV	0.300	
51	SHRGGNVTL	0.300	
206	NAGWLSDGS	0.300	
62	KFYRDPTAF	0.300	
183	DQDAVIASF	0.300	
270	LTYDEAVQA	0.300	
42	VEAEQAKVF	0.200	
53	RGGNVTLPC	0.200	
59	LPCKFYRDP	0.200	
306	AGWLADGSV	0.200	
137	YKCEVIEGL	0.200	
227	GGQNTVPGV	0.200	
37	GPHLLVEAE	0.200	
161	FPYFPRLGR	0.200	
336	GFPDKKHKL	0.200	
48	KVFSHRGGN	0.200	

Table XVII: v.2-B35-9mers: 151P3D4			
Pos	123456789	Score	SeqID
352	KPKSENNSW	90.000	
169	APHEVGWKY	80.000	
228	SPRGLGFIF	60.000	
308	SPYGPRNPL	20.000	
125	NPSRRPYHF	20.000	
276	VPAASPAAW	10.000	
81	KQRKDKVLL	9.000	
39	VPTKVTGII	8.000	
205	LQKQAEKNM	6.000	
212	NMKKKIDKY	6.000	
109	RNKLKYLAF	6.000	
299	TSSSTYDSL	5.000	
262	SSAHRPPAL	5.000	
321	HSPSGGGGL	5.000	
279	ASPAAWLPL	5.000	
302	STYDSLSPY	4.000	
129	RPYHFQVPS	4.000	
266	RPPALSARA	4.000	
9	FPLRALHIV	4.000	
293	RPSSCPTSS	4.000	
107	FCRNKLKYL	3.000	
372	GSGYCGALW	2.500	
316	LPNPRHSPS	2.000	
274	APVPAASPA	2.000	
152	CPQGHASEA	2.000	
252	HPGGRTPRA	2.000	
296	SCPTSSSTY	2.000	
240	APLAATRAT	2.000	
114	YLAFLHKRM	2.000	
227	GSPRGLGFI	2.000	
123	NTNPSRRPY	2.000	
59	FVGSYKLAY	2.000	
289	TPWTRPSSC	2.000	
314	NPLPNPRHS	2.000	
400	KAENGPHLL	1.800	
242	LAATRATRI	1.200	
393	KQKDKERKA	1.200	
156	HASEAYKKV	1.200	
371	AGSGYCGAL	1.000	
99	EGINISGSF	1.000	
336	CQGQKHNVL	1.000	
104	SGSFCRNKL	1.000	
234	FIFKTIAPL	1.000	
378	ALWKAIESL	1.000	
57	VQFVGSYKL	1.000	
46	IITQGAKDF	1.000	
226	GGSPRGLGF	1.000	
96	VSCEGINIS	1.000	
67	YSNDGEHWT	1.000	
271	SARAPVPAA	0.900	

Table XVII: v.2-B35-9mers: 151P3D4			
Pos	123456789	Score	SeqID
366	RPADLAGSG	0.800	
257	TPRAGSSAH	0.600	
318	NPRHSPSGG	0.600	
195	HYRKNKQLM	0.600	
95	VVSCEGINI	0.600	
12	RALHIVVES	0.600	
354	KSENNSWYV	0.600	
311	GPRNPLPNP	0.600	
30	KQDKKVDLL	0.600	
261	GSSAHRPPA	0.500	
300	SSSTYDSLS	0.500	
270	LSARAPVPA	0.500	
167	SGAPHEVGW	0.500	
295	SSCPTSSST	0.500	
149	GSCCPQGHA	0.500	
61	GSYKLAYSN	0.500	
133	FQVPSRIFW	0.500	
69	NDGEHWTVY	0.400	
13	ALHIVVESI	0.400	
231	GLGFIFKTI	0.400	
38	LVPTKVTGI	0.400	
375	YCGALWKAI	0.400	
348	KPQRKPKSE	0.400	
86	KVLLGRKAV	0.400	
93	AVVVSCEGI	0.400	
399	RKAENGPHL	0.400	
331	KPARHCQGQ	0.400	
328	GLKKPARHC	0.300	
277	PAASPAAWL	0.300	
239	IAPLAATRA	0.300	
89	LGRKAVVVS	0.300	
49	QGAKDFGHV	0.300	
382	AIESLEEGL	0.300	
254	GGRTPRAGS	0.300	
291	WTRPSSCPT	0.300	
377	GALWKAIES	0.300	
263	SAHRPPALS	0.300	
159	EAYKKVCLS	0.300	
1	MLEHTTKTF	0.300	
370	LAGSGYCGA	0.300	
115	LAFLHKRMN	0.300	
5	TTKTFPLRA	0.300	
230	RGLGFIFKT	0.200	
280	SPAAWLPLR	0.200	
138	RIFWRQEKA	0.200	
322	SPSGGGGLK	0.200	
288	RTPWTRPSS	0.200	
297	CPTSSSTYD	0.200	
249	RIGHPGGRT	0.200	
204	RLQKQAEKN	0.200	

Table XVIII: v.1-B35-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
161	FPYFPRLGRY	40.000	
221	KPREPCGGQN	24.000	
254	TSNFNGRFYY	10.000	
96	VSMGYHKKTY	10.000	
232	VPGVRNYGFW	10.000	
326	SPTEAAVRFV	8.000	
164	FPRLGRYNLN	6.000	
152	VALDLQGVVF	6.000	
122	ASLVITDLTL	5.000	
325	CSPTEAAVRF	5.000	
189	ASFDQLYDAW	5.000	
50	FSHRGGNVTL	5.000	
125	VITDLTLEDY	4.000	
185	DAVIASFDQL	3.000	
128	DLTLEDYGRY	3.000	
245	KSRYDVFCFT	3.000	
55	GNVTLPCKFY	2.000	
115	KGGSDSDASL	2.000	
59	LPCKFYRDPT	2.000	
217	YPITKPREPC	2.000	
229	QNTVPGVRNY	2.000	
253	FTSNFNGRFY	2.000	
32	IQAENGPHLL	2.000	
193	QLYDAWRGGL	2.000	
263	YLIHPTKLTY	2.000	
186	AVIASFDQLY	2.000	
316	YPISRPRRRC	2.000	
266	HPTKLTYDEA	2.000	
277	QACLNDGAQI	1.800	
68	TAFGSGIHKI	1.200	
179	QACLDQDAVI	1.200	
283	GAQIAKVGQI	1.200	
320	RPRRRCSPTE	1.200	
284	AQIAKVGQIF	1.000	
335	VGFPDKKHKL	1.000	
299	LGYDRCDAGW	1.000	
105	YGGYQGRVFL	1.000	
290	GQIFAAWKIL	1.000	
255	SNFNGRFYYL	1.000	
158	GVVFPYFPRL	1.000	
231	TVPGVRNYGF	1.000	
2	KSLLLLVLIS	1.000	
200	GGLDWCNAGW	1.000	
31	HIQAENGPHL	1.000	
54	GGNVTLPCKF	1.000	
9	LISICWADHL	1.000	
155	DLQGVVFPYF	1.000	
88	YLKEVDVFVS	0.900	
286	IAKVGQIFAA	0.900	
91	EVDVFVSMGY	0.600	

Table XVIII: v.1-B35-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
210	LSDGSVQYPI	0.600	
305	DAGWLADGSV	0.600	
136	RYKCEVIEGL	0.600	
206	NAGWLSDGSV	0.600	
117	GSDSDASLVI	0.600	
339	DKKHKLYGVY	0.600	
143	EGLEDDTVVV	0.600	
116	GGSDSDASLV	0.600	
239	GFWDKDKSRY	0.600	
76	KIRIKWTKLT	0.600	
341	KHKLYGVYCF	0.600	
40	LLVEAEQAKV	0.600	
10	ISICWADHLS	0.500	
5	LLLVLISICW	0.500	
72	SGIHKIRIKW	0.500	
103	KTYGGYQGRV	0.400	
336	GFPDKKHKLY	0.400	
13	CWADHLSDNY	0.400	
48	KVFSHRGGNV	0.400	
3	SLLLLVLISI	0.400	
289	VGQIFAAWKI	0.400	
70	FGSGIHKIRI	0.400	
83	KLTSDYLKEV	0.400	
309	LADGSVRYPI	0.360	
297	KILGYDRCDA	0.300	
109	QGRVFLKGGS	0.300	
269	KLTYDEAVQA	0.300	
180	ACLDQDAVIA	0.300	
201	GLDWCNAGWL	0.300	
121	DASLVITDLT	0.300	
41	LVEAEQAKVF	0.300	
196	DAWRGGLDWC	0.300	
188	IASFDQLYDA	0.300	
150	VVVALDLQGV	0.300	
178	QQACLDQDAV	0.300	
113	FLKGGSDSDA	0.300	
85	TSDYLKEVDV	0.300	
111	RVFLKGGSDS	0.200	
151	VVALDLQGVV	0.200	
344	LYGVYCFRAY	0.200	
343	KLYGVYCFRA	0.200	
307	GWLADGSVRY	0.200	
292	IFAAWKILGY	0.200	
80	KWTKLTSDYL	0.200	
182	LDQDAVIASF	0.200	
66	DPTAFGSGIH	0.200	
270	LTYDEAVQAC	0.200	
99	GYHKKTYGGY	0.200	
226	CGGQNTVPGV	0.200	
224	EPCGGQNTVP	0.200	

Table XVIII: v.2-B35-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
352	KPKSENNSWY	240.000	
366	RPADLAGSGY	160.000	
152	CPQGHASEAY	40.000	
276	VPAASPAAWL	20.000	
223	SPGGGSPRGL	20.000	
50	GAKDFGHVQF	18.000	
20	SIRDHSGQKM	12.000	
381	KAIESLEEGL	12.000	
301	SSTYDSLSPY	10.000	
105	GSFCRNKLKY	10.000	
295	SSCPTSSSTY	10.000	
109	RNKLKYLAFL	6.000	
168	GAPHEVGWKY	6.000	
28	KMKQDKKVDL	6.000	
227	GSPRGLGFIF	5.000	
261	GSSAHRPPAL	5.000	
307	LSPYGPRNPL	5.000	
103	ISGSFCRNKL	5.000	
348	KPQRKPKSEN	4.000	
9	FPLRALHIVV	4.000	
211	KNMKKKIDKY	4.000	
293	RPSSCPTSSS	4.000	
204	RLQKQAEKNM	4.000	
67	YSNDGEHWTV	3.000	
370	LAGSGYCGAL	3.000	
278	AASPAAWLPL	3.000	
377	GALWKAIESL	3.000	
5	TTKTFPLRAL	3.000	
166	LSGAPHEVGW	2.500	
187	KRKEKAEIHY	2.400	
12	RALHIVVESI	2.400	
92	KAVVVSCEGI	2.400	
65	LAYSNDGEHW	2.250	
39	VPTKVTGIIT	2.000	
297	CPTSSSTYDS	2.000	
280	SPAAWLPLRT	2.000	
274	APVPAASPAA	2.000	
54	FGHVQFVGSY	2.000	
122	MNTNPSRRPY	2.000	
282	AAWLPLRTPW	1.500	
157	ASEAYKKVCL	1.500	
56	HVQFVGSYKL	1.000	
193	EIHYRKNKQL	1.000	
45	GIITQGAKDF	1.000	
225	GGGSPRGLGF	1.000	
335	HCQGQKHNVL	1.000	
124	TNPSRRPYHF	1.000	
271	SARAPVPAAS	0.900	
7	KTFPLRALHI	0.800	
230	RGLGFIFKTI	0.800	

Table XVIII: v.2-B35-10mers: 151P3D4			
Pos	1234567890	Score	SeqID
68	SNDGEHWTVY	0.600	
311	GPRNPLPNPR	0.600	
94	VVVSCEGINI	0.600	
273	RAPVPAASPA	0.600	
228	SPRGLGFIFK	0.600	
156	HASEAYKKVC	0.600	
257	TPRAGSSAHR	0.600	
346	RGKPQRKPKS	0.600	
26	GQKMKQDKKV	0.600	
318	NPRHSPSGGG	0.600	
371	AGSGYCGALW	0.500	
299	TSSSTYDSLS	0.500	
149	GSCCPQGHAS	0.500	
305	DSLSPYGPRN	0.500	
270	LSARAPVPAA	0.500	
262	SSAHRPPALS	0.500	
364	NGRPADLAGS	0.450	
86	KVLLGRKAVV	0.400	
399	RKAENGPHLL	0.400	
226	GGSPRGLGFI	0.400	
266	RPPALSARAP	0.400	
37	LLVPTKVTGI	0.400	
129	RPYHFQVPSR	0.400	
113	KYLAFLHKRM	0.400	
169	APHEVGWKYQ	0.400	
38	LVPTKVTGII	0.400	
267	PPALSARAPV	0.400	
331	KPARHCQGQK	0.400	
208	QAEKNMKKKI	0.360	
400	KAENGPHLLV	0.360	
79	DEKQRKDKVL	0.300	
107	FCRNKLKYLA	0.300	
115	LAFLHKRMNT	0.300	
398	ERKAENGPHL	0.300	
239	IAPLAATRAT	0.300	
361	YVENGRPADL	0.300	
291	WTRPSSCPTS	0.300	
263	SAHRPPALSA	0.300	
212	NMKKKIDKYT	0.300	
196	YRKNKQLMRL	0.300	
254	GGRTPRAGSS	0.300	
126	PSRRPYHFQV	0.300	
89	LGRKAVVVSC	0.300	
48	TQGAKDFGHV	0.300	
314	NPLPNPRHSP	0.200	
194	IHYRKNKQLM	0.200	
322	SPSGGGGLKK	0.200	
164	VCLSGAPHEV	0.200	
288	RTPWTRPSSC	0.200	
42	KVTGIITQGA	0.200	

Table XIX: Frequently Occurring Motifs

Name	avrg. % identity	Description	Potential Function
zf-C2H2	34%	Zinc finger, C2H2 type	Nucleic acid-binding protein functions as transcription factor, nuclear location probable
cytochrome_b_N	68%	Cytochrome b(N-terminal)/b6/petB	membrane bound oxidase, generate superoxide
ig	19%	Immunoglobulin domain	domains are one hundred amino acids long and include a conserved intradomain disulfide bond.
WD40	18%	WD domain, G-beta repeat	tandem repeats of about 40 residues, each containing a Trp-Asp motif. Function in signal transduction and protein interaction
PDZ	23%	PDZ domain	may function in targeting signaling molecules to sub-membranous sites
LRR	28%	Leucine Rich Repeat	short sequence motifs involved in protein-protein interactions
pkinase	23%	Protein kinase domain	conserved catalytic core common to both serine/threonine and tyrosine protein kinases containing an ATP binding site and a catalytic site
PH	16%	PH domain	pleckstrin homology involved in intracellular signaling or as constituents of the cytoskeleton
EGF	34%	EGF-like domain	30-40 amino-acid long found in the extracellular domain of membrane-bound proteins or in secreted proteins
rvt	49%	Reverse transcriptase (RNA-dependent DNA polymerase)	
ank	25%	Ank repeat	Cytoplasmic protein, associates integral membrane proteins to the cytoskeleton
oxidored_q1	32%	NADH-Ubiquinone/plastoquinone (complex I), various chains	membrane associated. Involved in proton translocation across the membrane

Table XIX, continued: Frequently Occurring Motifs			
Name	**avrg. % identity**	**Description**	**Potential Function**
efhand	24%	EF hand	calcium-binding domain, consists of a12 residue loop flanked on both sides by a 12 residue alpha-helical domain
rvp	79%	Retroviral aspartyl protease	Aspartyl or acid proteases, centered on a catalytic aspartyl residue
Collagen	42%	Collagen triple helix repeat (20 copies)	extracellular structural proteins involved in formation of connective tissue. The sequence consists of the G-X-Y and the polypeptide chains forms a triple helix.
fn3	20%	Fibronectin type III domain	Located in the extracellular ligand-binding region of receptors and is about 200 amino acid residues long with two pairs of cysteines involved in disulfide bonds
7tm_1	19%	7 transmembrane receptor (rhodopsin family)	seven hydrophobic transmembrane regions, with the N-terminus located extracellularly while the C-terminus is cytoplasmic. Signal through G proteins

Table XX: Motifs and Post-translational Modifications of 151P3D4

N-glycosylation site.
21 - 24 NYTL
56 - 59 NVTL

cAMP- and cGMP-dependent protein kinase phosphorylation site
323 - 326 RRcS

Protein kinase C phosphorylation site
51 - 53 ShR
313 - 315 SvR

Casein kinase II phosphorylation site
118 - 121 SdsD
130 - 133 TleD
246 - 249 SryD
271 - 274 TydE
326 - 329 SptE

N-myristoylation site
54 - 59 GGnvTL
106 - 111 GGyqGR
116 - 121 GGsdSD
201 - 206 GLdwCN
227 - 232 GGqnTV
283 - 288 GAqiAK
290 - 295 GQifAA

TABLE XXI: Protein Properties of 151P3D4

151P3D4 V.1	Bioinformatic Program	URL	Outcome
ORF	ORF finder		bp316-1380 (includes stop)
Protein length			354 aa
Transmembrane region	TM Pred	http://www.ch.embnet.org/	no TM
	HMMTop	http://www.enzim.hu/hmmtop/	no TM, intracellular
	Sosui	http://www.genome.ad.jp/SOSui/	no TM, soluble protein
	TMHMM	http://www.cbs.dtu.dk/services/TMHMM	no TM
Signal Peptide	Signal P	http://www.cbs.dtu.dk/services/SignalP/	yes
pI	pI/MW tool	http://www.expasy.ch/tools/	7.1
Molecular weight	pI/MW tool	http://www.expasy.ch/tools/	40.1 kDa
Localization	PSORT	http://psort.nibb.ac.jp/	53% outside, 51% lysosome
	PSORT II	http://psort.nibb.ac.jp/	66% extracellular, 11% cytoplasmic
Motifs	Pfam	http://www.sanger.ac.uk/Pfam/	Ig domain, extracellular link domain
	Prints	http://www.biochem.ucl.ac.uk/	Link module
	Blocks	http://www.blocks.fhcrc.org/	Link motif, C-type lectin domain, receptor tyrosine kinase class III

151P3D4 V.2	Bioinformatic Program	URL	Outcome
ORF	ORF finder		bp1-2166 (includes stop)
Protein length			721aa
Transmembrane region	TM Pred	http://www.ch.embnet.org/	no TM
	HMMTop	http://www.enzim.hu/hmmtop/	no TM, extracellular
	Sosui	http://www.genome.ad.jp/SOSui/	no TM, soluble protein
	TMHMM	http://www.cbs.dtu.dk/services/TMHMM	no TM
Signal Peptide	Signal P	http://www.cbs.dtu.dk/services/SignalP/	none
pI	pI/MW tool	http://www.expasy.ch/tools/	pI9.6
Molecular weight	pI/MW tool	http://www.expasy.ch/tools/	80.7kDa
Localization	PSORT	http://psort.nibb.ac.jp/	82% nucleus, 42% peroxisome
	PSORT II	http://psort.nibb.ac.jp/	52% nuclear, 26% cytoplasmic
Motifs	Pfam	http://www.sanger.ac.uk/Pfam/	F5/8 type C domain, Ig domain extracellular link domain
	Prints	http://www.biochem.ucl.ac.uk/	link module signature
	Blocks	http://www.blocks.fhcrc.org/	Link motif, coagulation factor 5/8 type c domain (FA58C), ribosomal protein L13, C-type lectin domain, receptor tyrosine kinase class III

TABLE XXII 151P3D4 v.1: HLA Peptide Scoring Results A1 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
126	I T D L T L E D Y	31	
230	N T V P G V R N Y	28	
337	F P D K K H K L Y	28	
240	F W D K D K S R Y	26	
14	W A D H L S D N Y	25	
264	L I H P T K L T Y	25	
293	F A A W K I L G Y	22	
18	L S D N Y T L D H	21	
129	L T L E D Y G R Y	21	
155	D L Q G V V F P Y	20	
254	T S N F N G R F Y	20	
255	S N F N G R F Y Y	20	
345	Y G V Y C F R A Y	20	
162	P Y F P R L G R Y	19	
92	V D V F V S M G Y	18	
187	V I A S F D Q L Y	18	
209	W L S D G S V Q Y	18	
303	R C D A G W L A D	18	
308	W L A D G S V R Y	18	
97	S M G Y H K K T Y	17	
100	Y H K K T Y G G Y	17	
327	P T E A A V R F V	17	
56	N V T L P C K F Y	16	
64	Y R D P T A F G S	16	
117	G S D S D A S L V	16	
153	A L D L Q G V V F	16	
210	L S D G S V Q Y P	16	
340	K K H K L Y G V Y	16	
80	K W T K L T S D Y	15	
85	T S D Y L K E V D	15	
108	Y Q G R V F L K G	15	
131	L E D Y G R Y K C	15	
222	P R E P C G G Q N	15	
280	L N D G A Q I A K	15	
33	Q A E N G P H L L	14	
119	D S D A S L V I T	14	
148	D T V V V A L D L	14	
272	Y D E A V Q A C L	14	
130	T L E D Y G R Y K	13	
146	E D D T V V V A L	13	
174	F H E A Q Q A C L	13	
23	T L D H D R A I H	12	
41	L V E A E Q A K V	12	
89	L K E V D V F V S	12	
91	E V D V F V S M G	12	
138	K C E V I E G L E	12	
141	V I E G L E D D T	12	
144	G L E D D T V V V	12	
145	L E D D T V V V A	12	
183	D Q D A V I A S F	12	
190	S F D Q L Y D A W	12	
201	G L D W C N A G W	12	
309	L A D G S V R Y P	12	

TABLE XXII 151P3D4 v.1: HLA Peptide Scoring Results A1 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
34	A E N G P H L L V	11	
35	E N G P H L L V E	11	
57	V T L P C K F Y R	11	
181	C L D Q D A V I A	11	
194	L Y D A W R G G L	11	
242	D K D K S R Y D V	11	
271	T Y D E A V Q A C	11	
3	S L L L L V L I S	10	
25	D H D R A I H I Q	10	
43	E A E Q A K V F S	10	
219	I T K P R E P C G	10	
247	R Y D V F C F T S	10	
300	G Y D R C D A G W	10	
50	F S H R G G N V T	9	
83	K L T S D Y L K E	9	
96	V S M G Y H K K T	9	
103	K T Y G G Y Q G R	9	
118	S D S D A S L V I	9	
123	S L V I T D L T L	9	
159	V V F P Y F P R L	9	
161	F P Y F P R L G R	9	
166	R L G R Y N L N F	9	
196	D A W R G G L D W	9	
213	G S V Q Y P I T K	9	
312	G S V R Y P I S R	9	
318	I S R P R R R C S	9	
22	Y T L D H D R A I	8	
53	R G G N V T L P C	8	
67	P T A F G S G I H	8	
71	G S G I H K I R I	8	
204	W C N A G W L S D	8	
253	F T S N F N G R F	8	
1	M K S L L L L V L	7	
4	L L L L V L I S I	7	
73	G I H K I R I K W	7	
84	L T S D Y L K E V	7	
120	S D A S L V I T D	7	
122	A S L V I T D L T	7	
125	V I T D L T L E D	7	
139	C E V I E G L E D	7	
150	V V V A L D L Q G	7	
189	A S F D Q L Y D A	7	
246	S R Y D V F C F T	7	
258	N G R F Y Y L I H	7	
2	K S L L L L V L I	6	
12	I C W A D H L S D	6	
51	S H R G G N V T L	6	
68	T A F G S G I H K	6	
78	R I K W T K L T S	6	
81	W T K L T S D Y L	6	
105	Y G G Y Q G R V F	6	
176	E A Q Q A C L D Q	6	
188	I A S F D Q L Y D	6	

TABLE XXII 151P3D4 v.1: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
235	V R N Y G F W D K	6	
263	Y L I H P T K L T	6	
267	P T K L T Y D E A	6	
270	L T Y D E A V Q A	6	
274	E A V Q A C L N D	6	
286	I A K V G Q I F A	6	
292	I F A A W K I L G	6	
332	V R F V G F P D K	6	
338	P D K K H K L Y G	6	
6	L L V L I S I C W	5	
45	E Q A K V F S H R	5	
69	A F G S G I H K I	5	
88	Y L K E V D V F V	5	
90	K E V D V F V S M	5	
95	F V S M G Y H K K	5	
113	F L K G G S D S D	5	
136	R Y K C E V I E G	5	
147	D D T V V V A L D	5	
156	L Q G V V F P Y F	5	
182	L D Q D A V I A S	5	
195	Y D A W R G G L D	5	
214	S V Q Y P I T K P	5	
215	V Q Y P I T K P R	5	
225	P C G G Q N T V P	5	
245	K S R Y D V F C F	5	
248	Y D V F C F T S N	5	
259	G R F Y Y L I H P	5	
314	V R Y P I S R P R	5	
325	C S P T E A A V R	5	
335	V G F P D K K H K	5	
10	I S I C W A D H L	4	
11	S I C W A D H L S	4	
24	L D H D R A I H I	4	
26	H D R A I H I Q A	4	
42	V E A E Q A K V F	4	
52	H R G G N V T L P	4	
58	T L P C K F Y R D	4	
107	G Y Q G R V F L K	4	
112	V F L K G G S D S	4	
137	Y K C E V I E G L	4	
164	F P R L G R Y N L	4	
175	H E A Q Q A C L D	4	
180	A C L D Q D A V I	4	
186	A V I A S F D Q L	4	
197	A W R G G L D W C	4	
211	S D G S V Q Y P I	4	
231	T V P G V R N Y G	4	
238	Y G F W D K D K S	4	
256	N F N G R F Y Y L	4	
262	Y Y L I H P T K L	4	
273	D E A V Q A C L N	4	
281	N D G A Q I A K V	4	
287	A K V G Q I F A A	4	

TABLE XXII 151P3D4 v.1: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
310	A D G S V R Y P I	4	
324	R C S P T E A A V	4	
328	T E A A V R F V G	4	
331	A V R F V G F P D	4	
334	F V G F P D K K H	4	
343	K L Y G V Y C F R	4	
17	H L S D N Y T L D	3	
29	A I H I Q A E N G	3	
65	R D P T A F G S G	3	
102	K K T Y G G Y Q G	3	
106	G G Y Q G R V F L	3	
134	Y G R Y K C E V I	3	
154	L D L Q G V V F P	3	
160	V F P Y F P R L G	3	
163	Y F P R L G R Y N	3	
165	P R L G R Y N L N	3	
169	R Y N L N F H E A	3	
203	D W C N A G W L S	3	
223	R E P C G G Q N T	3	
224	E P C G G Q N T V	3	
228	G Q N T V P G V R	3	
236	R N Y G F W D K D	3	
252	C F T S N F N G R	3	
257	F N G R F Y Y L I	3	
279	C L N D G A Q I A	3	
285	Q I A K V G Q I F	3	
288	K V G Q I F A A W	3	
302	D R C D A G W L A	3	
313	S V R Y P I S R P	3	
319	S R P R R R C S P	3	
329	E A A V R F V G F	3	
333	R F V G F P D K K	3	
342	H K L Y G V Y C F	3	
8	V L I S I C W A D	2	
19	S D N Y T L D H D	2	
38	P H L L V E A E Q	2	
44	A E Q A K V F S H	2	
49	V F S H R G G N V	2	
55	G N V T L P C K F	2	
60	P C K F Y R D P T	2	
63	F Y R D P T A F G	2	
70	F G S G I H K I R	2	
72	S G I H K I R I K	2	
76	K I R I K W T K L	2	
77	I R I K W T K L T	2	
82	T K L T S D Y L K	2	
86	S D Y L K E V D V	2	
87	D Y L K E V D V F	2	
94	V F V S M G Y H K	2	
101	H K K T Y G G Y Q	2	
104	T Y G G Y Q G R V	2	
121	D A S L V I T D L	2	
124	L V I T D L T L E	2	

TABLE XXII 151P3D4 v.1: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
140	E	V	I	E	G	L	E	D	D	2	
149	T	V	V	V	A	L	D	L	Q	2	
152	V	A	L	D	L	Q	G	V	V	2	
170	Y	N	L	N	F	H	E	A	Q	2	
191	F	D	Q	L	Y	D	A	W	R	2	
208	G	W	L	S	D	G	S	V	Q	2	
212	D	G	S	V	Q	Y	P	I	T	2	
217	Y	P	I	T	K	P	R	E	P	2	
218	P	I	T	K	P	R	E	P	C	2	
229	Q	N	T	V	P	G	V	R	N	2	
232	V	P	G	V	R	N	Y	G	F	2	
234	G	V	R	N	Y	G	F	W	D	2	
251	F	C	F	T	S	N	F	N	G	2	
269	K	L	T	Y	D	E	A	V	Q	2	
276	V	Q	A	C	L	N	D	G	A	2	
278	A	C	L	N	D	G	A	Q	I	2	
284	A	Q	I	A	K	V	G	Q	I	2	
290	G	Q	I	F	A	A	W	K	I	2	
295	A	W	K	I	L	G	Y	D	R	2	
296	W	K	I	L	G	Y	D	R	C	2	
297	K	I	L	G	Y	D	R	C	D	2	
298	I	L	G	Y	D	R	C	D	A	2	
301	Y	D	R	C	D	A	G	W	L	2	
307	G	W	L	A	D	G	S	V	R	2	
316	Y	P	I	S	R	P	R	R	R	2	
317	P	I	S	R	P	R	R	R	C	2	
326	S	P	T	E	A	A	V	R	F	2	
330	A	A	V	R	F	V	G	F	P	2	
336	G	F	P	D	K	K	H	K	L	2	
341	K	H	K	L	Y	G	V	Y	C	2	
5	L	L	L	V	L	I	S	I	C	1	
15	A	D	H	L	S	D	N	Y	T	1	
16	D	H	L	S	D	N	Y	T	L	1	
31	H	I	Q	A	E	N	G	P	H	1	
32	I	Q	A	E	N	G	P	H	L	1	
37	G	P	H	L	L	V	E	A	E	1	
39	H	L	L	V	E	A	E	Q	A	1	
40	L	L	V	E	A	E	Q	A	K	1	
47	A	K	V	F	S	H	R	G	G	1	
48	K	V	F	S	H	R	G	G	N	1	
66	D	P	T	A	F	G	S	G	I	1	
111	R	V	F	L	K	G	G	S	D	1	
114	L	K	G	G	S	D	S	D	A	1	
128	D	L	T	L	E	D	Y	G	R	1	
132	E	D	Y	G	R	Y	K	C	E	1	
133	D	Y	G	R	Y	K	C	E	V	1	
143	E	G	L	E	D	D	T	V	V	1	
151	V	V	A	L	D	L	Q	G	V	1	
158	G	V	V	F	P	Y	F	P	R	1	
168	G	R	Y	N	L	N	F	H	E	1	
171	N	L	N	F	H	E	A	Q	Q	1	
177	A	Q	Q	A	C	L	D	Q	D	1	
193	Q	L	Y	D	A	W	R	G	G	1	

TABLE XXII 151P3D4 v.1: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
198	W	R	G	G	L	D	W	C	N	1	
205	C	N	A	G	W	L	S	D	G	1	
207	A	G	W	L	S	D	G	S	V	1	
221	K	P	R	E	P	C	G	G	Q	1	
227	G	G	Q	N	T	V	P	G	V	1	
243	K	D	K	S	R	Y	D	V	F	1	
244	D	K	S	R	Y	D	V	F	C	1	
250	V	F	C	F	T	S	N	F	N	1	
261	F	Y	Y	L	I	H	P	T	K	1	
268	T	K	L	T	Y	D	E	A	V	1	
275	A	V	Q	A	C	L	N	D	G	1	
282	D	G	A	Q	I	A	K	V	G	1	
289	V	G	Q	I	F	A	A	W	K	1	
294	A	A	W	K	I	L	G	Y	D	1	
304	C	D	A	G	W	L	A	D	G	1	
306	A	G	W	L	A	D	G	S	V	1	
315	R	Y	P	I	S	R	P	R	R	1	
323	R	R	C	S	P	T	E	A	A	1	
344	L	Y	G	V	Y	C	F	R	A	1	
346	G	V	Y	C	F	R	A	Y	N	1	

TABLE XXII 151P3D4 v.2: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
188	R	K	E	K	A	E	I	H	Y	29	
123	N	T	N	P	S	R	R	P	Y	26	
367	P	A	D	L	A	G	S	G	Y	26	
106	S	F	C	R	N	K	L	K	Y	25	
59	F	V	G	S	Y	K	L	A	Y	23	
302	S	T	Y	D	S	L	S	P	Y	23	
169	A	P	H	E	V	G	W	K	Y	21	
220	Y	T	E	S	P	G	G	G	S	20	
83	R	K	D	K	V	L	L	G	R	18	
97	S	C	E	G	I	N	I	S	G	18	
157	A	S	E	A	Y	K	K	V	C	17	
212	N	M	K	K	K	I	D	K	Y	17	
296	S	C	P	T	S	S	S	T	Y	17	
55	G	H	V	Q	F	V	G	S	Y	16	
69	N	D	G	E	H	W	T	V	Y	16	
323	P	S	G	G	G	G	L	K	K	16	
353	P	K	S	E	N	N	S	W	Y	16	
153	P	Q	G	H	A	S	E	A	Y	15	
361	Y	V	E	N	G	R	P	A	D	15	
385	S	L	E	E	G	L	G	G	K	15	
77	Y	Q	D	E	K	Q	R	K	D	14	
354	K	S	E	N	N	S	W	Y	V	14	
386	L	E	E	G	L	G	G	K	Q	14	
400	K	A	E	N	G	P	H	L	L	14	
7	K	T	F	P	L	R	A	L	H	13	
21	I	R	D	H	S	G	Q	K	M	13	
30	K	Q	D	K	K	V	D	L	L	13	
51	A	K	D	F	G	H	V	Q	F	13	

TABLE XXII 151P3D4 v.2: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
68	S	N	D	G	E	H	W	T	V	13	
78	Q	D	E	K	Q	R	K	D	K	13	
145	K	A	D	G	G	S	C	C	P	13	
5	T	T	K	T	F	P	L	R	A	12	
17	V	V	E	S	I	R	D	H	S	12	
170	P	H	E	V	G	W	K	Y	Q	12	
183	T	L	E	E	K	R	K	E	K	12	
184	L	E	E	K	R	K	E	K	A	12	
191	K	A	E	I	H	Y	R	K	N	12	
208	Q	A	E	K	N	M	K	K	K	12	
244	A	T	R	A	T	R	I	G	H	12	
264	A	H	R	P	P	A	L	S	A	12	
301	S	S	T	Y	D	S	L	S	P	12	
1	M	L	E	H	T	T	K	T	F	11	
4	H	T	T	K	T	F	P	L	R	11	
34	K	V	D	L	L	V	P	T	K	11	
40	P	T	K	V	T	G	I	I	T	11	
216	K	I	D	K	Y	T	E	S	P	11	
226	G	G	S	P	R	G	L	G	F	11	
279	A	S	P	A	A	W	L	P	L	11	
382	A	I	E	S	L	E	E	G	L	11	
384	E	S	L	E	E	G	L	G	G	11	
394	Q	K	D	K	E	R	K	A	E	11	
31	Q	D	K	K	V	D	L	L	V	10	
70	D	G	E	H	W	T	V	Y	Q	10	
74	W	T	V	Y	Q	D	E	K	Q	10	
133	F	Q	V	P	S	R	I	F	W	10	
142	R	Q	E	K	A	D	G	G	S	10	
291	W	T	R	P	S	S	C	P	T	10	
295	S	S	C	P	T	S	S	S	T	10	
303	T	Y	D	S	L	S	P	Y	G	10	
364	N	G	R	P	A	D	L	A	G	10	
373	S	G	Y	C	G	A	L	W	K	10	
396	D	K	E	R	K	A	E	N	G	10	
82	Q	R	K	D	K	V	L	L	G	9	
112	L	K	Y	L	A	F	L	H	K	9	
150	S	C	C	P	Q	G	H	A	S	9	
160	A	Y	K	K	V	C	L	S	G	9	
180	V	T	A	T	L	E	E	K	R	9	
182	A	T	L	E	E	K	R	K	E	9	
196	Y	R	K	N	K	Q	L	M	R	9	
229	P	R	G	L	G	F	I	F	K	9	
247	A	T	R	I	G	H	P	G	G	9	
300	S	S	S	T	Y	D	S	L	S	9	
306	S	L	S	P	Y	G	P	R	N	9	
67	Y	S	N	D	G	E	H	W	T	8	
222	E	S	P	G	G	G	S	P	R	8	
310	Y	G	P	R	N	P	L	P	N	8	
322	S	P	S	G	G	G	G	L	K	8	
32	D	K	K	V	D	L	L	V	P	7	
43	V	T	G	I	I	T	Q	G	A	7	
47	I	T	Q	G	A	K	D	F	G	7	
96	V	S	C	E	G	I	N	I	S	7	
105	G	S	F	C	R	N	K	L	K	7	
127	S	R	R	P	Y	H	F	Q	V	7	
199	N	K	Q	L	M	R	L	Q	K	7	
221	T	E	S	P	G	G	G	S	P	7	
236	F	K	T	I	A	P	L	A	A	7	
237	K	T	I	A	P	L	A	A	T	7	
250	I	G	H	P	G	G	R	T	P	7	
256	R	T	P	R	A	G	S	S	A	7	
272	A	R	A	P	V	P	A	A	S	7	
278	A	A	S	P	A	A	W	L	P	7	
288	R	T	P	W	T	R	P	S	S	7	
309	P	Y	G	P	R	N	P	L	P	7	
321	H	S	P	S	G	G	G	G	L	7	
324	S	G	G	G	G	L	K	K	P	7	
338	G	Q	K	H	N	V	L	A	R	7	
346	R	G	K	P	Q	R	K	P	K	7	
372	G	S	G	Y	C	G	A	L	W	7	
8	T	F	P	L	R	A	L	H	I	6	
10	P	L	R	A	L	H	I	V	V	6	
41	T	K	V	T	G	I	I	T	Q	6	
54	F	G	H	V	Q	F	V	G	S	6	
95	V	V	S	C	E	G	I	N	I	6	
109	R	N	K	L	K	Y	L	A	F	6	
166	L	S	G	A	P	H	E	V	G	6	
167	S	G	A	P	H	E	V	G	W	6	
178	Q	A	V	T	A	T	L	E	E	6	
227	G	S	P	R	G	L	G	F	I	6	
262	S	S	A	H	R	P	P	A	L	6	
281	P	A	A	W	L	P	L	R	T	6	
283	A	W	L	P	L	R	T	P	W	6	
298	P	T	S	S	S	T	Y	D	S	6	
307	L	S	P	Y	G	P	R	N	P	6	
333	A	R	H	C	Q	G	Q	K	H	6	
358	N	S	W	Y	V	E	N	G	R	6	
380	W	K	A	I	E	S	L	E	E	6	
13	A	L	H	I	V	V	E	S	I	5	
23	D	H	S	G	Q	K	M	K	Q	5	
35	V	D	L	L	V	P	T	K	V	5	
37	L	L	V	P	T	K	V	T	G	5	
45	G	I	I	T	Q	G	A	K	D	5	
57	V	Q	F	V	G	S	Y	K	L	5	
104	S	G	S	F	C	R	N	K	L	5	
126	P	S	R	R	P	Y	H	F	Q	5	
149	G	S	C	C	P	Q	G	H	A	5	
204	R	L	Q	K	Q	A	E	K	N	5	
223	S	P	G	G	G	S	P	R	G	5	
261	G	S	S	A	H	R	P	P	A	5	
263	S	A	H	R	P	P	A	L	S	5	
274	A	P	V	P	A	A	S	P	A	5	
294	P	S	S	C	P	T	S	S	S	5	
305	D	S	L	S	P	Y	G	P	R	5	
308	S	P	Y	G	P	R	N	P	L	5	
320	R	H	S	P	S	G	G	G	G	5	

TABLE XXII 151P3D4 v.2: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
329	L K K P A R H C Q	5	
388	E G L G G K Q K D	5	
15	H I V V E S I R D	4	
19	E S I R D H S G Q	4	
24	H S G Q K M K Q D	4	
27	Q K M K Q D K K V	4	
61	G S Y K L A Y S N	4	
87	V L L G R K A V V	4	
102	N I S G S F C R N	4	
103	I S G S F C R N K	4	
128	R R P Y H F Q V P	4	
131	Y H F Q V P S R I	4	
135	V P S R I F W R Q	4	
136	P S R I F W R Q E	4	
177	Y Q A V T A T L E	4	
211	K N M K K K I D K	4	
225	G G G S P R G L G	4	
228	S P R G L G F I F	4	
231	G L G F I F K T I	4	
233	G F I F K T I A P	4	
238	T I A P L A A T R	4	
251	G H P G G R T P R	4	
255	G R T P R A G S S	4	
265	H R P P A L S A R	4	
270	L S A R A P V P A	4	
271	S A R A P V P A A	4	
280	S P A A W L P L R	4	
287	L R T P W T R P S	4	
299	T S S S T Y D S L	4	
312	P R N P L P N P R	4	
314	N P L P N P R H S	4	
316	L P N P R H S P S	4	
343	V L A R G K P Q R	4	
345	A R G K P Q R K P	4	
350	Q R K P K S E N N	4	
377	G A L W K A I E S	4	
390	L G G K Q K D K E	4	
22	R D H S G Q K M K	3	
36	D L L V P T K V T	3	
39	V P T K V T G I I	3	
49	Q G A K D F G H V	3	
53	D F G H V Q F V G	3	
56	H V Q F V G S Y K	3	
58	Q F V G S Y K L A	3	
63	Y K L A Y S N D G	3	
85	D K V L L G R K A	3	
86	K V L L G R K A V	3	
90	G R K A V V V S C	3	
91	R K A V V V S C E	3	
111	K L K Y L A F L H	3	
114	Y L A F L H K R M	3	
130	P Y H F Q V P S R	3	
137	S R I F W R Q E K	3	

TABLE XXII 151P3D4 v.2: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
144	E K A D G G S C C	3	
159	E A Y K K V C L S	3	
164	V C L S G A P H E	3	
173	V G W K Y Q A V T	3	
192	A E I H Y R K N K	3	
207	K Q A E K N M K K	3	
209	A E K N M K K K I	3	
230	R G L G F I F K T	3	
269	A L S A R A P V P	3	
315	P L P N P R H S P	3	
335	H C Q G Q K H N V	3	
337	Q G Q K H N V L A	3	
341	H N V L A R G K P	3	
355	S E N N S W Y V E	3	
359	S W Y V E N G R P	3	
363	E N G R P A D L A	3	
368	A D L A G S G Y C	3	
369	D L A G S G Y C G	3	
371	A G S G Y C G A L	3	
374	G Y C G A L W K A	3	
387	E E G L G G K Q K	3	
14	L H I V V E S I R	2	
20	S I R D H S G Q K	2	
25	S G Q K M K Q D K	2	
26	G Q K M K Q D K K	2	
46	I I T Q G A K D F	2	
50	G A K D F G H V Q	2	
52	K D F G H V Q F V	2	
62	S Y K L A Y S N D	2	
64	K L A Y S N D G E	2	
66	A Y S N D G E H W	2	
72	E H W T V Y Q D E	2	
79	D E K Q R K D K V	2	
81	K Q R K D K V L L	2	
88	L L G R K A V V V	2	
89	L G R K A V V V S	2	
92	K A V V V S C E G	2	
101	I N I S G S F C R	2	
108	C R N K L K Y L A	2	
113	K Y L A F L H K R	2	
116	A F L H K R M N T	2	
117	F L H K R M N T N	2	
138	R I F W R Q E K A	2	
139	I F W R Q E K A D	2	
146	A D G G S C C P Q	2	
151	C C P Q G H A S E	2	
155	G H A S E A Y K K	2	
156	H A S E A Y K K V	2	
158	S E A Y K K V C L	2	
161	Y K K V C L S G A	2	
165	C L S G A P H E V	2	
174	G W K Y Q A V T A	2	
176	K Y Q A V T A T L	2	

TABLE XXII 151P3D4 v.2: HLA Peptide Scoring Results A1 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
193	E	I	H	Y	R	K	N	K	Q	2	
195	H	Y	R	K	N	K	Q	L	M	2	
197	R	K	N	K	Q	L	M	R	L	2	
198	K	N	K	Q	L	M	R	L	Q	2	
200	K	Q	L	M	R	L	Q	K	Q	2	
202	L	M	R	L	Q	K	Q	A	E	2	
235	I	F	K	T	I	A	P	L	A	2	
241	P	L	A	A	T	R	A	T	R	2	
249	R	I	G	H	P	G	G	R	T	2	
254	G	G	R	T	P	R	A	G	S	2	
257	T	P	R	A	G	S	S	A	H	2	
282	A	A	W	L	P	L	R	T	P	2	
286	P	L	R	T	P	W	T	R	P	2	
304	Y	D	S	L	S	P	Y	G	P	2	
313	R	N	P	L	P	N	P	R	H	2	
328	G	L	K	K	P	A	R	H	C	2	
334	R	H	C	Q	G	Q	K	H	N	2	
339	Q	K	H	N	V	L	A	R	G	2	
347	G	K	P	Q	R	K	P	K	S	2	
357	N	N	S	W	Y	V	E	N	G	2	
362	V	E	N	G	R	P	A	D	L	2	
370	L	A	G	S	G	Y	C	G	A	2	
375	Y	C	G	A	L	W	K	A	I	2	
378	A	L	W	K	A	I	E	S	L	2	
379	L	W	K	A	I	E	S	L	E	2	
383	I	E	S	L	E	E	G	L	G	2	
389	G	L	G	G	K	Q	K	D	K	2	
393	K	Q	K	D	K	E	R	K	A	2	
6	T	K	T	F	P	L	R	A	L	1	
9	F	P	L	R	A	L	H	I	V	1	
11	L	R	A	L	H	I	V	V	E	1	
12	R	A	L	H	I	V	V	E	S	1	
18	V	E	S	I	R	D	H	S	G	1	
28	K	M	K	Q	D	K	K	V	D	1	
38	L	V	P	T	K	V	T	G	I	1	
42	K	V	T	G	I	I	T	Q	G	1	
60	V	G	S	Y	K	L	A	Y	S	1	
71	G	E	H	W	T	V	Y	Q	D	1	
73	H	W	T	V	Y	Q	D	E	K	1	
76	V	Y	Q	D	E	K	Q	R	K	1	
80	E	K	Q	R	K	D	K	V	L	1	
93	A	V	V	V	S	C	E	G	I	1	
94	V	V	V	S	C	E	G	I	N	1	
100	G	I	N	I	S	G	S	F	C	1	
107	F	C	R	N	K	L	K	Y	L	1	
110	N	K	L	K	Y	L	A	F	L	1	
115	L	A	F	L	H	K	R	M	N	1	
118	L	H	K	R	M	N	T	N	P	1	
120	K	R	M	N	T	N	P	S	R	1	
122	M	N	T	N	P	S	R	R	P	1	
124	T	N	P	S	R	R	P	Y	H	1	
132	H	F	Q	V	P	S	R	I	F	1	
140	F	W	R	Q	E	K	A	D	G	1	
143	Q	E	K	A	D	G	G	S	C	1	
152	C	P	Q	G	H	A	S	E	A	1	
163	K	V	C	L	S	G	A	P	H	1	
168	G	A	P	H	E	V	G	W	K	1	
171	H	E	V	G	W	K	Y	Q	A	1	
175	W	K	Y	Q	A	V	T	A	T	1	
179	A	V	T	A	T	L	E	E	K	1	
194	I	H	Y	R	K	N	K	Q	L	1	
201	Q	L	M	R	L	Q	K	Q	A	1	
206	Q	K	Q	A	E	K	N	M	K	1	
224	P	G	G	G	S	P	R	G	L	1	
234	F	I	F	K	T	I	A	P	L	1	
240	A	P	L	A	A	T	R	A	T	1	
243	A	A	T	R	A	T	R	I	G	1	
246	R	A	T	R	I	G	H	P	G	1	
248	T	R	I	G	H	P	G	G	R	1	
252	H	P	G	G	R	T	P	R	A	1	
258	P	R	A	G	S	S	A	H	R	1	
260	A	G	S	S	A	H	R	P	P	1	
268	P	A	L	S	A	R	A	P	V	1	
273	R	A	P	V	P	A	A	S	P	1	
276	V	P	A	A	S	P	A	A	W	1	
277	P	A	A	S	P	A	A	W	L	1	
284	W	L	P	L	R	T	P	W	T	1	
290	P	W	T	R	P	S	S	C	P	1	
311	G	P	R	N	P	L	P	N	P	1	
319	P	R	H	S	P	S	G	G	G	1	
325	G	G	G	G	L	K	K	P	A	1	
336	C	Q	G	Q	K	H	N	V	L	1	
342	N	V	L	A	R	G	K	P	Q	1	
344	L	A	R	G	K	P	Q	R	K	1	
349	P	Q	R	K	P	K	S	E	N	1	
352	K	P	K	S	E	N	N	S	W	1	
360	W	Y	V	E	N	G	R	P	A	1	
398	E	R	K	A	E	N	G	P	H	1	
399	R	K	A	E	N	G	P	H	L	1	

TABLE XXIII 151P3D4 v.1: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
4	L	L	L	L	V	L	I	S	I	28	
88	Y	L	K	E	V	D	V	F	V	25	
123	S	L	V	I	T	D	L	T	L	25	
144	G	L	E	D	D	T	V	V	V	25	
84	L	T	S	D	Y	L	K	E	V	23	
76	K	I	R	I	K	W	T	K	L	22	
151	V	V	A	L	D	L	Q	G	V	22	
3	S	L	L	L	L	V	L	I	S	20	
51	S	H	R	G	G	N	V	T	L	20	
159	V	V	F	P	Y	F	P	R	L	20	
263	Y	L	I	H	P	T	K	L	T	20	
5	L	L	L	V	L	I	S	I	C	19	

TABLE XXIII 151P3D4 v.1: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
41	L V E A E Q A K V	19	
69	A F G S G I H K I	19	
137	Y K C E V I E G L	19	
152	V A L D L Q G V V	19	
2	K S L L L L V L I	18	
22	Y T L D H D R A I	18	
186	A V I A S F D Q L	18	
279	C L N D G A Q I A	18	
281	N D G A Q I A K V	18	
291	Q I F A A W K I L	18	
32	I Q A E N G P H L	17	
34	A E N G P H L L V	17	
121	D A S L V I T D L	17	
227	G G Q N T V P G V	17	
284	A Q I A K V G Q I	17	
308	W L A D G S V R Y	17	
1	M K S L L L L V L	16	
7	L V L I S I C W A	16	
33	Q A E N G P H L L	16	
39	H L L V E A E Q A	16	
86	S D Y L K E V D V	16	
106	G G Y Q G R V F L	16	
113	F L K G G S D S D	16	
116	G G S D S D A S L	16	
181	C L D Q D A V I A	16	
262	Y Y L I H P T K L	16	
336	G F P D K K H K L	16	
40	L L V E A E Q A K	15	
125	V I T D L T L E D	15	
141	V I E G L E D D T	15	
155	D L Q G V V F P Y	15	
179	Q A C L D Q D A V	15	
180	A C L D Q D A V I	15	
207	A G W L S D G S V	15	
209	W L S D G S V Q Y	15	
264	L I H P T K L T Y	15	
298	I L G Y D R C D A	15	
306	A G W L A D G S V	15	
324	R C S P T E A A V	15	
339	D K K H K L Y G V	15	
8	V L I S I C W A D	14	
10	I S I C W A D H L	14	
16	D H L S D N Y T L	14	
142	I E G L E D D T V	14	
146	E D D T V V V A L	14	
148	D T V V V A L D L	14	
153	A L D L Q G V V F	14	
164	F P R L G R Y N L	14	
201	G L D W C N A G W	14	
224	E P C G G Q N T V	14	
256	N F N G R F Y Y L	14	
268	T K L T Y D E A V	14	
270	L T Y D E A V Q A	14	

TABLE XXIII 151P3D4 v.1: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
278	A C L N D G A Q I	14	
293	F A A W K I L G Y	14	
297	K I L G Y D R C D	14	
327	P T E A A V R F V	14	
343	K L Y G V Y C F R	14	
36	N G P H L L V E A	13	
81	W T K L T S D Y L	13	
83	K L T S D Y L K E	13	
104	T Y G G Y Q G R V	13	
145	L E D D T V V V A	13	
189	A S F D Q L Y D A	13	
193	Q L Y D A W R G G	13	
194	L Y D A W R G G L	13	
202	L D W C N A G W L	13	
272	Y D E A V Q A C L	13	
287	A K V G Q I F A A	13	
6	L L V L I S I C W	12	
9	L I S I C W A D H	12	
23	T L D H D R A I H	12	
58	T L P C K F Y R D	12	
118	S D S D A S L V I	12	
124	L V I T D L T L E	12	
133	D Y G R Y K C E V	12	
154	L D L Q G V V F P	12	
166	R L G R Y N L N F	12	
171	N L N F H E A Q Q	12	
174	F H E A Q Q A C L	12	
187	V I A S F D Q L Y	12	
214	S V Q Y P I T K P	12	
230	N T V P G V R N Y	12	
290	G Q I F A A W K I	12	
301	Y D R C D A G W L	12	
309	L A D G S V R Y P	12	
11	S I C W A D H L S	11	
17	H L S D N Y T L D	11	
24	L D H D R A I H I	11	
49	V F S H R G G N V	11	
73	G I H K I R I K W	11	
103	K T Y G G Y Q G R	11	
117	G S D S D A S L V	11	
120	S D A S L V I T D	11	
130	T L E D Y G R Y K	11	
140	E V I E G L E D D	11	
143	E G L E D D T V V	11	
211	S D G S V Q Y P I	11	
257	F N G R F Y Y L I	11	
269	K L T Y D E A V Q	11	
275	A V Q A C L N D G	11	
286	I A K V G Q I F A	11	
294	A A W K I L G Y D	11	
310	A D G S V R Y P I	11	
330	A A V R F V G F P	11	
28	R A I H I Q A E N	10	

TABLE XXIII 151P3D4 v.1: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
29	AIHIQAENG	10	
78	RIKWTKLTS	10	
79	IKWTKLTSD	10	
90	KEVDVFVSM	10	
95	FVSMGYHKK	10	
96	VSMGYHKKT	10	
97	SMGYHKKTY	10	
122	ASLVITDLT	10	
126	ITDLTLEDY	10	
128	DLTLEDYGR	10	
129	LTLEDYGRY	10	
134	YGRYKCEVI	10	
197	AWRGGLDWC	10	
242	DKDKSRYDV	10	
260	RFYYLIHPT	10	
285	QIAKVGQIF	10	
304	CDAGWLADG	10	
313	SVRYPISRP	10	
44	AEQAKVFSH	9	
57	VTLPCKFYR	9	
71	GSGIHKIRI	9	
72	SGIHKIRIK	9	
77	IRIKWTKLT	9	
119	DSDASLVIT	9	
276	VQACLNDGA	9	
346	GVYCFRAYN	9	
31	HIQAENGPH	8	
50	FSHRGGNVT	8	
66	DPTAFGSGI	8	
74	IHKIRIKWT	8	
111	RVFLKGGSD	8	
114	LKGGSDSDA	8	
149	TVVVALDLQ	8	
169	RYNLNFHEA	8	
182	LDQDAVIAS	8	
205	CNAGWLSDG	8	
210	LSDGSVQYP	8	
219	ITKPREPCG	8	
246	SRYDVFCFT	8	
283	GAQIAKVGQ	8	
288	KVGQIFAAW	8	
323	RRCSPTEAA	8	
342	HKLYGVYCF	8	
13	CWADHLSDN	7	
15	ADHLSDNYT	7	
37	GPHLLVEAE	7	
48	KVFSHRGGN	7	
54	GGNVTLPCK	7	
61	CKFYRDPTA	7	
63	FYRDPTAFG	7	
68	TAFGSGIHK	7	
107	GYQGRVFLK	7	
150	VVVALDLQG	7	

TABLE XXIII 151P3D4 v.1: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
172	LNFHEAQQA	7	
178	QQACLDQDA	7	
183	DQDAVIASF	7	
196	DAWRGGLDW	7	
217	YPITKPREP	7	
231	TVPGVRNYG	7	
249	DVFCFTSNF	7	
265	IHPTKLTYD	7	
271	TYDEAVQAC	7	
344	LYGVYCFRA	7	
12	ICWADHLSD	6	
18	LSDNYTLDH	6	
19	SDNYTLDHD	6	
27	DRAIHIQAE	6	
30	IHIQAENGP	6	
52	HRGGNVTLP	6	
91	EVDVFVSMG	6	
99	GYHKKTYGG	6	
131	LEDYGRYKC	6	
167	LGRYNLNFH	6	
170	YNLNFHEAQ	6	
177	AQQACLDQD	6	
188	IASFDQLYD	6	
200	GGLDWCNAG	6	
204	WCNAGWLSD	6	
206	NAGWLSDGS	6	
223	REPCGGQNT	6	
234	GVRNYGFWD	6	
236	RNYGFWDKD	6	
253	FTSNFNGRF	6	
259	GRFYYLIHP	6	
267	PTKLTYDEA	6	
317	PISRPRRRC	6	
322	RRRCSPTEA	6	
329	EAAVRFVGF	6	
334	FVGFPDKKH	6	
14	WADHLSDNY	5	
46	QAKVFSHRG	5	
64	YRDPTAFGS	5	
87	DYLKEVDVF	5	
89	LKEVDVFVS	5	
108	YQGRVFLKG	5	
109	QGRVFLKGG	5	
112	VFLKGGSDS	5	
136	RYKCEVIEG	5	
158	GVVFPYFPR	5	
215	VQYPITKPR	5	
218	PITKPREPC	5	
221	KPREPCGGQ	5	
238	YGFWDKDKS	5	
239	GFWDKDKSR	5	
255	SNFNGRFYY	5	
261	FYYLIHPTK	5	

TABLE XXIII 151P3D4 v.1: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
277	Q A C L N D G A Q	5	
280	L N D G A Q I A K	5	
299	L G Y D R C D A G	5	
305	D A G W L A D G S	5	
326	S P T E A A V R F	5	
331	A V R F V G F P D	5	
332	V R F V G F P D K	5	
333	R F V G F P D K K	5	
25	D H D R A I H I Q	4	
26	H D R A I H I Q A	4	
35	E N G P H L L V E	4	
42	V E A E Q A K V F	4	
55	G N V T L P C K F	4	
67	P T A F G S G I H	4	
75	H K I R I K W T K	4	
93	D V F V S M G Y H	4	
135	G R Y K C E V I E	4	
147	D D T V V V A L D	4	
161	F P Y F P R L G R	4	
162	P Y F P R L G R Y	4	
190	S F D Q L Y D A W	4	
191	F D Q L Y D A W R	4	
195	Y D A W R G G L D	4	
199	R G G L D W C N A	4	
212	D G S V Q Y P I T	4	
213	G S V Q Y P I T K	4	
226	C G G Q N T V P G	4	
245	K S R Y D V F C F	4	
289	V G Q I F A A W K	4	
292	I F A A W K I L G	4	
296	W K I L G Y D R C	4	
300	G Y D R C D A G W	4	
302	D R C D A G W L A	4	
303	R C D A G W L A D	4	
312	G S V R Y P I S R	4	
314	V R Y P I S R P R	4	
316	Y P I S R P R R R	4	
318	I S R P R R R C S	4	
319	S R P R R R C S P	4	
320	R P R R R C S P T	4	
21	N Y T L D H D R A	3	
38	P H L L V E A E Q	3	
53	R G G N V T L P C	3	
56	N V T L P C K F Y	3	
59	L P C K F Y R D P	3	
62	K F Y R D P T A F	3	
80	K W T K L T S D Y	3	
82	T K L T S D Y L K	3	
127	T D L T L E D Y G	3	
139	C E V I E G L E D	3	
156	L Q G V V F P Y F	3	
163	Y F P R L G R Y N	3	
168	G R Y N L N F H E	3	

TABLE XXIII 151P3D4 v.1: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
173	N F H E A Q Q A C	3	
185	D A V I A S F D Q	3	
198	W R G G L D W C N	3	
208	G W L S D G S V Q	3	
232	V P G V R N Y G F	3	
235	V R N Y G F W D K	3	
247	R Y D V F C F T S	3	
248	Y D V F C F T S N	3	
266	H P T K L T Y D E	3	
295	A W K I L G Y D R	3	
307	G W L A D G S V R	3	
335	V G F P D K K H K	3	
341	K H K L Y G V Y C	3	
20	D N Y T L D H D R	2	
43	E A E Q A K V F S	2	
47	A K V F S H R G G	2	
65	R D P T A F G S G	2	
70	F G S G I H K I R	2	
94	V F V S M G Y H K	2	
98	M G Y H K K T Y G	2	
100	Y H K K T Y G G Y	2	
102	K K T Y G G Y Q G	2	
110	G R V F L K G G S	2	
115	K G G S D S D A S	2	
157	Q G V V F P Y F P	2	
165	P R L G R Y N L N	2	
175	H E A Q Q A C L D	2	
176	E A Q Q A C L D Q	2	
184	Q D A V I A S F D	2	
228	G Q N T V P G V R	2	
229	Q N T V P G V R N	2	
244	D K S R Y D V F C	2	
251	F C F T S N F N G	2	
274	E A V Q A C L N D	2	
325	C S P T E A A V R	2	
328	T E A A V R F V G	2	
340	K K H K L Y G V Y	2	
345	Y G V Y C F R A Y	2	
92	V D V F V S M G Y	1	
105	Y G G Y Q G R V F	1	
160	V F P Y F P R L G	1	
216	Q Y P I T K P R E	1	
220	T K P R E P C G G	1	
240	F W D K D K S R Y	1	
241	W D K D K S R Y D	1	
250	V F C F T S N F N	1	
252	C F T S N F N G R	1	
258	N G R F Y Y L I H	1	
273	D E A V Q A C L N	1	
315	R Y P I S R P R R	1	
337	F P D K K H K L Y	1	
45	E Q A K V F S H R	-1	
132	E D Y G R Y K C E	-1	

TABLE XXIII 151P3D4 v.1: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
203	D W C N A G W L S	-1	
225	P C G G Q N T V P	-1	
222	P R E P C G G Q N	-2	
237	N Y G F W D K D K	-2	
233	P G V R N Y G F W	-3	
338	P D K K H K L Y G	-3	

TABLE XXIII 151P3D4 v.2: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
378	A L W K A I E S L	29	
87	V L L G R K A V V	27	
13	A L H I V V E S I	26	
234	F I F K T I A P L	26	
88	L L G R K A V V V	25	
165	C L S G A P H E V	25	
382	A I E S L E E G L	21	
38	L V P T K V T G I	20	
385	S L E E G L G G K	20	
86	K V L L G R K A V	19	
110	N K L K Y L A F L	19	
231	G L G F I F K T I	19	
237	K T I A P L A A T	19	
9	F P L R A L H I V	18	
10	P L R A L H I V V	18	
37	L L V P T K V T G	18	
52	K D F G H V Q F V	18	
36	D L L V P T K V T	17	
57	V Q F V G S Y K L	17	
114	Y L A F L H K R M	17	
156	H A S E A Y K K V	17	
176	K Y Q A V T A T L	17	
238	T I A P L A A T R	17	
271	S A R A P V P A A	17	
284	W L P L R T P W T	17	
308	S P Y G P R N P L	17	
400	K A E N G P H L L	17	
30	K Q D K K V D L L	16	
68	S N D G E H W T V	16	
158	S E A Y K K V C L	16	
242	L A A T R A T R I	16	
262	S S A H R P P A L	16	
277	P A A S P A A W L	16	
306	S L S P Y G P R N	16	
343	V L A R G K P Q R	16	
362	V E N G R P A D L	16	
371	A G S G Y C G A L	16	
35	V D L L V P T K V	15	
45	G I I T Q G A K D	15	
93	A V V V S C E G I	15	
107	F C R N K L K Y L	15	
127	S R R P Y H F Q V	15	

TABLE XXIII 151P3D4 v.2: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
138	R I F W R Q E K A	15	
197	R K N K Q L M R L	15	
201	Q L M R L Q K Q A	15	
227	G S P R G L G F I	15	
230	R G L G F I F K T	15	
268	P A L S A R A P V	15	
381	K A I E S L E E G	15	
399	R K A E N G P H L	15	
6	T K T F P L R A L	14	
12	R A L H I V V E S	14	
29	M K Q D K K V D L	14	
104	S G S F C R N K L	14	
117	F L H K R M N T N	14	
212	N M K K K I D K Y	14	
216	K I D K Y T E S P	14	
282	A A W L P L R T P	14	
369	D L A G S G Y C G	14	
33	K K V D L L V P T	13	
34	K V D L L V P T K	13	
64	K L A Y S N D G E	13	
81	K Q R K D K V L L	13	
95	V V S C E G I N I	13	
172	E V G W K Y Q A V	13	
183	T L E E K R K E K	13	
194	I H Y R K N K Q L	13	
241	P L A A T R A T R	13	
249	R I G H P G G R T	13	
269	A L S A R A P V P	13	
279	A S P A A W L P L	13	
321	H S P S G G G G L	13	
335	H C Q G Q K H N V	13	
370	L A G S G Y C G A	13	
374	G Y C G A L W K A	13	
389	G L G G K Q K D K	13	
1	M L E H T T K T F	12	
16	I V V E S I R D H	12	
27	Q K M K Q D K K V	12	
43	V T G I I T Q G A	12	
49	Q G A K D F G H V	12	
182	A T L E E K R K E	12	
204	R L Q K Q A E K N	12	
264	A H R P P A L S A	12	
299	T S S S T Y D S L	12	
302	S T Y D S L S P Y	12	
336	C Q G Q K H N V L	12	
7	K T F P L R A L H	11	
20	S I R D H S G Q K	11	
67	Y S N D G E H W T	11	
113	K Y L A F L H K R	11	
131	Y H F Q V P S R I	11	
179	A V T A T L E E K	11	
202	L M R L Q K Q A E	11	
240	A P L A A T R A T	11	

TABLE XXIII 151P3D4 v.2: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
315	P L P N P R H S P	11	
324	S G G G G L K K P	11	
328	G L K K P A R H C	11	
375	Y C G A L W K A I	11	
11	L R A L H I V V E	10	
31	Q D K K V D L L V	10	
39	V P T K V T G I I	10	
42	K V T G I I T Q G	10	
46	I I T Q G A K D F	10	
79	D E K Q R K D K V	10	
96	V S C E G I N I S	10	
100	G I N I S G S F C	10	
102	N I S G S F C R N	10	
111	K L K Y L A F L H	10	
161	Y K K V C L S G A	10	
175	W K Y Q A V T A T	10	
180	V T A T L E E K R	10	
209	A E K N M K K K I	10	
224	P G G G S P R G L	10	
239	I A P L A A T R A	10	
247	A T R I G H P G G	10	
256	R T P R A G S S A	10	
270	L S A R A P V P A	10	
291	W T R P S S C P T	10	
295	S S C P T S S S T	10	
354	K S E N N S W Y V	10	
377	G A L W K A I E S	10	
3	E H T T K T F P L	9	
5	T T K T F P L R A	9	
8	T F P L R A L H I	9	
65	L A Y S N D G E H	9	
116	A F L H K R M N T	9	
121	R M N T N P S R R	9	
145	K A D G G S C C P	9	
167	S G A P H E V G W	9	
168	G A P H E V G W K	9	
173	V G W K Y Q A V T	9	
178	Q A V T A T L E E	9	
186	E K R K E K A E I	9	
200	K Q L M R L Q K Q	9	
252	H P G G R T P R A	9	
263	S A H R P P A L S	9	
272	A R A P V P A A S	9	
273	R A P V P A A S P	9	
280	S P A A W L P L R	9	
281	P A A W L P L R T	9	
344	L A R G K P Q R K	9	
361	Y V E N G R P A D	9	
15	H I V V E S I R D	8	
21	I R D H S G Q K M	8	
41	T K V T G I I T Q	8	
47	I T Q G A K D F G	8	
55	G H V Q F V G S Y	8	

TABLE XXIII 151P3D4 v.2: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
59	F V G S Y K L A Y	8	
89	L G R K A V V V S	8	
90	G R K A V V V S C	8	
134	Q V P S R I F W R	8	
152	C P Q G H A S E A	8	
207	K Q A E K N M K K	8	
232	L G F I F K T I A	8	
250	I G H P G G R T P	8	
274	A P V P A A S P A	8	
278	A A S P A A W L P	8	
286	P L R T P W T R P	8	
365	G R P A D L A G S	8	
393	K Q K D K E R K A	8	
28	K M K Q D K K V D	7	
50	G A K D F G H V Q	7	
60	V G S Y K L A Y S	7	
77	Y Q D E K Q R K D	7	
80	E K Q R K D K V L	7	
92	K A V V V S C E G	7	
108	C R N K L K Y L A	7	
115	L A F L H K R M N	7	
123	N T N P S R R P Y	7	
159	E A Y K K V C L S	7	
163	K V C L S G A P H	7	
171	H E V G W K Y Q A	7	
174	G W K Y Q A V T A	7	
184	L E E K R K E K A	7	
193	E I H Y R K N K Q	7	
203	M R L Q K Q A E K	7	
215	K K I D K Y T E S	7	
220	Y T E S P G G G S	7	
223	S P G G G S P R G	7	
243	A A T R A T R I G	7	
244	A T R A T R I G H	7	
265	H R P P A L S A R	7	
266	R P P A L S A R A	7	
275	P V P A A S P A A	7	
283	A W L P L R T P W	7	
288	R T P W T R P S S	7	
311	G P R N P L P N P	7	
325	G G G G L K K P A	7	
61	G S Y K L A Y S N	6	
63	Y K L A Y S N D G	6	
71	G E H W T V Y Q D	6	
82	Q R K D K V L L G	6	
83	R K D K V L L G R	6	
85	D K V L L G R K A	6	
91	R K A V V V S C E	6	
101	I N I S G S F C R	6	
149	G S C C P Q G H A	6	
150	S C C P Q G H A S	6	
151	C C P Q G H A S E	6	
155	G H A S E A Y K K	6	

TABLE XXIII 151P3D4 v.2: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
164	V C L S G A P H E	6	
169	A P H E V G W K Y	6	
191	K A E I H Y R K N	6	
221	T E S P G G G S P	6	
233	G F I F K T I A P	6	
235	I F K T I A P L A	6	
236	F K T I A P L A A	6	
245	T R A T R I G H P	6	
261	G S S A H R P P A	6	
276	V P A A S P A A W	6	
285	L P L R T P W T R	6	
322	S P S G G G G L K	6	
327	G G L K K P A R H	6	
337	Q G Q K H N V L A	6	
338	G Q K H N V L A R	6	
339	Q K H N V L A R G	6	
360	W Y V E N G R P A	6	
366	R P A D L A G S G	6	
368	A D L A G S G Y C	6	
373	S G Y C G A L W K	6	
386	L E E G L G G K Q	6	
395	K D K E R K A E N	6	
51	A K D F G H V Q F	5	
58	Q F V G S Y K L A	5	
74	W T V Y Q D E K Q	5	
84	K D K V L L G R K	5	
94	V V V S C E G I N	5	
97	S C E G I N I S G	5	
98	C E G I N I S G S	5	
106	S F C R N K L K Y	5	
120	K R M N T N P S R	5	
137	S R I F W R Q E K	5	
189	K E K A E I H Y R	5	
226	G G S P R G L G F	5	
228	S P R G L G F I F	5	
248	T R I G H P G G R	5	
251	G H P G G R T P R	5	
254	G G R T P R A G S	5	
259	R A G S S A H R P	5	
287	L R T P W T R P S	5	
316	L P N P R H S P S	5	
342	N V L A R G K P Q	5	
345	A R G K P Q R K P	5	
357	N N S W Y V E N G	5	
380	W K A I E S L E E	5	
388	E G L G G K Q K D	5	
4	H T T K T F P L R	4	
14	L H I V V E S I R	4	
17	V V E S I R D H S	4	
18	V E S I R D H S G	4	
40	P T K V T G I I T	4	
54	F G H V Q F V G S	4	
75	T V Y Q D E K Q R	4	

TABLE XXIII 151P3D4 v.2: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
112	L K Y L A F L H K	4	
129	R P Y H F Q V P S	4	
141	W R Q E K A D G G	4	
146	A D G G S C C P Q	4	
160	A Y K K V C L S G	4	
177	Y Q A V T A T L E	4	
192	A E I H Y R K N K	4	
195	H Y R K N K Q L M	4	
205	L Q K Q A E K N M	4	
208	Q A E K N M K K K	4	
246	R A T R I G H P G	4	
255	G R T P R A G S S	4	
296	S C P T S S S T Y	4	
298	P T S S S T Y D S	4	
304	Y D S L S P Y G P	4	
314	N P L P N P R H S	4	
323	P S G G G G L K K	4	
326	G G G L K K P A R	4	
329	L K K P A R H C Q	4	
331	K P A R H C Q G Q	4	
333	A R H C Q G Q K H	4	
340	K H N V L A R G K	4	
347	G K P Q R K P K S	4	
355	S E N N S W Y V E	4	
364	N G R P A D L A G	4	
376	C G A L W K A I E	4	
390	L G G K Q K D K E	4	
23	D H S G Q K M K Q	3	
26	G Q K M K Q D K K	3	
32	D K K V D L L V P	3	
44	T G I I T Q G A K	3	
56	H V Q F V G S Y K	3	
103	I S G S F C R N K	3	
119	H K R M N T N P S	3	
130	P Y H F Q V P S R	3	
133	F Q V P S R I F W	3	
139	I F W R Q E K A D	3	
140	F W R Q E K A D G	3	
162	K K V C L S G A P	3	
166	L S G A P H E V G	3	
187	K R K E K A E I H	3	
196	Y R K N K Q L M R	3	
211	K N M K K K I D K	3	
214	K K K I D K Y T E	3	
219	K Y T E S P G G G	3	
257	T P R A G S S A H	3	
258	P R A G S S A H R	3	
289	T P W T R P S S C	3	
292	T R P S S C P T S	3	
300	S S S T Y D S L S	3	
301	S S T Y D S L S P	3	
307	L S P Y G P R N P	3	
310	Y G P R N P L P N	3	

TABLE XXIII 151P3D4 v.2: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
320	R H S P S G G G G	3	
348	K P Q R K P K S E	3	
352	K P K S E N N S W	3	
359	S W Y V E N G R P	3	
384	E S L E E G L G G	3	
397	K E R K A E N G P	3	
2	L E H T T K T F P	2	
25	S G Q K M K Q D K	2	
48	T Q G A K D F G H	2	
66	A Y S N D G E H W	2	
69	N D G E H W T V Y	2	
70	D G E H W T V Y Q	2	
73	H W T V Y Q D E K	2	
76	V Y Q D E K Q R K	2	
109	R N K L K Y L A F	2	
144	E K A D G G S C C	2	
148	G G S C C P Q G H	2	
154	Q G H A S E A Y K	2	
181	T A T L E E K R K	2	
190	E K A E I H Y R K	2	
213	M K K K I D K Y T	2	
218	D K Y T E S P G G	2	
225	G G G S P R G L G	2	
260	A G S S A H R P P	2	
293	R P S S C P T S S	2	
294	P S S C P T S S S	2	
303	T Y D S L S P Y G	2	
305	D S L S P Y G P R	2	
312	P R N P L P N P R	2	
313	R N P L P N P R H	2	
341	H N V L A R G K P	2	
350	Q R K P K S E N N	2	
356	E N N S W Y V E N	2	
358	N S W Y V E N G R	2	
363	E N G R P A D L A	2	
367	P A D L A G S G Y	2	
372	G S G Y C G A L W	2	
383	I E S L E E G L G	2	
391	G G K Q K D K E R	2	
22	R D H S G Q K M K	1	
62	S Y K L A Y S N D	1	
99	E G I N I S G S F	1	
105	G S F C R N K L K	1	
118	L H K R M N T N P	1	
124	T N P S R R P Y H	1	
125	N P S R R P Y H F	1	
132	H F Q V P S R I F	1	
135	V P S R I F W R Q	1	
143	Q E K A D G G S C	1	
157	A S E A Y K K V C	1	
198	K N K Q L M R L Q	1	
199	N K Q L M R L Q K	1	
206	Q K Q A E K N M K	1	

TABLE XXIII 151P3D4 v.2: HLA Peptide Scoring Results A*0201 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
222	E S P G G G S P R	1	
318	N P R H S P S G G	1	
330	K K P A R H C Q G	1	
332	P A R H C Q G Q K	1	
334	R H C Q G Q K H N	1	
351	R K P K S E N N S	1	
379	L W K A I E S L E	1	
392	G K Q K D K E R K	1	
53	D F G H V Q F V G	-1	
126	P S R R P Y H F Q	-1	
128	R R P Y H F Q V P	-1	
188	R K E K A E I H Y	-1	
229	P R G L G F I F K	-1	
297	C P T S S S T Y D	-1	
319	P R H S P S G G G	-1	
353	P K S E N N S W Y	-1	
396	D K E R K A E N G	-1	
72	E H W T V Y Q D E	-2	
78	Q D E K Q R K D K	-2	
136	P S R I F W R Q E	-2	
153	P Q G H A S E A Y	-2	
210	E K N M K K K I D	-2	
253	P G G R T P R A G	-2	
387	E E G L G G K Q K	-2	
170	P H E V G W K Y Q	-3	
185	E E K R K E K A E	-3	
290	P W T R P S S C P	-3	
398	E R K A E N G P H	-4	

TABLE XXIV 151P3D4: HLA Peptide Scoring Results A*0202 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
	NO DATA		

TABLE XXV 151P3D4: HLA Peptide Scoring Results A*0203 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
	NO DATA		

TABLE XXVI 151P3D4 v.1: HLA Peptide Scoring Results A3 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
153	A L D L Q G V V F	29	
209	W L S D G S V Q Y	26	
130	T L E D Y G R Y K	24	
166	R L G R Y N L N F	24	
264	L I H P T K L T Y	24	
308	W L A D G S V R Y	24	
343	K L Y G V Y C F R	24	
40	L L V E A E Q A K	22	

TABLE XXVI 151P3D4 v.1: HLA Peptide Scoring Results A3 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
95	F V S M G Y H K K	22	
111	R V F L K G G S D	22	
186	A V I A S F D Q L	21	
75	H K I R I K W T K	20	
78	R I K W T K L T S	20	
269	K L T Y D E A V Q	20	
331	A V R F V G F P D	20	
123	S L V I T D L T L	19	
144	G L E D D T V V V	19	
155	D L Q G V V F P Y	19	
261	F Y Y L I H P T K	19	
285	Q I A K V G Q I F	19	
23	T L D H D R A I H	18	
39	H L L V E A E Q A	18	
150	V V V A L D L Q G	18	
234	G V R N Y G F W D	18	
289	V G Q I F A A W K	18	
307	G W L A D G S V R	18	
346	G V Y C F R A Y N	18	
3	S L L L L V L I S	17	
56	N V T L P C K F Y	17	
62	K F Y R D P T A F	17	
76	K I R I K W T K L	17	
88	Y L K E V D V F V	17	
113	F L K G G S D S D	17	
181	C L D Q D A V I A	17	
193	Q L Y D A W R G G	17	
249	D V F C F T S N F	17	
288	K V G Q I F A A W	17	
313	S V R Y P I S R P	17	
333	R F V G F P D K K	17	
4	L L L L V L I S I	16	
9	L I S I C W A D H	16	
51	S H R G G N V T L	16	
83	K L T S D Y L K E	16	
140	E V I E G L E D D	16	
171	N L N F H E A Q Q	16	
279	C L N D G A Q I A	16	
5	L L L V L I S I C	15	
29	A I H I Q A E N G	15	
31	H I Q A E N G P H	15	
41	L V E A E Q A K V	15	
48	K V F S H R G G N	15	
68	T A F G S G I H K	15	
72	S G I H K I R I K	15	
93	D V F V S M G Y H	15	
103	K T Y G G Y Q G R	15	
128	D L T L E D Y G R	15	
187	V I A S F D Q L Y	15	
213	G S V Q Y P I T K	15	
270	L T Y D E A V Q A	15	
275	A V Q A C L N D G	15	
278	A C L N D G A Q I	15	

TABLE XXVI 151P3D4 v.1: HLA Peptide Scoring Results A3 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
297	K I L G Y D R C D	15	
320	R P R R R C S P T	15	
7	L V L I S I C W A	14	
8	V L I S I C W A D	14	
91	E V D V F V S M G	14	
107	G Y Q G R V F L K	14	
124	L V I T D L T L E	14	
158	G V V F P Y F P R	14	
231	T V P G V R N Y G	14	
243	K D K S R Y D V F	14	
325	C S P T E A A V R	14	
334	F V G F P D K K H	14	
340	K K H K L Y G V Y	14	
42	V E A E Q A K V F	13	
94	V F V S M G Y H K	13	
159	V V F P Y F P R L	13	
180	A C L D Q D A V I	13	
201	G L D W C N A G W	13	
263	Y L I H P T K L T	13	
280	L N D G A Q I A K	13	
284	A Q I A K V G Q I	13	
298	I L G Y D R C D A	13	
326	S P T E A A V R F	13	
335	V G F P D K K H K	13	
17	H L S D N Y T L D	12	
44	A E Q A K V F S H	12	
50	F S H R G G N V T	12	
80	K W T K L T S D Y	12	
82	T K L T S D Y L K	12	
125	V I T D L T L E D	12	
151	V V A L D L Q G V	12	
161	F P Y F P R L G R	12	
162	P Y F P R L G R Y	12	
183	D Q D A V I A S F	12	
208	G W L S D G S V Q	12	
214	S V Q Y P I T K P	12	
235	V R N Y G F W D K	12	
291	Q I F A A W K I L	12	
295	A W K I L G Y D R	12	
303	R C D A G W L A D	12	
317	P I S R P R R R C	12	
332	V R F V G F P D K	12	
341	K H K L Y G V Y C	12	
6	L L V L I S I C W	11	
58	T L P C K F Y R D	11	
86	S D Y L K E V D V	11	
90	K E V D V F V S M	11	
97	S M G Y H K K T Y	11	
102	K K T Y G G Y Q G	11	
105	Y G G Y Q G R V F	11	
106	G G Y Q G R V F L	11	
196	D A W R G G L D W	11	
197	A W R G G L D W C	11	

TABLE XXVI 151P3D4 v.1: HLA Peptide Scoring Results A3 9-mers SYFPEITHI											
Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
215	V	Q	Y	P	I	T	K	P	R	11	
228	G	Q	N	T	V	P	G	V	R	11	
230	N	T	V	P	G	V	R	N	Y	11	
255	S	N	F	N	G	R	F	Y	Y	11	
293	F	A	A	W	K	I	L	G	Y	11	
314	V	R	Y	P	I	S	R	P	R	11	
318	I	S	R	P	R	R	R	C	S	11	
324	R	C	S	P	T	E	A	A	V	11	
329	E	A	A	V	R	F	V	G	F	11	
2	K	S	L	L	L	L	V	L	I	10	
28	R	A	I	H	I	Q	A	E	N	10	
35	E	N	G	P	H	L	L	V	E	10	
54	G	G	N	V	T	L	P	C	K	10	
87	D	Y	L	K	E	V	D	V	F	10	
112	V	F	L	K	G	G	S	D	S	10	
129	L	T	L	E	D	Y	G	R	Y	10	
141	V	I	E	G	L	E	D	D	T	10	
149	T	V	V	V	A	L	D	L	Q	10	
222	P	R	E	P	C	G	G	Q	N	10	
236	R	N	Y	G	F	W	D	K	D	10	
237	N	Y	G	F	W	D	K	D	K	10	
245	K	S	R	Y	D	V	F	C	F	10	
258	N	G	R	F	Y	Y	L	I	H	10	
312	G	S	V	R	Y	P	I	S	R	10	
315	R	Y	P	I	S	R	P	R	R	10	
316	Y	P	I	S	R	P	R	R	R	10	
321	P	R	R	R	C	S	P	T	E	10	
11	S	I	C	W	A	D	H	L	S	9	
12	I	C	W	A	D	H	L	S	D	9	
45	E	Q	A	K	V	F	S	H	R	9	
53	R	G	G	N	V	T	L	P	C	9	
57	V	T	L	P	C	K	F	Y	R	9	
73	G	I	H	K	I	R	I	K	W	9	
118	S	D	S	D	A	S	L	V	I	9	
126	I	T	D	L	T	L	E	D	Y	9	
145	L	E	D	D	T	V	V	V	A	9	
184	Q	D	A	V	I	A	S	F	D	9	
191	F	D	Q	L	Y	D	A	W	R	9	
204	W	C	N	A	G	W	L	S	D	9	
218	P	I	T	K	P	R	E	P	C	9	
223	R	E	P	C	G	G	Q	N	T	9	
229	Q	N	T	V	P	G	V	R	N	9	
240	F	W	D	K	D	K	S	R	Y	9	
254	T	S	N	F	N	G	R	F	Y	9	
319	S	R	P	R	R	R	C	S	P	9	
322	R	R	R	C	S	P	T	E	A	9	
328	T	E	A	A	V	R	F	V	G	9	
1	M	K	S	L	L	L	L	V	L	8	
10	I	S	I	C	W	A	D	H	L	8	
18	L	S	D	N	Y	T	L	D	H	8	
20	D	N	Y	T	L	D	H	D	R	8	
26	H	D	R	A	I	H	I	Q	A	8	
34	A	E	N	G	P	H	L	L	V	8	

TABLE XXVI 151P3D4 v.1: HLA Peptide Scoring Results A3 9-mers SYFPEITHI											
Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
66	D	P	T	A	F	G	S	G	I	8	
67	P	T	A	F	G	S	G	I	H	8	
92	V	D	V	F	V	S	M	G	Y	8	
100	Y	H	K	K	T	Y	G	G	Y	8	
132	E	D	Y	G	R	Y	K	C	E	8	
134	Y	G	R	Y	K	C	E	V	I	8	
135	G	R	Y	K	C	E	V	I	E	8	
143	E	G	L	E	D	D	T	V	V	8	
152	V	A	L	D	L	Q	G	V	V	8	
154	L	D	L	Q	G	V	V	F	P	8	
177	A	Q	Q	A	C	L	D	Q	D	8	
219	I	T	K	P	R	E	P	C	G	8	
221	K	P	R	E	P	C	G	G	Q	8	
224	E	P	C	G	G	Q	N	T	V	8	
239	G	F	W	D	K	D	K	S	R	8	
247	R	Y	D	V	F	C	F	T	S	8	
260	R	F	Y	Y	L	I	H	P	T	8	
282	D	G	A	Q	I	A	K	V	G	8	
299	L	G	Y	D	R	C	D	A	G	8	
301	Y	D	R	C	D	A	G	W	L	8	
342	H	K	L	Y	G	V	Y	C	F	8	
32	I	Q	A	E	N	G	P	H	L	7	
38	P	H	L	L	V	E	A	E	Q	7	
63	F	Y	R	D	P	T	A	F	G	7	
65	R	D	P	T	A	F	G	S	G	7	
74	I	H	K	I	R	I	K	W	T	7	
108	Y	Q	G	R	V	F	L	K	G	7	
139	C	E	V	I	E	G	L	E	D	7	
142	I	E	G	L	E	D	D	T	V	7	
148	D	T	V	V	V	A	L	D	L	7	
164	F	P	R	L	G	R	Y	N	L	7	
167	L	G	R	Y	N	L	N	F	H	7	
195	Y	D	A	W	R	G	G	L	D	7	
207	A	G	W	L	S	D	G	S	V	7	
225	P	C	G	G	Q	N	T	V	P	7	
244	D	K	S	R	Y	D	V	F	C	7	
246	S	R	Y	D	V	F	C	F	T	7	
306	A	G	W	L	A	D	G	S	V	7	
330	A	A	V	R	F	V	G	F	P	7	
337	F	P	D	K	K	H	K	L	Y	7	
345	Y	G	V	Y	C	F	R	A	Y	7	
14	W	A	D	H	L	S	D	N	Y	6	
16	D	H	L	S	D	N	Y	T	L	6	
24	L	D	H	D	R	A	I	H	I	6	
33	Q	A	E	N	G	P	H	L	L	6	
49	V	F	S	H	R	G	G	N	V	6	
61	C	K	F	Y	R	D	P	T	A	6	
64	Y	R	D	P	T	A	F	G	S	6	
70	F	G	S	G	I	H	K	I	R	6	
79	I	K	W	T	K	L	T	S	D	6	
98	M	G	Y	H	K	K	T	Y	G	6	
116	G	G	S	D	S	D	A	S	L	6	
117	G	S	D	S	D	A	S	L	V	6	

TABLE XXVI 151P3D4 v.1: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
119	D S D A S L V I T	6	
120	S D A S L V I T D	6	
146	E D D T V V V A L	6	
163	Y F P R L G R Y N	6	
165	P R L G R Y N L N	6	
172	L N F H E A Q Q A	6	
205	C N A G W L S D G	6	
232	V P G V R N Y G F	6	
253	F T S N F N G R F	6	
272	Y D E A V Q A C L	6	
287	A K V G Q I F A A	6	
290	G Q I F A A W K I	6	
296	W K I L G Y D R C	6	
300	G Y D R C D A G W	6	
304	C D A G W L A D G	6	
13	C W A D H L S D N	5	
30	I H I Q A E N G P	5	
55	G N V T L P C K F	5	
69	A F G S G I H K I	5	
77	I R I K W T K L T	5	
101	H K K T Y G G Y Q	5	
109	Q G R V F L K G G	5	
114	L K G G S D S D A	5	
122	A S L V I T D L T	5	
136	R Y K C E V I E G	5	
156	L Q G V V F P Y F	5	
168	G R Y N L N F H E	5	
169	R Y N L N F H E A	5	
174	F H E A Q Q A C L	5	
188	I A S F D Q L Y D	5	
192	D Q L Y D A W R G	5	
199	R G G L D W C N A	5	
202	L D W C N A G W L	5	
217	Y P I T K P R E P	5	
262	Y Y L I H P T K L	5	
277	Q A C L N D G A Q	5	
281	N D G A Q I A K V	5	
283	G A Q I A K V G Q	5	
286	I A K V G Q I F A	5	
292	I F A A W K I L G	5	
310	A D G S V R Y P I	5	
323	R R C S P T E A A	5	
15	A D H L S D N Y T	4	
22	Y T L D H D R A I	4	
36	N G P H L L V E A	4	
43	E A E Q A K V F S	4	
85	T S D Y L K E V D	4	
89	L K E V D V F V S	4	
115	K G G S D S D A S	4	
138	K C E V I E G L E	4	
147	D D T V V V A L D	4	
170	Y N L N F H E A Q	4	
175	H E A Q Q A C L D	4	

TABLE XXVI 151P3D4 v.1: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
179	Q A C L D Q D A V	4	
189	A S F D Q L Y D A	4	
194	L Y D A W R G G L	4	
200	G G L D W C N A G	4	
203	D W C N A G W L S	4	
220	T K P R E P C G G	4	
226	C G G Q N T V P G	4	
233	P G V R N Y G F W	4	
252	C F T S N F N G R	4	
256	N F N G R F Y Y L	4	
265	I H P T K L T Y D	4	
273	D E A V Q A C L N	4	
294	A A W K I L G Y D	4	
302	D R C D A G W L A	4	
338	P D K K H K L Y G	4	
25	D H D R A I H I Q	3	
27	D R A I H I Q A E	3	
46	Q A K V F S H R G	3	
47	A K V F S H R G G	3	
52	H R G G N V T L P	3	
104	T Y G G Y Q G R V	3	
121	D A S L V I T D L	3	
131	L E D Y G R Y K C	3	
133	D Y G R Y K C E V	3	
157	Q G V V F P Y F P	3	
176	E A Q Q A C L D Q	3	
178	Q Q A C L D Q D A	3	
216	Q Y P I T K P R E	3	
241	W D K D K S R Y D	3	
248	Y D V F C F T S N	3	
257	F N G R F Y Y L I	3	
268	T K L T Y D E A V	3	
274	E A V Q A C L N D	3	
305	D A G W L A D G S	3	
37	G P H L L V E A E	2	
60	P C K F Y R D P T	2	
81	W T K L T S D Y L	2	
96	V S M G Y H K K T	2	
127	T D L T L E D Y G	2	
137	Y K C E V I E G L	2	
173	N F H E A Q Q A C	2	
182	L D Q D A V I A S	2	
190	S F D Q L Y D A W	2	
198	W R G G L D W C N	2	
210	L S D G S V Q Y P	2	
211	S D G S V Q Y P I	2	
267	P T K L T Y D E A	2	
271	T Y D E A V Q A C	2	
309	L A D G S V R Y P	2	
311	D G S V R Y P I S	2	
327	P T E A A V R F V	2	
336	G F P D K K H K L	2	
339	D K K H K L Y G V	2	

TABLE XXVI 151P3D4 v.1: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
19	S D N Y T L D H D	1	
21	N Y T L D H D R A	1	
71	G S G I H K I R I	1	
84	L T S D Y L K E V	1	
99	G Y H K K T Y G G	1	
110	G R V F L K G G S	1	
160	V F P Y F P R L G	1	
185	D A V I A S F D Q	1	
227	G G Q N T V P G V	1	
242	D K D K S R Y D V	1	
276	V Q A C L N D G A	1	

TABLE XXVI 151P3D4 v.2: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
34	K V D L L V P T K	28	
20	S I R D H S G Q K	27	
56	H V Q F V G S Y K	27	
238	T I A P L A A T R	26	
88	L L G R K A V V V	25	
179	A V T A T L E E K	25	
241	P L A A T R A T R	25	
385	S L E E G L G G K	25	
163	K V C L S G A P H	24	
269	A L S A R A P V P	24	
373	S G Y C G A L W K	24	
87	V L L G R K A V V	23	
183	T L E E K R K E K	23	
343	V L A R G K P Q R	23	
389	G L G G K Q K D K	23	
37	L L V P T K V T G	21	
75	T V Y Q D E K Q R	21	
111	K L K Y L A F L H	21	
59	F V G S Y K L A Y	20	
86	K V L L G R K A V	20	
323	P S G G G G L K K	20	
10	P L R A L H I V V	19	
42	K V T G I I T Q G	19	
46	I I T Q G A K D F	19	
134	Q V P S R I F W R	19	
322	S P S G G G G L K	19	
342	N V L A R G K P Q	19	
346	R G K P Q R K P K	19	
387	E E G L G G K Q K	19	
1	M L E H T T K T F	18	
112	L K Y L A F L H K	18	
199	N K Q L M R L Q K	18	
201	Q L M R L Q K Q A	18	
13	A L H I V V E S I	17	
16	I V V E S I R D H	17	
22	R D H S G Q K M K	17	
45	G I I T Q G A K D	17	
154	Q G H A S E A Y K	17	
192	A E I H Y R K N K	17	
204	R L Q K Q A E K N	17	
207	K Q A E K N M K K	17	
264	A H R P P A L S A	17	
306	S L S P Y G P R N	17	
332	P A R H C Q G Q K	17	
344	L A R G K P Q R K	17	
36	D L L V P T K V T	16	
44	T G I I T Q G A K	16	
51	A K D F G H V Q F	16	
117	F L H K R M N T N	16	
203	M R L Q K Q A E K	16	
249	R I G H P G G R T	16	
340	K H N V L A R G K	16	
369	D L A G S G Y C G	16	
84	K D K V L L G R K	15	
100	G I N I S G S F C	15	
109	R N K L K Y L A F	15	
137	S R I F W R Q E K	15	
206	Q K Q A E K N M K	15	
226	G G S P R G L G F	15	
256	R T P R A G S S A	15	
257	T P R A G S S A H	15	
302	S T Y D S L S P Y	15	
361	Y V E N G R P A D	15	
378	A L W K A I E S L	15	
7	K T F P L R A L H	14	
64	K L A Y S N D G E	14	
138	R I F W R Q E K A	14	
155	G H A S E A Y K K	14	
169	A P H E V G W K Y	14	
211	K N M K K K I D K	14	
222	E S P G G G S P R	14	
231	G L G F I F K T I	14	
250	I G H P G G R T P	14	
284	W L P L R T P W T	14	
285	L P L R T P W T R	14	
286	P L R T P W T R P	14	
296	S C P T S S S T Y	14	
315	P L P N P R H S P	14	
328	G L K K P A R H C	14	
78	Q D E K Q R K D K	13	
93	A V V V S C E G I	13	
95	V V S C E G I N I	13	
106	S F C R N K L K Y	13	
165	C L S G A P H E V	13	
176	K Y Q A V T A T L	13	
187	K R K E K A E I H	13	
194	I H Y R K N K Q L	13	
216	K I D K Y T E S P	13	
228	S P R G L G F I F	13	
229	P R G L G F I F K	13	

TABLE XXVI 151P3D4 v.2: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
244	A T R A T R I G H	13	
272	A R A P V P A A S	13	
275	P V P A A S P A A	13	
367	P A D L A G S G Y	13	
26	G Q K M K Q D K K	12	
38	L V P T K V T G I	12	
69	N D G E H W T V Y	12	
83	R K D K V L L G R	12	
103	I S G S F C R N K	12	
105	G S F C R N K L K	12	
121	R M N T N P S R R	12	
129	R P Y H F Q V P S	12	
168	G A P H E V G W K	12	
172	E V G W K Y Q A V	12	
174	G W K Y Q A V T A	12	
190	E K A E I H Y R K	12	
208	Q A E K N M K K K	12	
237	K T I A P L A A T	12	
273	R A P V P A A S P	12	
274	A P V P A A S P A	12	
366	R P A D L A G S G	12	
14	L H I V V E S I R	11	
17	V V E S I R D H S	11	
25	S G Q K M K Q D K	11	
76	V Y Q D E K Q R K	11	
89	L G R K A V V V S	11	
94	V V V S C E G I N	11	
99	E G I N I S G S F	11	
101	I N I S G S F C R	11	
113	K Y L A F L H K R	11	
114	Y L A F L H K R M	11	
143	Q E K A D G G S C	11	
181	T A T L E E K R K	11	
196	Y R K N K Q L M R	11	
221	T E S P G G G S P	11	
234	F I F K T I A P L	11	
248	T R I G H P G G R	11	
255	G R T P R A G S S	11	
265	H R P P A L S A R	11	
320	R H S P S G G G G	11	
327	G G L K K P A R H	11	
353	P K S E N N S W Y	11	
382	A I E S L E E G L	11	
11	L R A L H I V V E	10	
12	R A L H I V V E S	10	
73	H W T V Y Q D E K	10	
81	K Q R K D K V L L	10	
90	G R K A V V V S C	10	
102	N I S G S F C R N	10	
120	K R M N T N P S R	10	
123	N T N P S R R P Y	10	
125	N P S R R P Y H F	10	
127	S R R P Y H F Q V	10	

TABLE XXVI 151P3D4 v.2: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
144	E K A D G G S C C	10	
160	A Y K K V C L S G	10	
188	R K E K A E I H Y	10	
189	K E K A E I H Y R	10	
193	E I H Y R K N K Q	10	
246	R A T R I G H P G	10	
251	G H P G G R T P R	10	
258	P R A G S S A H R	10	
283	A W L P L R T P W	10	
330	K K P A R H C Q G	10	
333	A R H C Q G Q K H	10	
348	K P Q R K P K S E	10	
364	N G R P A D L A G	10	
368	A D L A G S G Y C	10	
392	G K Q K D K E R K	10	
395	K D K E R K A E N	10	
8	T F P L R A L H I	9	
19	E S I R D H S G Q	9	
50	G A K D F G H V Q	9	
55	G H V Q F V G S Y	9	
61	G S Y K L A Y S N	9	
65	L A Y S N D G E H	9	
91	R K A V V V S C E	9	
157	A S E A Y K K V C	9	
167	S G A P H E V G W	9	
214	K K K I D K Y T E	9	
215	K K I D K Y T E S	9	
247	A T R I G H P G G	9	
266	R P P A L S A R A	9	
270	L S A R A P V P A	9	
278	A A S P A A W L P	9	
295	S S C P T S S S T	9	
313	R N P L P N P R H	9	
338	G Q K H N V L A R	9	
384	E S L E E G L G G	9	
399	R K A E N G P H L	9	
15	H I V V E S I R D	8	
28	K M K Q D K K V D	8	
32	D K K V D L L V P	8	
33	K K V D L L V P T	8	
80	E K Q R K D K V L	8	
82	Q R K D K V L L G	8	
116	A F L H K R M N T	8	
128	R R P Y H F Q V P	8	
150	S C C P Q G H A S	8	
152	C P Q G H A S E A	8	
212	N M K K K I D K Y	8	
230	R G L G F I F K T	8	
240	A P L A A T R A T	8	
263	S A H R P P A L S	8	
276	V P A A S P A A W	8	
277	P A A S P A A W L	8	
279	A S P A A W L P L	8	

TABLE XXVI 151P3D4 v.2: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
280	S P A A W L P L R	8	
282	A A W L P L R T P	8	
289	T P W T R P S S C	8	
293	R P S S C P T S S	8	
308	S P Y G P R N P L	8	
312	P R N P L P N P R	8	
316	L P N P R H S P S	8	
362	V E N G R P A D L	8	
398	E R K A E N G P H	8	
31	Q D K K V D L L V	7	
48	T Q G A K D F G H	7	
66	A Y S N D G E H W	7	
68	S N D G E H W T V	7	
124	T N P S R R P Y H	7	
136	P S R I F W R Q E	7	
145	K A D G G S C C P	7	
151	C C P Q G H A S E	7	
153	P Q G H A S E A Y	7	
158	S E A Y K K V C L	7	
164	V C L S G A P H E	7	
173	V G W K Y Q A V T	7	
200	K Q L M R L Q K Q	7	
239	I A P L A A T R A	7	
242	L A A T R A T R I	.7	
254	G G R T P R A G S	7	
259	R A G S S A H R P	7	
271	S A R A P V P A A	7	
288	R T P W T R P S S	7	
305	D S L S P Y G P R	7	
310	Y G P R N P L P N	7	
318	N P R H S P S G G	7	
326	G G G L K K P A R	7	
331	K P A R H C Q G Q	7	
339	Q K H N V L A R G	7	
350	Q R K P K S E N N	7	
371	A G S G Y C G A L	7	
381	K A I E S L E E G	7	
396	D K E R K A E N G	7	
400	K A E N G P H L L	7	
29	M K Q D K K V D L	6	
35	V D L L V P T K V	6	
41	T K V T G I I T Q	6	
62	S Y K L A Y S N D	6	
126	P S R R P Y H F Q	6	
130	P Y H F Q V P S R	6	
139	I F W R Q E K A D	6	
140	F W R Q E K A D G	6	
166	L S G A P H E V G	6	
175	W K Y Q A V T A T	6	
182	A T L E E K R K E	6	
185	E E K R K E K A E	6	
186	E K R K E K A E I	6	
217	I D K Y T E S P G	6	

TABLE XXVI 151P3D4 v.2: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
219	K Y T E S P G G G	6	
227	G S P R G L G F I	6	
235	I F K T I A P L A	6	
236	F K T I A P L A A	6	
243	A A T R A T R I G	6	
262	S S A H R P P A L	6	
267	P P A L S A R A P	6	
268	P A L S A R A P V	6	
290	P W T R P S S C P	6	
291	W T R P S S C P T	6	
301	S S T Y D S L S P	6	
314	N P L P N P R H S	6	
321	H S P S G G G G L	6	
334	R H C Q G Q K H N	6	
337	Q G Q K H N V L A	6	
349	P Q R K P K S E N	6	
352	K P K S E N N S W	6	
355	S E N N S W Y V E	6	
359	S W Y V E N G R P	6	
363	E N G R P A D L A	6	
372	G S G Y C G A L W	6	
377	G A L W K A I E S	6	
379	L W K A I E S L E	6	
386	L E E G L G G K Q	6	
388	E G L G G K Q K D	6	
391	G G K Q K D K E R	6	
393	K Q K D K E R K A	6	
397	K E R K A E N G P	6	
5	T T K T F P L R A	5	
9	F P L R A L H I V	5	
18	V E S I R D H S G	5	
21	I R D H S G Q K M	5	
52	K D F G H V Q F V	5	
53	D F G H V Q F V G	5	
97	S C E G I N I S G	5	
107	F C R N K L K Y L	5	
110	N K L K Y L A F L	5	
118	L H K R M N T N P	5	
131	Y H F Q V P S R I	5	
141	W R Q E K A D G G	5	
142	R Q E K A D G G S	5	
146	A D G G S C C P Q	5	
148	G G S C C P Q G H	5	
159	E A Y K K V C L S	5	
162	K K V C L S G A P	5	
171	H E V G W K Y Q A	5	
177	Y Q A V T A T L E	5	
178	Q A V T A T L E E	5	
180	V T A T L E E K R	5	
197	R K N K Q L M R L	5	
202	L M R L Q K Q A E	5	
209	A E K N M K K K I	5	
223	S P G G G S P R G	5	

TABLE XXVI 151P3D4 v.2: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
233	G F I F K T I A P	5	
253	P G G R T P R A G	5	
281	P A A W L P L R T	5	
294	P S S C P T S S S	5	
309	P Y G P R N P L P	5	
317	P N P R H S P S G	5	
324	S G G G G L K K P	5	
329	L K K P A R H C Q	5	
336	C Q G Q K H N V L	5	
358	N S W Y V E N G R	5	
365	G R P A D L A G S	5	
376	C G A L W K A I E	5	
380	W K A I E S L E E	5	
4	H T T K T F P L R	4	
24	H S G Q K M K Q D	4	
30	K Q D K K V D L L	4	
40	P T K V T G I I T	4	
47	I T Q G A K D F G	4	
49	Q G A K D F G H V	4	
54	F G H V Q F V G S	4	
58	Q F V G S Y K L A	4	
60	V G S Y K L A Y S	4	
63	Y K L A Y S N D G	4	
67	Y S N D G E H W T	4	
70	D G E H W T V Y Q	4	
85	D K V L L G R K A	4	
92	K A V V V S C E G	4	
98	C E G I N I S G S	4	
132	H F Q V P S R I F	4	
133	F Q V P S R I F W	4	
161	Y K K V C L S G A	4	
191	K A E I H Y R K N	4	
198	K N K Q L M R L Q	4	
218	D K Y T E S P G G	4	
220	Y T E S P G G G S	4	
245	T R A T R I G H P	4	
252	H P G G R T P R A	4	
292	T R P S S C P T S	4	
300	S S S T Y D S L S	4	
311	G P R N P L P N P	4	
351	R K P K S E N N S	4	
354	K S E N N S W Y V	4	
356	E N N S W Y V E N	4	
360	W Y V E N G R P A	4	
383	I E S L E E G L G	4	
394	Q K D K E R K A E	4	
23	D H S G Q K M K Q	3	
71	G E H W T V Y Q D	3	
79	D E K Q R K D K V	3	
96	V S C E G I N I S	3	
119	H K R M N T N P S	3	
135	V P S R I F W R Q	3	
147	D G G S C C P Q G	3	

TABLE XXVI 151P3D4 v.2: HLA Peptide Scoring Results A3 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
195	H Y R K N K Q L M	3	
224	P G G G S P R G L	3	
260	A G S S A H R P P	3	
261	G S S A H R P P A	3	
287	L R T P W T R P S	3	
307	L S P Y G P R N P	3	
341	H N V L A R G K P	3	
345	A R G K P Q R K P	3	
375	Y C G A L W K A I	3	
27	Q K M K Q D K K V	2	
39	V P T K V T G I I	2	
57	V Q F V G S Y K L	2	
77	Y Q D E K Q R K D	2	
104	S G S F C R N K L	2	
115	L A F L H K R M N	2	
170	P H E V G W K Y Q	2	
184	L E E K R K E K A	2	
225	G G G S P R G L G	2	
232	L G F I F K T I A	2	
299	T S S S T Y D S L	2	
304	Y D S L S P Y G P	2	
325	G G G G L K K P A	2	
335	H C Q G Q K H N V	2	
347	G K P Q R K P K S	2	
370	L A G S G Y C G A	2	
374	G Y C G A L W K A	2	
2	L E H T T K T F P	1	
3	E H T T K T F P L	1	
6	T K T F P L R A L	1	
43	V T G I I T Q G A	1	
72	E H W T V Y Q D E	1	
122	M N T N P S R R P	1	
149	G S C C P Q G H A	1	
156	H A S E A Y K K V	1	
205	L Q K Q A E K N M	1	
210	E K N M K K K I D	1	
213	M K K K I D K Y T	1	
297	C P T S S S T Y D	1	
319	P R H S P S G G G	1	

TABLE XXVII 151P3D4 v.1: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
155	D L Q G V V F P Y	30	
249	D V F C F T S N F	30	
159	V V F P Y F P R L	28	
129	L T L E D Y G R Y	27	
230	N T V P G V R N Y	27	
186	A V I A S F D Q L	26	
126	I T D L T L E D Y	25	
140	E V I E G L E D D	24	
148	D T V V V A L D L	24	

TABLE XXVII 151P3D4 v.1: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
91	E V D V F V S M G	23	
93	D V F V S M G Y H	23	
183	D Q D A V I A S F	23	
187	V I A S F D Q L Y	23	
285	Q I A K V G Q I F	23	
329	E A A V R F V G F	23	
264	L I H P T K L T Y	22	
308	W L A D G S V R Y	22	
87	D Y L K E V D V F	21	
146	E D D T V V V A L	21	
153	A L D L Q G V V F	21	
209	W L S D G S V Q Y	21	
253	F T S N F N G R F	21	
56	N V T L P C K F Y	20	
76	K I R I K W T K L	20	
256	N F N G R F Y Y L	20	
291	Q I F A A W K I L	20	
81	W T K L T S D Y L	19	
162	P Y F P R L G R Y	19	
166	R L G R Y N L N F	19	
103	K T Y G G Y Q G R	18	
121	D A S L V I T D L	18	
336	G F P D K K H K L	18	
62	K F Y R D P T A F	17	
100	Y H K K T Y G G Y	17	
151	V V A L D L Q G V	17	
288	K V G Q I F A A W	17	
293	F A A W K I L G Y	17	
84	L T S D Y L K E V	16	
123	S L V I T D L T L	16	
124	L V I T D L T L E	16	
243	K D K S R Y D V F	16	
267	P T K L T Y D E A	16	
313	S V R Y P I S R P	16	
340	K K H K L Y G V Y	16	
7	L V L I S I C W A	15	
16	D H L S D N Y T L	15	
58	T L P C K F Y R D	15	
90	K E V D V F V S M	15	
95	F V S M G Y H K K	15	
128	D L T L E D Y G R	15	
137	Y K C E V I E G L	15	
156	L Q G V V F P Y F	15	
214	S V Q Y P I T K P	15	
345	Y G V Y C F R A Y	15	
5	L L L V L I S I C	14	
42	V E A E Q A K V F	14	
45	E Q A K V F S H R	14	
48	K V F S H R G G N	14	
83	K L T S D Y L K E	14	
111	R V F L K G G S D	14	
149	T V V V A L D L Q	14	
158	G V V F P Y F P R	14	

TABLE XXVII 151P3D4 v.1: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
190	S F D Q L Y D A W	14	
219	I T K P R E P C G	14	
240	F W D K D K S R Y	14	
245	K S R Y D V F C F	14	
275	A V Q A C L N D G	14	
326	S P T E A A V R F	14	
327	P T E A A V R F V	14	
342	H K L Y G V Y C F	14	
343	K L Y G V Y C F R	14	
1	M K S L L L L V L	13	
3	S L L L L V L I S	13	
4	L L L L V L I S I	13	
14	W A D H L S D N Y	13	
17	H L S D N Y T L D	13	
27	D R A I H I Q A E	13	
32	I Q A E N G P H L	13	
80	K W T K L T S D Y	13	
119	D S D A S L V I T	13	
125	V I T D L T L E D	13	
141	V I E G L E D D T	13	
231	T V P G V R N Y G	13	
270	L T Y D E A V Q A	13	
337	F P D K K H K L Y	13	
339	D K K H K L Y G V	13	
8	V L I S I C W A D	12	
22	Y T L D H D R A I	12	
29	A I H I Q A E N G	12	
35	E N G P H L L V E	12	
40	L L V E A E Q A K	12	
41	L V E A E Q A K V	12	
55	G N V T L P C K F	12	
57	V T L P C K F Y R	12	
69	A F G S G I H K I	12	
73	G I H K I R I K W	12	
88	Y L K E V D V F V	12	
92	V D V F V S M G Y	12	
113	F L K G G S D S D	12	
116	G G S D S D A S L	12	
132	E D Y G R Y K C E	12	
150	V V V A L D L Q G	12	
212	D G S V Q Y P I T	12	
252	C F T S N F N G R	12	
255	S N F N G R F Y Y	12	
297	K I L G Y D R C D	12	
9	L I S I C W A D H	11	
10	I S I C W A D H L	11	
25	D H D R A I H I Q	11	
51	S H R G G N V T L	11	
67	P T A F G S G I H	11	
78	R I K W T K L T S	11	
105	Y G G Y Q G R V F	11	
147	D D T V V V A L D	11	
181	C L D Q D A V I A	11	

TABLE XXVII 151P3D4 v.1: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
201	G L D W C N A G W	11	
218	P I T K P R E P C	11	
232	V P G V R N Y G F	11	
260	R F Y Y L I H P T	11	
311	D G S V R Y P I S	11	
317	P I S R P R R R C	11	
334	F V G F P D K K H	11	
346	G V Y C F R A Y N	11	
11	S I C W A D H L S	10	
23	T L D H D R A I H	10	
31	H I Q A E N G P H	10	
97	S M G Y H K K T Y	10	
106	G G Y Q G R V F L	10	
144	G L E D D T V V V	10	
171	N L N F H E A Q Q	10	
173	N F H E A Q Q A C	10	
174	F H E A Q Q A C L	10	
193	Q L Y D A W R G G	10	
194	L Y D A W R G G L	10	
234	G V R N Y G F W D	10	
254	T S N F N G R F Y	10	
263	Y L I H P T K L T	10	
279	C L N D G A Q I A	10	
331	A V R F V G F P D	10	
39	H L L V E A E Q A	9	
130	T L E D Y G R Y K	9	
164	F P R L G R Y N L	9	
210	L S D G S V Q Y P	9	
239	G F W D K D K S R	9	
242	D K D K S R Y D V	9	
262	Y Y L I H P T K L	9	
269	K L T Y D E A V Q	9	
271	T Y D E A V Q A C	9	
272	Y D E A V Q A C L	9	
333	R F V G F P D K K	9	
6	L L V L I S I C W	8	
33	Q A E N G P H L L	8	
36	N G P H L L V E A	8	
43	E A E Q A K V F S	8	
66	D P T A F G S G I	8	
94	V F V S M G Y H K	8	
112	V F L K G G S D S	8	
143	E G L E D D T V V	8	
163	Y F P R L G R Y N	8	
189	A S F D Q L Y D A	8	
202	L D W C N A G W L	8	
205	C N A G W L S D G	8	
224	E P C G G Q N T V	8	
273	D E A V Q A C L N	8	
274	E A V Q A C L N D	8	
282	D G A Q I A K V G	8	
284	A Q I A K V G Q I	8	
287	A K V G Q I F A A	8	

TABLE XXVII 151P3D4 v.1: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
298	I L G Y D R C D A	8	
301	Y D R C D A G W L	8	
304	C D A G W L A D G	8	
305	D A G W L A D G S	8	
309	L A D G S V R Y P	8	
13	C W A D H L S D N	7	
20	D N Y T L D H D R	7	
49	V F S H R G G N V	7	
72	S G I H K I R I K	7	
120	S D A S L V I T D	7	
133	D Y G R Y K C E V	7	
145	L E D D T V V V A	7	
160	V F P Y F P R L G	7	
176	E A Q Q A C L D Q	7	
192	D Q L Y D A W R G	7	
244	D K S R Y D V F C	7	
259	G R F Y Y L I H P	7	
281	N D G A Q I A K V	7	
292	I F A A W K I L G	7	
296	W K I L G Y D R C	7	
302	D R C D A G W L A	7	
332	V R F V G F P D K	7	
2	K S L L L L V L I	6	
37	G P H L L V E A E	6	
44	A E Q A K V F S H	6	
52	H R G G N V T L P	6	
65	R D P T A F G S G	6	
68	T A F G S G I H K	6	
79	I K W T K L T S D	6	
107	G Y Q G R V F L K	6	
136	R Y K C E V I E G	6	
154	L D L Q G V V F P	6	
165	P R L G R Y N L N	6	
182	L D Q D A V I A S	6	
185	D A V I A S F D Q	6	
196	D A W R G G L D W	6	
197	A W R G G L D W C	6	
203	D W C N A G W L S	6	
227	G G Q N T V P G V	6	
250	V F C F T S N F N	6	
265	I H P T K L T Y D	6	
19	S D N Y T L D H D	5	
54	G G N V T L P C K	5	
59	L P C K F Y R D P	5	
74	I H K I R I K W T	5	
108	Y Q G R V F L K G	5	
109	Q G R V F L K G G	5	
169	R Y N L N F H E A	5	
177	A Q Q A C L D Q D	5	
246	S R Y D V F C F T	5	
248	Y D V F C F T S N	5	
294	A A W K I L G Y D	5	
335	V G F P D K K H K	5	

TABLE XXVII 151P3D4 v.1: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
28	R A I H I Q A E N	4	
30	I H I Q A E N G P	4	
64	Y R D P T A F G S	4	
89	L K E V D V F V S	4	
114	L K G G S D S D A	4	
167	L G R Y N L N F H	4	
172	L N F H E A Q Q A	4	
217	Y P I T K P R E P	4	
233	P G V R N Y G F W	4	
235	V R N Y G F W D K	4	
251	F C F T S N F N G	4	
257	F N G R F Y Y L I	4	
258	N G R F Y Y L I H	4	
280	L N D G A Q I A K	4	
315	R Y P I S R P R R	4	
316	Y P I S R P R R R	4	
324	R C S P T E A A V	4	
330	A A V R F V G F P	4	
61	C K F Y R D P T A	3	
77	I R I K W T K L T	3	
96	V S M G Y H K K T	3	
99	G Y H K K T Y G G	3	
104	T Y G G Y Q G R V	3	
117	G S D S D A S L V	3	
175	H E A Q Q A C L D	3	
178	Q Q A C L D Q D A	3	
180	A C L D Q D A V I	3	
198	W R G G L D W C N	3	
216	Q Y P I T K P R E	3	
221	K P R E P C G G Q	3	
222	P R E P C G G Q N	3	
223	R E P C G G Q N T	3	
225	P C G G Q N T V P	3	
236	R N Y G F W D K D	3	
238	Y G F W D K D K S	3	
241	W D K D K S R Y D	3	
276	V Q A C L N D G A	3	
290	G Q I F A A W K I	3	
300	G Y D R C D A G W	3	
24	L D H D R A I H I	2	
34	A E N G P H L L V	2	
38	P H L L V E A E Q	2	
46	Q A K V F S H R G	2	
47	A K V F S H R G G	2	
63	F Y R D P T A F G	2	
70	F G S G I H K I R	2	
75	H K I R I K W T K	2	
85	T S D Y L K E V D	2	
86	S D Y L K E V D V	2	
110	G R V F L K G G S	2	
115	K G G S D S D A S	2	
131	L E D Y G R Y K C	2	
135	G R Y K C E V I E	2	

TABLE XXVII 151P3D4 v.1: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
152	V A L D L Q G V V	2	
168	G R Y N L N F H E	2	
184	Q D A V I A S F D	2	
200	G G L D W C N A G	2	
206	N A G W L S D G S	2	
207	A G W L S D G S V	2	
208	G W L S D G S V Q	2	
215	V Q Y P I T K P R	2	
220	T K P R E P C G G	2	
226	C G G Q N T V P G	2	
229	Q N T V P G V R N	2	
266	H P T K L T Y D E	2	
278	A C L N D G A Q I	2	
283	G A Q I A K V G Q	2	
295	A W K I L G Y D R	2	
299	L G Y D R C D A G	2	
303	R C D A G W L A D	2	
314	V R Y P I S R P R	2	
318	I S R P R R R C S	2	
319	S R P R R R C S P	2	
322	R R R C S P T E A	2	
323	R R C S P T E A A	2	
325	C S P T E A A V R	2	
338	P D K K H K L Y G	2	
341	K H K L Y G V Y C	2	
12	I C W A D H L S D	1	
15	A D H L S D N Y T	1	
18	L S D N Y T L D H	1	
21	N Y T L D H D R A	1	
26	H D R A I H I Q A	1	
60	P C K F Y R D P T	1	
71	G S G I H K I R I	1	
82	T K L T S D Y L K	1	
98	M G Y H K K T Y G	1	
101	H K K T Y G G Y Q	1	
102	K K T Y G G Y Q G	1	
118	S D S D A S L V I	1	
127	T D L T L E D Y G	1	
134	Y G R Y K C E V I	1	
139	C E V I E G L E D	1	
161	F P Y F P R L G R	1	
170	Y N L N F H E A Q	1	
179	Q A C L D Q D A V	1	
191	F D Q L Y D A W R	1	
195	Y D A W R G G L D	1	
199	R G G L D W C N A	1	
204	W C N A G W L S D	1	
211	S D G S V Q Y P I	1	
213	G S V Q Y P I T K	1	
247	R Y D V F C F T S	1	
261	F Y Y L I H P T K	1	
268	T K L T Y D E A V	1	
277	Q A C L N D G A Q	1	

TABLE XXVII 151P3D4 v.1: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
286	I A K V G Q I F A	1	
289	V G Q I F A A W K	1	
306	A G W L A D G S V	1	
307	G W L A D G S V R	1	
310	A D G S V R Y P I	1	
312	G S V R Y P I S R	1	
320	R P R R R C S P T	1	
321	P R R R C S P T E	1	
328	T E A A V R F V G	1	
344	L Y G V Y C F R A	1	

TABLE XXVII 151P3D4 v.2: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
302	S T Y D S L S P Y	27	
234	F I F K T I A P L	26	
123	N T N P S R R P Y	23	
172	E V G W K Y Q A V	23	
59	F V G S Y K L A Y	22	
378	A L W K A I E S L	22	
46	I I T Q G A K D F	21	
382	A I E S L E E G L	21	
99	E G I N I S G S F	19	
114	Y L A F L H K R M	19	
1	M L E H T T K T F	18	
102	N I S G S F C R N	18	
212	N M K K K I D K Y	18	
237	K T I A P L A A T	18	
369	D L A G S G Y C G	18	
16	I V V E S I R D H	17	
34	K V D L L V P T K	17	
38	L V P T K V T G I	17	
42	K V T G I I T Q G	17	
106	S F C R N K L K Y	17	
109	R N K L K Y L A F	17	
193	E I H Y R K N K Q	17	
4	H T T K T F P L R	16	
7	K T F P L R A L H	16	
55	G H V Q F V G S Y	16	
132	H F Q V P S R I F	16	
134	Q V P S R I F W R	16	
197	R K N K Q L M R L	16	
3	E H T T K T F P L	15	
30	K Q D K K V D L L	15	
45	G I I T Q G A K D	15	
80	E K Q R K D K V L	15	
179	A V T A T L E E K	15	
238	T I A P L A A T R	15	
385	S L E E G L G G K	15	
36	D L L V P T K V T	14	
110	N K L K Y L A F L	14	
299	T S S S T Y D S L	14	

TABLE XXVII 151P3D4 v.2: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
6	T K T F P L R A L	13	
13	A L H I V V E S I	13	
51	A K D F G H V Q F	13	
58	Q F V G S Y K L A	13	
107	F C R N K L K Y L	13	
117	F L H K R M N T N	13	
138	R I F W R Q E K A	13	
169	A P H E V G W K Y	13	
180	V T A T L E E K R	13	
182	A T L E E K R K E	13	
216	K I D K Y T E S P	13	
226	G G S P R G L G F	13	
228	S P R G L G F I F	13	
256	R T P R A G S S A	13	
275	P V P A A S P A A	13	
288	R T P W T R P S S	13	
291	W T R P S S C P T	13	
296	S C P T S S S T Y	13	
353	P K S E N N S W Y	13	
356	E N N S W Y V E N	13	
367	P A D L A G S G Y	13	
399	R K A E N G P H L	13	
5	T T K T F P L R A	12	
17	V V E S I R D H S	12	
20	S I R D H S G Q K	12	
21	I R D H S G Q K M	12	
43	V T G I I T Q G A	12	
47	I T Q G A K D F G	12	
53	D F G H V Q F V G	12	
69	N D G E H W T V Y	12	
74	W T V Y Q D E K Q	12	
75	T V Y Q D E K Q R	12	
93	A V V V S C E G I	12	
100	G I N I S G S F C	12	
159	E A Y K K V C L S	12	
163	K V C L S G A P H	12	
183	T L E E K R K E K	12	
188	R K E K A E I H Y	12	
220	Y T E S P G G G S	12	
224	P G G G S P R G L	12	
231	G L G F I F K T I	12	
247	A T R I G H P G G	12	
298	P T S S S T Y D S	12	
306	S L S P Y G P R N	12	
361	Y V E N G R P A D	12	
15	H I V V E S I R D	11	
23	D H S G Q K M K Q	11	
29	M K Q D K K V D L	11	
32	D K K V D L L V P	11	
37	L L V P T K V T G	11	
40	P T K V T G I I T	11	
56	H V Q F V G S Y K	11	
57	V Q F V G S Y K L	11	

TABLE XXVII 151P3D4 v.2: HLA Peptide Scoring Results A26 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
64	K	L	A	Y	S	N	D	G	E	11	
72	E	H	W	T	V	Y	Q	D	E	11	
86	K	V	L	L	G	R	K	A	V	11	
87	V	L	L	G	R	K	A	V	V	11	
94	V	V	V	S	C	E	G	I	N	11	
95	V	V	S	C	E	G	I	N	I	11	
125	N	P	S	R	R	P	Y	H	F	11	
153	P	Q	G	H	A	S	E	A	Y	11	
158	S	E	A	Y	K	K	V	C	L	11	
165	C	L	S	G	A	P	H	E	V	11	
204	R	L	Q	K	Q	A	E	K	N	11	
205	L	Q	K	Q	A	E	K	N	M	11	
244	A	T	R	A	T	R	I	G	H	11	
249	R	I	G	H	P	G	G	R	T	11	
262	S	S	A	H	R	P	P	A	L	11	
277	P	A	A	S	P	A	A	W	L	11	
305	D	S	L	S	P	Y	G	P	R	11	
321	H	S	P	S	G	G	G	G	L	11	
328	G	L	K	K	P	A	R	H	C	11	
343	V	L	A	R	G	K	P	Q	R	11	
362	V	E	N	G	R	P	A	D	L	11	
371	A	G	S	G	Y	C	G	A	L	11	
389	G	L	G	G	K	Q	K	D	K	11	
19	E	S	I	R	D	H	S	G	Q	10	
81	K	Q	R	K	D	K	V	L	L	10	
88	L	L	G	R	K	A	V	V	V	10	
111	K	L	K	Y	L	A	F	L	H	10	
190	E	K	A	E	I	H	Y	R	K	10	
194	I	H	Y	R	K	N	K	Q	L	10	
195	H	Y	R	K	N	K	Q	L	M	10	
201	Q	L	M	R	L	Q	K	Q	A	10	
222	E	S	P	G	G	G	S	P	R	10	
233	G	F	I	F	K	T	I	A	P	10	
241	P	L	A	A	T	R	A	T	R	10	
284	W	L	P	L	R	T	P	W	T	10	
308	S	P	Y	G	P	R	N	P	L	10	
315	P	L	P	N	P	R	H	S	P	10	
336	C	Q	G	Q	K	H	N	V	L	10	
342	N	V	L	A	R	G	K	P	Q	10	
381	K	A	I	E	S	L	E	E	G	10	
388	E	G	L	G	G	K	Q	K	D	10	
10	P	L	R	A	L	H	I	V	V	9	
52	K	D	F	G	H	V	Q	F	V	9	
79	D	E	K	Q	R	K	D	K	V	9	
104	S	G	S	F	C	R	N	K	L	9	
116	A	F	L	H	K	R	M	N	T	9	
144	E	K	A	D	G	G	S	C	C	9	
147	D	G	G	S	C	C	P	Q	G	9	
176	K	Y	Q	A	V	T	A	T	L	9	
185	E	E	K	R	K	E	K	A	E	9	
186	E	K	R	K	E	K	A	E	I	9	
215	K	K	I	D	K	Y	T	E	S	9	
265	H	R	P	P	A	L	S	A	R	9	

TABLE XXVII 151P3D4 v.2: HLA Peptide Scoring Results A26 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
269	A	L	S	A	R	A	P	V	P	9	
279	A	S	P	A	A	W	L	P	L	9	
286	P	L	R	T	P	W	T	R	P	9	
384	E	S	L	E	E	G	L	G	G	9	
8	T	F	P	L	R	A	L	H	I	8	
85	D	K	V	L	L	G	R	K	A	8	
139	I	F	W	R	Q	E	K	A	D	8	
218	D	K	Y	T	E	S	P	G	G	8	
235	I	F	K	T	I	A	P	L	A	8	
396	D	K	E	R	K	A	E	N	G	8	
400	K	A	E	N	G	P	H	L	L	8	
24	H	S	G	Q	K	M	K	Q	D	7	
33	K	K	V	D	L	L	V	P	T	7	
49	Q	G	A	K	D	F	G	H	V	7	
54	F	G	H	V	Q	F	V	G	S	7	
62	S	Y	K	L	A	Y	S	N	D	7	
70	D	G	E	H	W	T	V	Y	Q	7	
82	Q	R	K	D	K	V	L	L	G	7	
83	R	K	D	K	V	L	L	G	R	7	
84	K	D	K	V	L	L	G	R	K	7	
90	G	R	K	A	V	V	V	S	C	7	
130	P	Y	H	F	Q	V	P	S	R	7	
156	H	A	S	E	A	Y	K	K	V	7	
161	Y	K	K	V	C	L	S	G	A	7	
198	K	N	K	Q	L	M	R	L	Q	7	
210	E	K	N	M	K	K	K	I	D	7	
230	R	G	L	G	F	I	F	K	T	7	
324	S	G	G	G	G	L	K	K	P	7	
365	G	R	P	A	D	L	A	G	S	7	
374	G	Y	C	G	A	L	W	K	A	7	
387	E	E	G	L	G	G	K	Q	K	7	
398	E	R	K	A	E	N	G	P	H	7	
11	L	R	A	L	H	I	V	V	E	6	
12	R	A	L	H	I	V	V	E	S	6	
60	V	G	S	Y	K	L	A	Y	S	6	
89	L	G	R	K	A	V	V	V	S	6	
91	R	K	A	V	V	V	S	C	E	6	
96	V	S	C	E	G	I	N	I	S	6	
98	C	E	G	I	N	I	S	G	S	6	
128	R	R	P	Y	H	F	Q	V	P	6	
175	W	K	Y	Q	A	V	T	A	T	6	
200	K	Q	L	M	R	L	Q	K	Q	6	
207	K	Q	A	E	K	N	M	K	K	6	
208	Q	A	E	K	N	M	K	K	K	6	
245	T	R	A	T	R	I	G	H	P	6	
258	P	R	A	G	S	S	A	H	R	6	
271	S	A	R	A	P	V	P	A	A	6	
280	S	P	A	A	W	L	P	L	R	6	
311	G	P	R	N	P	L	P	N	P	6	
338	G	Q	K	H	N	V	L	A	R	6	
339	Q	K	H	N	V	L	A	R	G	6	
363	E	N	G	R	P	A	D	L	A	6	
370	L	A	G	S	G	Y	C	G	A	6	

TABLE XXVII 151P3D4 v.2: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
71	G E H W T V Y Q D	5	
77	Y Q D E K Q R K D	5	
112	L K Y L A F L H K	5	
113	K Y L A F L H K R	5	
131	Y H F Q V P S R I	5	
135	V P S R I F W R Q	5	
167	S G A P H E V G W	5	
168	G A P H E V G W K	5	
189	K E K A E I H Y R	5	
191	K A E I H Y R K N	5	
227	G S P R G L G F I	5	
248	T R I G H P G G R	5	
272	A R A P V P A A S	5	
344	L A R G K P Q R K	5	
350	Q R K P K S E N N	5	
357	N N S W Y V E N G	5	
395	K D K E R K A E N	5	
9	F P L R A L H I V	4	
41	T K V T G I I T Q	4	
126	P S R R P Y H F Q	4	
137	S R I F W R Q E K	4	
141	W R Q E K A D G G	4	
150	S C C P Q G H A S	4	
151	C C P Q G H A S E	4	
152	C P Q G H A S E A	4	
187	K R K E K A E I H	4	
203	M R L Q K Q A E K	4	
219	K Y T E S P G G G	4	
223	S P G G G S P R G	4	
229	P R G L G F I F K	4	
252	H P G G R T P R A	4	
266	R P P A L S A R A	4	
276	V P A A S P A A W	4	
282	A A W L P L R T P	4	
292	T R P S S C P T S	4	
295	S S C P T S S S T	4	
303	T Y D S L S P Y G	4	
320	R H S P S G G G G	4	
327	G G L K K P A R H	4	
335	H C Q G Q K H N V	4	
346	R G K P Q R K P K	4	
347	G K P Q R K P K S	4	
351	R K P K S E N N S	4	
366	R P A D L A G S G	4	
386	L E E G L G G K Q	4	
391	G G K Q K D K E R	4	
393	K Q K D K E R K A	4	
14	L H I V V E S I R	3	
26	G Q K M K Q D K K	3	
27	Q K M K Q D K K V	3	
44	T G I I T Q G A K	3	
61	G S Y K L A Y S N	3	
68	S N D G E H W T V	3	

TABLE XXVII 151P3D4 v.2: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
76	V Y Q D E K Q R K	3	
97	S C E G I N I S G	3	
101	I N I S G S F C R	3	
115	L A F L H K R M N	3	
124	T N P S R R P Y H	3	
127	S R R P Y H F Q V	3	
133	F Q V P S R I F W	3	
145	K A D G G S C C P	3	
146	A D G G S C C P Q	3	
155	G H A S E A Y K K	3	
160	A Y K K V C L S G	3	
164	V C L S G A P H E	3	
171	H E V G W K Y Q A	3	
174	G W K Y Q A V T A	3	
192	A E I H Y R K N K	3	
196	Y R K N K Q L M R	3	
202	L M R L Q K Q A E	3	
221	T E S P G G G S P	3	
251	G H P G G R T P R	3	
255	G R T P R A G S S	3	
259	R A G S S A H R P	3	
264	A H R P P A L S A	3	
267	P P A L S A R A P	3	
273	R A P V P A A S P	3	
274	A P V P A A S P A	3	
281	P A A W L P L R T	3	
283	A W L P L R T P W	3	
309	P Y G P R N P L P	3	
312	P R N P L P N P R	3	
313	R N P L P N P R H	3	
314	N P L P N P R H S	3	
316	L P N P R H S P S	3	
317	P N P R H S P S G	3	
318	N P R H S P S G G	3	
323	P S G G G G L K K	3	
325	G G G G L K K P A	3	
326	G G G L K K P A R	3	
329	L K K P A R H C Q	3	
331	K P A R H C Q G Q	3	
333	A R H C Q G Q K H	3	
349	P Q R K P K S E N	3	
352	K P K S E N N S W	3	
364	N G R P A D L A G	3	
390	L G G K Q K D K E	3	
394	Q K D K E R K A E	3	
22	R D H S G Q K M K	2	
25	S G Q K M K Q D K	2	
28	K M K Q D K K V D	2	
31	Q D K K V D L L V	2	
48	T Q G A K D F G H	2	
50	G A K D F G H V Q	2	
65	L A Y S N D G E H	2	
78	Q D E K Q R K D K	2	

TABLE XXVII 151P3D4 v.2: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
103	I S G S F C R N K	2	
105	G S F C R N K L K	2	
108	C R N K L K Y L A	2	
118	L H K R M N T N P	2	
120	K R M N T N P S R	2	
121	R M N T N P S R R	2	
140	F W R Q E K A D G	2	
142	R Q E K A D G G S	2	
143	Q E K A D G G S C	2	
148	G G S C C P Q G H	2	
154	Q G H A S E A Y K	2	
162	K K V C L S G A P	2	
173	V G W K Y Q A V T	2	
184	L E E K R K E K A	2	
209	A E K N M K K K I	2	
211	K N M K K K I D K	2	
213	M K K K I D K Y T	2	
217	I D K Y T E S P G	2	
232	L G F I F K T I A	2	
239	I A P L A A T R A	2	
242	L A A T R A T R I	2	
250	I G H P G G R T P	2	
254	G G R T P R A G S	2	
257	T P R A G S S A H	2	
268	P A L S A R A P V	2	
270	L S A R A P V P A	2	
278	A A S P A A W L P	2	
287	L R T P W T R P S	2	
289	T P W T R P S S C	2	
293	R P S S C P T S S	2	
294	P S S C P T S S S	2	
297	C P T S S S T Y D	2	
304	Y D S L S P Y G P	2	
307	L S P Y G P R N P	2	
319	P R H S P S G G G	2	
322	S P S G G G G L K	2	
330	K K P A R H C Q G	2	
334	R H C Q G Q K H N	2	
337	Q G Q K H N V L A	2	
340	K H N V L A R G K	2	
345	A R G K P Q R K P	2	
348	K P Q R K P K S E	2	
360	W Y V E N G R P A	2	
375	Y C G A L W K A I	2	
376	C G A L W K A I E	2	
377	G A L W K A I E S	2	
379	L W K A I E S L E	2	
380	W K A I E S L E E	2	
392	G K Q K D K E R K	2	
397	K E R K A E N G P	2	
18	V E S I R D H S G	1	
35	V D L L V P T K V	1	
39	V P T K V T G I I	1	

TABLE XXVII 151P3D4 v.2: HLA Peptide Scoring Results A26 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
66	A Y S N D G E H W	1	
67	Y S N D G E H W T	1	
73	H W T V Y Q D E K	1	
92	K A V V V S C E G	1	
122	M N T N P S R R P	1	
129	R P Y H F Q V P S	1	
136	P S R I F W R Q E	1	
149	G S C C P Q G H A	1	
177	Y Q A V T A T L E	1	
178	Q A V T A T L E E	1	
181	T A T L E E K R K	1	
199	N K Q L M R L Q K	1	
206	Q K Q A E K N M K	1	
214	K K K I D K Y T E	1	
225	G G G S P R G L G	1	
236	F K T I A P L A A	1	
240	A P L A A T R A T	1	
253	P G G R T P R A G	1	
260	A G S S A H R P P	1	
261	G S S A H R P P A	1	
263	S A H R P P A L S	1	
290	P W T R P S S C P	1	
300	S S S T Y D S L S	1	
301	S S T Y D S L S P	1	
310	Y G P R N P L P N	1	
332	P A R H C Q G Q K	1	
341	H N V L A R G K P	1	
355	S E N N S W Y V E	1	
358	N S W Y V E N G R	1	
359	S W Y V E N G R P	1	
372	G S G Y C G A L W	1	

TABLE XXVIII 151P3D4 v.1: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
164	F P R L G R Y N L	23	
320	R P R R R C S P T	20	
224	E P C G G Q N T V	19	
66	D P T A F G S G I	18	
326	S P T E A A V R F	18	
232	V P G V R N Y G F	17	
51	S H R G G N V T L	16	
146	E D D T V V V A L	16	
161	F P Y F P R L G R	16	
221	K P R E P C G G Q	16	
1	M K S L L L L V L	15	
34	A E N G P H L L V	15	
32	I Q A E N G P H L	14	
76	K I R I K W T K L	14	
106	G G Y Q G R V F L	14	
186	A V I A S F D Q L	14	
116	G G S D S D A S L	13	

TABLE XXVIII 151P3D4 v.1: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
121	D A S L V I T D L	13	
153	A L D L Q G V V F	13	
159	V V F P Y F P R L	13	
194	L Y D A W R G G L	13	
256	N F N G R F Y Y L	13	
37	G P H L L V E A E	12	
123	S L V I T D L T L	12	
148	D T V V V A L D L	12	
174	F H E A Q Q A C L	12	
266	H P T K L T Y D E	12	
272	Y D E A V Q A C L	12	
301	Y D R C D A G W L	12	
323	R R C S P T E A A	12	
324	R C S P T E A A V	12	
337	F P D K K H K L Y	12	
10	I S I C W A D H L	11	
59	L P C K F Y R D P	11	
118	S D S D A S L V I	11	
145	L E D D T V V V A	11	
262	Y Y L I H P T K L	11	
287	A K V G Q I F A A	11	
291	Q I F A A W K I L	11	
310	A D G S V R Y P I	11	
329	E A A V R F V G F	11	
16	D H L S D N Y T L	10	
33	Q A E N G P H L L	10	
81	W T K L T S D Y L	10	
90	K E V D V F V S M	10	
119	D S D A S L V I T	10	
137	Y K C E V I E G L	10	
144	G L E D D T V V V	10	
166	R L G R Y N L N F	10	
180	A C L D Q D A V I	10	
202	L D W C N A G W L	10	
217	Y P I T K P R E P	10	
245	K S R Y D V F C F	10	
263	Y L I H P T K L T	10	
278	A C L N D G A Q I	10	
284	A Q I A K V G Q I	10	
316	Y P I S R P R R R	10	
322	R R R C S P T E A	10	
336	G F P D K K H K L	10	
2	K S L L L L V L I	9	
26	H D R A I H I Q A	9	
49	V F S H R G G N V	9	
62	K F Y R D P T A F	9	
69	A F G S G I H K I	9	
77	I R I K W T K L T	9	
87	D Y L K E V D V F	9	
88	Y L K E V D V F V	9	
96	V S M G Y H K K T	9	
104	T Y G G Y Q G R V	9	
105	Y G G Y Q G R V F	9	

TABLE XXVIII 151P3D4 v.1: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
114	L K G G S D S D A	9	
122	A S L V I T D L T	9	
134	Y G R Y K C E V I	9	
143	E G L E D D T V V	9	
156	L Q G V V F P Y F	9	
181	C L D Q D A V I A	9	
183	D Q D A V I A S F	9	
212	D G S V Q Y P I T	9	
242	D K D K S R Y D V	9	
281	N D G A Q I A K V	9	
285	Q I A K V G Q I F	9	
298	I L G Y D R C D A	9	
327	P T E A A V R F V	9	
15	A D H L S D N Y T	8	
36	N G P H L L V E A	8	
41	L V E A E Q A K V	8	
42	V E A E Q A K V F	8	
50	F S H R G G N V T	8	
60	P C K F Y R D P T	8	
63	F Y R D P T A F G	8	
84	L T S D Y L K E V	8	
86	S D Y L K E V D V	8	
141	V I E G L E D D T	8	
142	I E G L E D D T V	8	
169	R Y N L N F H E A	8	
189	A S F D Q L Y D A	8	
199	R G G L D W C N A	8	
207	A G W L S D G S V	8	
211	S D G S V Q Y P I	8	
223	R E P C G G Q N T	8	
227	G G Q N T V P G V	8	
243	K D K S R Y D V F	8	
246	S R Y D V F C F T	8	
253	F T S N F N G R F	8	
260	R F Y Y L I H P T	8	
270	L T Y D E A V Q A	8	
286	I A K V G Q I F A	8	
306	A G W L A D G S V	8	
22	Y T L D H D R A I	7	
61	C K F Y R D P T A	7	
71	G S G I H K I R I	7	
74	I H K I R I K W T	7	
117	G S D S D A S L V	7	
133	D Y G R Y K C E V	7	
151	V V A L D L Q G V	7	
152	V A L D L Q G V V	7	
178	Q Q A C L D Q D A	7	
179	Q A C L D Q D A V	7	
249	D V F C F T S N F	7	
257	F N G R F Y Y L I	7	
268	T K L T Y D E A V	7	
276	V Q A C L N D G A	7	
302	D R C D A G W L A	7	

TABLE XXVIII 151P3D4 v.1: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
342	H K L Y G V Y C F	7	
344	L Y G V Y C F R A	7	
4	L L L L V L I S I	6	
7	L V L I S I C W A	6	
21	N Y T L D H D R A	6	
24	L D H D R A I H I	6	
35	E N G P H L L V E	6	
39	H L L V E A E Q A	6	
53	R G G N V T L P C	6	
55	G N V T L P C K F	6	
172	L N F H E A Q Q A	6	
197	A W R G G L D W C	6	
218	P I T K P R E P C	6	
229	Q N T V P G V R N	6	
267	P T K L T Y D E A	6	
279	C L N D G A Q I A	6	
290	G Q I F A A W K I	6	
303	R C D A G W L A D	6	
317	P I S R P R R R C	6	
331	A V R F V G F P D	6	
339	D K K H K L Y G V	6	
52	H R G G N V T L P	5	
188	I A S F D Q L Y D	5	
225	P C G G Q N T V P	5	
226	C G G Q N T V P G	5	
244	D K S R Y D V F C	5	
288	K V G Q I F A A W	5	
313	S V R Y P I S R P	5	
318	I S R P R R R C S	5	
12	I C W A D H L S D	4	
18	L S D N Y T L D H	4	
43	E A E Q A K V F S	4	
44	A E Q A K V F S H	4	
45	E Q A K V F S H R	4	
56	N V T L P C K F Y	4	
70	F G S G I H K I R	4	
108	Y Q G R V F L K G	4	
154	L D L Q G V V F P	4	
155	D L Q G V V F P Y	4	
158	G V V F P Y F P R	4	
209	W L S D G S V Q Y	4	
210	L S D G S V Q Y P	4	
214	S V Q Y P I T K P	4	
258	N G R F Y Y L I H	4	
280	L N D G A Q I A K	4	
304	C D A G W L A D G	4	
309	L A D G S V R Y P	4	
328	T E A A V R F V G	4	
330	A A V R F V G F P	4	
334	F V G F P D K K H	4	
341	K H K L Y G V Y C	4	
343	K L Y G V Y C F R	4	
3	S L L L L V L I S	3	

TABLE XXVIII 151P3D4 v.1: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
9	L I S I C W A D H	3	
17	H L S D N Y T L D	3	
23	T L D H D R A I H	3	
68	T A F G S G I H K	3	
78	R I K W T K L T S	3	
80	K W T K L T S D Y	3	
83	K L T S D Y L K E	3	
91	E V D V F V S M G	3	
103	K T Y G G Y Q G R	3	
107	G Y Q G R V F L K	3	
115	K G G S D S D A S	3	
125	V I T D L T L E D	3	
132	E D Y G R Y K C E	3	
135	G R Y K C E V I E	3	
139	C E V I E G L E D	3	
150	V V V A L D L Q G	3	
167	L G R Y N L N F H	3	
176	E A Q Q A C L D Q	3	
177	A Q Q A C L D Q D	3	
196	D A W R G G L D W	3	
198	W R G G L D W C N	3	
204	W C N A G W L S D	3	
205	C N A G W L S D G	3	
215	V Q Y P I T K P R	3	
219	I T K P R E P C G	3	
231	T V P G V R N Y G	3	
234	G V R N Y G F W D	3	
236	R N Y G F W D K D	3	
264	L I H P T K L T Y	3	
269	K L T Y D E A V Q	3	
271	T Y D E A V Q A C	3	
274	E A V Q A C L N D	3	
275	A V Q A C L N D G	3	
292	I F A A W K I L G	3	
293	F A A W K I L G Y	3	
294	A A W K I L G Y D	3	
295	A W K I L G Y D R	3	
297	K I L G Y D R C D	3	
307	G W L A D G S V R	3	
308	W L A D G S V R Y	3	
311	D G S V R Y P I S	3	
315	R Y P I S R P R R	3	
321	P R R R C S P T E	3	
333	R F V G F P D K K	3	
338	P D K K H K L Y G	3	
340	K K H K L Y G V Y	3	
27	D R A I H I Q A E	2	
28	R A I H I Q A E N	2	
29	A I H I Q A E N G	2	
31	H I Q A E N G P H	2	
47	A K V F S H R G G	2	
48	K V F S H R G G N	2	
64	Y R D P T A F G S	2	

TABLE XXVIII 151P3D4 v.1: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
65	R D P T A F G S G	2	
73	G I H K I R I K W	2	
79	I K W T K L T S D	2	
85	T S D Y L K E V D	2	
89	L K E V D V F V S	2	
95	F V S M G Y H K K	2	
99	G Y H K K T Y G G	2	
102	K K T Y G G Y Q G	2	
109	Q G R V F L K G G	2	
111	R V F L K G G S D	2	
112	V F L K G G S D S	2	
113	F L K G G S D S D	2	
120	S D A S L V I T D	2	
126	I T D L T L E D Y	2	
131	L E D Y G R Y K C	2	
136	R Y K C E V I E G	2	
147	D D T V V V A L D	2	
165	P R L G R Y N L N	2	
182	L D Q D A V I A S	2	
184	Q D A V I A S F D	2	
190	S F D Q L Y D A W	2	
195	Y D A W R G G L D	2	
201	G L D W C N A G W	2	
208	G W L S D G S V Q	2	
222	P R E P C G G Q N	2	
230	N T V P G V R N Y	2	
240	F W D K D K S R Y	2	
247	R Y D V F C F T S	2	
248	Y D V F C F T S N	2	
254	T S N F N G R F Y	2	
265	I H P T K L T Y D	2	
282	D G A Q I A K V G	2	
283	G A Q I A K V G Q	2	
300	G Y D R C D A G W	2	
314	V R Y P I S R P R	2	
325	C S P T E A A V R	2	
332	V R F V G F P D K	2	
345	Y G V Y C F R A Y	2	
346	G V Y C F R A Y N	2	
8	V L I S I C W A D	1	
13	C W A D H L S D N	1	
14	W A D H L S D N Y	1	
25	D H D R A I H I Q	1	
30	I H I Q A E N G P	1	
38	P H L L V E A E Q	1	
40	L L V E A E Q A K	1	
54	G G N V T L P C K	1	
57	V T L P C K F Y R	1	
58	T L P C K F Y R D	1	
67	P T A F G S G I H	1	
94	V F V S M G Y H K	1	
97	S M G Y H K K T Y	1	
98	M G Y H K K T Y G	1	

TABLE XXVIII 151P3D4 v.1: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
100	Y H K K T Y G G Y	1	
101	H K K T Y G G Y Q	1	
124	L V I T D L T L E	1	
130	T L E D Y G R Y K	1	
138	K C E V I E G L E	1	
140	E V I E G L E D D	1	
157	Q G V V F P Y F P	1	
162	P Y F P R L G R Y	1	
163	Y F P R L G R Y N	1	
170	Y N L N F H E A Q	1	
171	N L N F H E A Q Q	1	
173	N F H E A Q Q A C	1	
175	H E A Q Q A C L D	1	
187	V I A S F D Q L Y	1	
191	F D Q L Y D A W R	1	
200	G G L D W C N A G	1	
203	D W C N A G W L S	1	
206	N A G W L S D G S	1	
216	Q Y P I T K P R E	1	
228	G Q N T V P G V R	1	
233	P G V R N Y G F W	1	
235	V R N Y G F W D K	1	
237	N Y G F W D K D K	1	
250	V F C F T S N F N	1	
252	C F T S N F N G R	1	
255	S N F N G R F Y Y	1	
261	F Y Y L I H P T K	1	
273	D E A V Q A C L N	1	
277	Q A C L N D G A Q	1	
289	V G Q I F A A W K	1	
299	L G Y D R C D A G	1	
305	D A G W L A D G S	1	
319	S R P R R R C S P	1	
335	V G F P D K K H K	1	

TABLE XXVIII 151P3D4 v.2: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
308	S P Y G P R N P L	27	
228	S P R G L G F I F	21	
240	A P L A A T R A T	21	
252	H P G G R T P R A	21	
274	A P V P A A S P A	20	
266	R P P A L S A R A	19	
39	V P T K V T G I I	18	
125	N P S R R P Y H F	18	
152	C P Q G H A S E A	18	
371	A G S G Y C G A L	17	
9	F P L R A L H I V	16	
81	K Q R K D K V L L	16	
264	A H R P P A L S A	16	
279	A S P A A W L P L	16	

TABLE XXVIII 151P3D4 v.2: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
311	G P R N P L P N P	16	
271	S A R A P V P A A	15	
277	P A A S P A A W L	15	
322	S P S G G G G L K	15	
6	T K T F P L R A L	14	
30	K Q D K K V D L L	14	
129	R P Y H F Q V P S	14	
176	K Y Q A V T A T L	14	
223	S P G G G S P R G	14	
257	T P R A G S S A H	14	
276	V P A A S P A A W	14	
293	R P S S C P T S S	14	
399	R K A E N G P H L	14	
3	E H T T K T F P L	13	
104	S G S F C R N K L	13	
110	N K L K Y L A F L	13	
135	V P S R I F W R Q	13	
158	S E A Y K K V C L	13	
169	A P H E V G W K Y	13	
224	P G G G S P R G L	13	
234	F I F K T I A P L	13	
237	K T I A P L A A T	13	
262	S S A H R P P A L	13	
280	S P A A W L P L R	13	
362	V E N G R P A D L	13	
378	A L W K A I E S L	13	
29	M K Q D K K V D L	12	
80	E K Q R K D K V L	12	
107	F C R N K L K Y L	12	
197	R K N K Q L M R L	12	
226	G G S P R G L G F	12	
249	R I G H P G G R T	12	
261	G S S A H R P P A	12	
267	P P A L S A R A P	12	
299	T S S S T Y D S L	12	
316	L P N P R H S P S	12	
318	N P R H S P S G G	12	
331	K P A R H C Q G Q	12	
336	C Q G Q K H N V L	12	
366	R P A D L A G S G	12	
382	A I E S L E E G L	12	
36	D L L V P T K V T	11	
51	A K D F G H V Q F	11	
52	K D F G H V Q F V	11	
186	E K R K E K A E I	11	
194	I H Y R K N K Q L	11	
297	C P T S S S T Y D	11	
314	N P L P N P R H S	11	
321	H S P S G G G G L	11	
348	K P Q R K P K S E	11	
352	K P K S E N N S W	11	
363	E N G R P A D L A	11	
400	K A E N G P H L L	11	

TABLE XXVIII 151P3D4 v.2: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
10	P L R A L H I V V	10	
33	K K V D L L V P T	10	
57	V Q F V G S Y K L	10	
87	V L L G R K A V V	10	
88	L L G R K A V V V	10	
109	R N K L K Y L A F	10	
165	C L S G A P H E V	10	
270	L S A R A P V P A	10	
285	L P L R T P W T R	10	
289	T P W T R P S S C	10	
291	W T R P S S C P T	10	
325	G G G G L K K P A	10	
13	A L H I V V E S I	9	
21	I R D H S G Q K M	9	
31	Q D K K V D L L V	9	
49	Q G A K D F G H V	9	
68	S N D G E H W T V	9	
86	K V L L G R K A V	9	
95	V V S C E G I N I	9	
116	A F L H K R M N T	9	
127	S R R P Y H F Q V	9	
132	H F Q V P S R I F	9	
149	G S C C P Q G H A	9	
172	E V G W K Y Q A V	9	
173	V G W K Y Q A V T	9	
175	W K Y Q A V T A T	9	
195	H Y R K N K Q L M	9	
230	R G L G F I F K T	9	
236	F K T I A P L A A	9	
268	P A L S A R A P V	9	
275	P V P A A S P A A	9	
281	P A A W L P L R T	9	
337	Q G Q K H N V L A	9	
375	Y C G A L W K A I	9	
5	T T K T F P L R A	8	
8	T F P L R A L H I	8	
27	Q K M K Q D K K V	8	
38	L V P T K V T G I	8	
43	V T G I I T Q G A	8	
58	Q F V G S Y K L A	8	
93	A V V V S C E G I	8	
156	H A S E A Y K K V	8	
171	H E V G W K Y Q A	8	
174	G W K Y Q A V T A	8	
209	A E K N M K K K I	8	
231	G L G F I F K T I	8	
235	I F K T I A P L A	8	
239	I A P L A A T R A	8	
242	L A A T R A T R I	8	
256	R T P R A G S S A	8	
284	W L P L R T P W T	8	
335	H C Q G Q K H N V	8	
360	W Y V E N G R P A	8	

TABLE XXVIII 151P3D4 v.2: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
374	G Y C G A L W K A	8	
1	M L E H T T K T F	7	
35	V D L L V P T K V	7	
40	P T K V T G I I T	7	
46	I I T Q G A K D F	7	
85	D K V L L G R K A	7	
89	L G R K A V V V S	7	
99	E G I N I S G S F	7	
108	C R N K L K Y L A	7	
114	Y L A F L H K R M	7	
138	R I F W R Q E K A	7	
184	L E E K R K E K A	7	
201	Q L M R L Q K Q A	7	
213	M K K K I D K Y T	7	
227	G S P R G L G F I	7	
232	L G F I F K T I A	7	
254	G G R T P R A G S	7	
269	A L S A R A P V P	7	
295	S S C P T S S S T	7	
345	A R G K P Q R K P	7	
354	K S E N N S W Y V	7	
370	L A G S G Y C G A	7	
393	K Q K D K E R K A	7	
67	Y S N D G E H W T	6	
79	D E K Q R K D K V	6	
126	P S R R P Y H F Q	6	
131	Y H F Q V P S R I	6	
146	A D G G S C C P Q	6	
161	Y K K V C L S G A	6	
166	L S G A P H E V G	6	
205	L Q K Q A E K N M	6	
244	A T R A T R I G H	6	
272	A R A P V P A A S	6	
283	A W L P L R T P W	6	
286	P L R T P W T R P	6	
294	P S S C P T S S S	6	
323	P S G G G G L K K	6	
349	P Q R K P K S E N	6	
364	N G R P A D L A G	6	
66	A Y S N D G E H W	5	
83	R K D K V L L G R	5	
102	N I S G S F C R N	5	
160	A Y K K V C L S G	5	
222	E S P G G G S P R	5	
225	G G G S P R G L G	5	
247	A T R I G H P G G	5	
251	G H P G G R T P R	5	
260	A G S S A H R P P	5	
273	R A P V P A A S P	5	
278	A A S P A A W L P	5	
282	A A W L P L R T P	5	
306	S L S P Y G P R N	5	
313	R N P L P N P R H	5	

TABLE XXVIII 151P3D4 v.2: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
320	R H S P S G G G G	5	
7	K T F P L R A L H	4	
11	L R A L H I V V E	4	
12	R A L H I V V E S	4	
23	D H S G Q K M K Q	4	
34	K V D L L V P T K	4	
42	K V T G I I T Q G	4	
47	I T Q G A K D F G	4	
59	F V G S Y K L A Y	4	
90	G R K A V V V S C	4	
119	H K R M N T N P S	4	
145	K A D G G S C C P	4	
157	A S E A Y K K V C	4	
163	K V C L S G A P H	4	
167	S G A P H E V G W	4	
216	K I D K Y T E S P	4	
220	Y T E S P G G G S	4	
221	T E S P G G G S P	4	
241	P L A A T R A T R	4	
258	P R A G S S A H R	4	
263	S A H R P P A L S	4	
305	D S L S P Y G P R	4	
315	P L P N P R H S P	4	
328	G L K K P A R H C	4	
338	G Q K H N V L A R	4	
344	L A R G K P Q R K	4	
346	R G K P Q R K P K	4	
369	D L A G S G Y C G	4	
384	E S L E E G L G G	4	
394	Q K D K E R K A E	4	
397	K E R K A E N G P	4	
4	H T T K T F P L R	3	
32	D K K V D L L V P	3	
37	L L V P T K V T G	3	
54	F G H V Q F V G S	3	
60	V G S Y K L A Y S	3	
69	N D G E H W T V Y	3	
70	D G E H W T V Y Q	3	
82	Q R K D K V L L G	3	
91	R K A V V V S C E	3	
112	L K Y L A F L H K	3	
120	K R M N T N P S R	3	
122	M N T N P S R R P	3	
123	N T N P S R R P Y	3	
128	R R P Y H F Q V P	3	
133	F Q V P S R I F W	3	
140	F W R Q E K A D G	3	
144	E K A D G G S C C	3	
150	S C C P Q G H A S	3	
159	E A Y K K V C L S	3	
178	Q A V T A T L E E	3	
179	A V T A T L E E K	3	
192	A E I H Y R K N K	3	

TABLE XXVIII 151P3D4 v.2: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
199	N K Q L M R L Q K	3	
202	L M R L Q K Q A E	3	
211	K N M K K K I D K	3	
229	P R G L G F I F K	3	
238	T I A P L A A T R	3	
243	A A T R A T R I G	3	
246	R A T R I G H P G	3	
250	I G H P G G R T P	3	
287	L R T P W T R P S	3	
288	R T P W T R P S S	3	
290	P W T R P S S C P	3	
298	P T S S S T Y D S	3	
309	P Y G P R N P L P	3	
310	Y G P R N P L P N	3	
319	P R H S P S G G G	3	
324	S G G G G L K K P	3	
326	G G G L K K P A R	3	
333	A R H C Q G Q K H	3	
342	N V L A R G K P Q	3	
356	E N N S W Y V E N	3	
357	N N S W Y V E N G	3	
361	Y V E N G R P A D	3	
368	A D L A G S G Y C	3	
372	G S G Y C G A L W	3	
380	W K A I E S L E E	3	
383	I E S L E E G L G	3	
386	L E E G L G G K Q	3	
387	E E G L G G K Q K	3	
388	E G L G G K Q K D	3	
389	G L G G K Q K D K	3	
398	E R K A E N G P H	3	
2	L E H T T K T F P	2	
18	V E S I R D H S G	2	
20	S I R D H S G Q K	2	
28	K M K Q D K K V D	2	
45	G I I T Q G A K D	2	
48	T Q G A K D F G H	2	
50	G A K D F G H V Q	2	
53	D F G H V Q F V G	2	
64	K L A Y S N D G E	2	
78	Q D E K Q R K D K	2	
97	S C E G I N I S G	2	
100	G I N I S G S F C	2	
103	I S G S F C R N K	2	
106	S F C R N K L K Y	2	
113	K Y L A F L H K R	2	
124	T N P S R R P Y H	2	
130	P Y H F Q V P S R	2	
136	P S R I F W R Q E	2	
139	I F W R Q E K A D	2	
142	R Q E K A D G G S	2	
143	Q E K A D G G S C	2	
147	D G G S C C P Q G	2	

TABLE XXVIII 151P3D4 v.2: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
148	G G S C C P Q G H	2	
153	P Q G H A S E A Y	2	
154	Q G H A S E A Y K	2	
162	K K V C L S G A P	2	
177	Y Q A V T A T L E	2	
182	A T L E E K R K E	2	
185	E E K R K E K A E	2	
188	R K E K A E I H Y	2	
189	K E K A E I H Y R	2	
190	E K A E I H Y R K	2	
196	Y R K N K Q L M R	2	
204	R L Q K Q A E K N	2	
207	K Q A E K N M K K	2	
215	K K I D K Y T E S	2	
217	I D K Y T E S P G	2	
233	G F I F K T I A P	2	
248	T R I G H P G G R	2	
253	P G G R T P R A G	2	
259	R A G S S A H R P	2	
265	H R P P A L S A R	2	
300	S S S T Y D S L S	2	
301	S S T Y D S L S P	2	
303	T Y D S L S P Y G	2	
304	Y D S L S P Y G P	2	
312	P R N P L P N P R	2	
327	G G L K K P A R H	2	
329	L K K P A R H C Q	2	
330	K K P A R H C Q G	2	
332	P A R H C Q G Q K	2	
343	V L A R G K P Q R	2	
351	R K P K S E N N S	2	
353	P K S E N N S W Y	2	
365	G R P A D L A G S	2	
367	P A D L A G S G Y	2	
373	S G Y C G A L W K	2	
376	C G A L W K A I E	2	
390	L G G K Q K D K E	2	
395	K D K E R K A E N	2	
16	I V V E S I R D H	1	
17	V V E S I R D H S	1	
19	E S I R D H S G Q	1	
22	R D H S G Q K M K	1	
24	H S G Q K M K Q D	1	
25	S G Q K M K Q D K	1	
44	T G I I T Q G A K	1	
55	G H V Q F V G S Y	1	
56	H V Q F V G S Y K	1	
61	G S Y K L A Y S N	1	
63	Y K L A Y S N D G	1	
71	G E H W T V Y Q D	1	
72	E H W T V Y Q D E	1	
77	Y Q D E K Q R K D	1	
84	K D K V L L G R K	1	

TABLE XXVIII 151P3D4 v.2: HLA Peptide Scoring Results B*0702 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
92	K A V V V S C E G	1	
98	C E G I N I S G S	1	
101	I N I S G S F C R	1	
111	K L K Y L A F L H	1	
117	F L H K R M N T N	1	
118	L H K R M N T N P	1	
121	R M N T N P S R R	1	
137	S R I F W R Q E K	1	
151	C C P Q G H A S E	1	
155	G H A S E A Y K K	1	
164	V C L S G A P H E	1	
168	G A P H E V G W K	1	
180	V T A T L E E K R	1	
183	T L E E K R K E K	1	
187	K R K E K A E I H	1	
191	K A E I H Y R K N	1	
193	E I H Y R K N K Q	1	
198	K N K Q L M R L Q	1	
200	K Q L M R L Q K Q	1	
203	M R L Q K Q A E K	1	
206	Q K Q A E K N M K	1	
208	Q A E K N M K K K	1	
210	E K N M K K K I D	1	
212	N M K K K I D K Y	1	
214	K K K I D K Y T E	1	
218	D K Y T E S P G G	1	
219	K Y T E S P G G G	1	
245	T R A T R I G H P	1	
255	G R T P R A G S S	1	
292	T R P S S C P T S	1	
302	S T Y D S L S P Y	1	
317	P N P R H S P S G	1	
334	R H C Q G Q K H N	1	
339	Q K H N V L A R G	1	
340	K H N V L A R G K	1	
341	H N V L A R G K P	1	
347	G K P Q R K P K S	1	
350	Q R K P K S E N N	1	
355	S E N N S W Y V E	1	
379	L W K A I E S L E	1	
381	K A I E S L E E G	1	
392	G K Q K D K E R K	1	

TABLE XXIX 151P3D4 v.1: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
76	K I R I K W T K L	30	
164	F P R L G R Y N L	24	
243	K D K S R Y D V F	24	
134	Y G R Y K C E V I	23	
232	V P G V R N Y G F	23	
329	E A A V R F V G F	22	

TABLE XXIX 151P3D4 v.1: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
74	I H K I R I K W T	21	
81	W T K L T S D Y L	21	
336	G F P D K K H K L	21	
51	S H R G G N V T L	20	
241	W D K D K S R Y D	20	
320	R P R R R C S P T	20	
339	D K K H K L Y G V	20	
88	Y L K E V D V F V	19	
219	I T K P R E P C G	19	
123	S L V I T D L T L	18	
256	N F N G R F Y Y L	18	
337	F P D K K H K L Y	18	
113	F L K G G S D S D	17	
217	Y P I T K P R E P	17	
284	A Q I A K V G Q I	17	
326	S P T E A A V R F	17	
58	T L P C K F Y R D	16	
121	D A S L V I T D L	16	
286	I A K V G Q I F A	16	
293	F A A W K I L G Y	16	
301	Y D R C D A G W L	16	
46	Q A K V F S H R G	15	
146	E D D T V V V A L	15	
291	Q I F A A W K I L	15	
318	I S R P R R R C S	15	
24	L D H D R A I H I	14	
33	Q A E N G P H L L	14	
78	R I K W T K L T S	14	
86	S D Y L K E V D V	14	
153	A L D L Q G V V F	14	
221	K P R E P C G G Q	14	
245	K S R Y D V F C F	14	
316	Y P I S R P R R R	14	
4	L L L L V L I S I	13	
32	I Q A E N G P H L	13	
72	S G I H K I R I K	13	
137	Y K C E V I E G L	13	
166	R L G R Y N L N F	13	
66	D P T A F G S G I	12	
106	G G Y Q G R V F L	12	
136	R Y K C E V I E G	12	
239	G F W D K D K S R	12	
267	P T K L T Y D E A	12	
341	K H K L Y G V Y C	12	
1	M K S L L L L V L	11	
10	I S I C W A D H L	11	
16	D H L S D N Y T L	11	
44	A E Q A K V F S H	11	
79	I K W T K L T S D	11	
99	G Y H K K T Y G G	11	
101	H K K T Y G G Y Q	11	
111	R V F L K G G S D	11	
116	G G S D S D A S L	11	

TABLE XXIX 151P3D4 v.1: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
132	E D Y G R Y K C E	11	
148	D T V V V A L D L	11	
159	V V F P Y F P R L	11	
174	F H E A Q Q A C L	11	
265	I H P T K L T Y D	11	
3	S L L L L V L I S	10	
37	G P H L L V E A E	10	
42	V E A E Q A K V F	10	
60	P C K F Y R D P T	10	
98	M G Y H K K T Y G	10	
100	Y H K K T Y G G Y	10	
107	G Y Q G R V F L K	10	
186	A V I A S F D Q L	10	
194	L Y D A W R G G L	10	
202	L D W C N A G W L	10	
262	Y Y L I H P T K L	10	
272	Y D E A V Q A C L	10	
285	Q I A K V G Q I F	10	
295	A W K I L G Y D R	10	
313	S V R Y P I S R P	10	
319	S R P R R R C S P	10	
338	P D K K H K L Y G	10	
40	L L V E A E Q A K	9	
49	V F S H R G G N V	9	
61	C K F Y R D P T A	9	
299	L G Y D R C D A G	9	
311	D G S V R Y P I S	9	
342	H K L Y G V Y C F	9	
2	K S L L L L V L I	8	
5	L L L V L I S I C	8	
8	V L I S I C W A D	8	
39	H L L V E A E Q A	8	
109	Q G R V F L K G G	8	
118	S D S D A S L V I	8	
144	G L E D D T V V V	8	
162	P Y F P R L G R Y	8	
165	P R L G R Y N L N	8	
195	Y D A W R G G L D	8	
201	G L D W C N A G W	8	
211	S D G S V Q Y P I	8	
224	E P C G G Q N T V	8	
253	F T S N F N G R F	8	
298	I L G Y D R C D A	8	
6	L L V L I S I C W	7	
17	H L S D N Y T L D	7	
22	Y T L D H D R A I	7	
26	H D R A I H I Q A	7	
43	E A E Q A K V F S	7	
55	G N V T L P C K F	7	
62	K F Y R D P T A F	7	
63	F Y R D P T A F G	7	
69	A F G S G I H K I	7	
71	G S G I H K I R I	7	

TABLE XXIX 151P3D4 v.1: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
87	D Y L K E V D V F	7	
105	Y G G Y Q G R V F	7	
128	D L T L E D Y G R	7	
155	D L Q G V V F P Y	7	
156	L Q G V V F P Y F	7	
161	F P Y F P R L G R	7	
167	L G R Y N L N F H	7	
181	C L D Q D A V I A	7	
183	D Q D A V I A S F	7	
209	W L S D G S V Q Y	7	
234	G V R N Y G F W D	7	
257	F N G R F Y Y L I	7	
263	Y L I H P T K L T	7	
266	H P T K L T Y D E	7	
269	K L T Y D E A V Q	7	
290	G Q I F A A W K I	7	
308	W L A D G S V R Y	7	
322	R R R C S P T E A	7	
11	S I C W A D H L S	6	
23	T L D H D R A I H	6	
31	H I Q A E N G P H	6	
59	L P C K F Y R D P	6	
83	K L T S D Y L K E	6	
125	V I T D L T L E D	6	
130	T L E D Y G R Y K	6	
171	N L N F H E A Q Q	6	
176	E A Q Q A C L D Q	6	
179	Q A C L D Q D A V	6	
180	A C L D Q D A V I	6	
193	Q L Y D A W R G G	6	
197	A W R G G L D W C	6	
249	D V F C F T S N F	6	
258	N G R F Y Y L I H	6	
274	E A V Q A C L N D	6	
277	Q A C L N D G A Q	6	
278	A C L N D G A Q I	6	
279	C L N D G A Q I A	6	
283	G A Q I A K V G Q	6	
310	A D G S V R Y P I	6	
321	P R R R C S P T E	6	
331	A V R F V G F P D	6	
343	K L Y G V Y C F R	6	
28	R A I H I Q A E N	5	
73	G I H K I R I K W	5	
141	V I E G L E D D T	5	
152	V A L D L Q G V V	5	
187	V I A S F D Q L Y	5	
188	I A S F D Q L Y D	5	
309	L A D G S V R Y P	5	
330	A A V R F V G F P	5	
9	L I S I C W A D H	4	
14	W A D H L S D N Y	4	
29	A I H I Q A E N G	4	

TABLE XXIX 151P3D4 v.1: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
68	T A F G S G I H K	4	
91	E V D V F V S M G	4	
97	S M G Y H K K T Y	4	
140	E V I E G L E D D	4	
143	E G L E D D T V V	4	
185	D A V I A S F D Q	4	
196	D A W R G G L D W	4	
206	N A G W L S D G S	4	
214	S V Q Y P I T K P	4	
218	P I T K P R E P C	4	
264	L I H P T K L T Y	4	
271	T Y D E A V Q A C	4	
294	A A W K I L G Y D	4	
297	K I L G Y D R C D	4	
305	D A G W L A D G S	4	
317	P I S R P R R R C	4	
19	S D N Y T L D H D	3	
120	S D A S L V I T D	3	
173	N F H E A Q Q A C	3	
190	S F D Q L Y D A W	3	
27	D R A I H I Q A E	2	
35	E N G P H L L V E	2	
36	N G P H L L V E A	2	
38	P H L L V E A E Q	2	
45	E Q A K V F S H R	2	
52	H R G G N V T L P	2	
54	G G N V T L P C K	2	
56	N V T L P C K F Y	2	
70	F G S G I H K I R	2	
77	I R I K W T K L T	2	
84	L T S D Y L K E V	2	
89	L K E V D V F V S	2	
96	V S M G Y H K K T	2	
126	I T D L T L E D Y	2	
129	L T L E D Y G R Y	2	
135	G R Y K C E V I E	2	
142	I E G L E D D T V	2	
145	L E D D T V V V A	2	
147	D D T V V V A L D	2	
151	V V A L D L Q G V	2	
154	L D L Q G V V F P	2	
160	V F P Y F P R L G	2	
168	G R Y N L N F H E	2	
169	R Y N L N F H E A	2	
182	L D Q D A V I A S	2	
191	F D Q L Y D A W R	2	
200	G G L D W C N A G	2	
215	V Q Y P I T K P R	2	
227	G G Q N T V P G V	2	
229	Q N T V P G V R N	2	
235	V R N Y G F W D K	2	
246	S R Y D V F C F T	2	
251	F C F T S N F N G	2	

TABLE XXIX 151P3D4 v.1: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
255	S N F N G R F Y Y	2	
259	G R F Y Y L I H P	2	
260	R F Y Y L I H P T	2	
261	F Y Y L I H P T K	2	
276	V Q A C L N D G A	2	
287	A K V G Q I F A A	2	
332	V R F V G F P D K	2	
334	F V G F P D K K H	2	
335	V G F P D K K H K	2	
345	Y G V Y C F R A Y	2	
7	L V L I S I C W A	1	
12	I C W A D H L S D	1	
15	A D H L S D N Y T	1	
21	N Y T L D H D R A	1	
25	D H D R A I H I Q	1	
30	I H I Q A E N G P	1	
50	F S H R G G N V T	1	
57	V T L P C K F Y R	1	
75	H K I R I K W T K	1	
85	T S D Y L K E V D	1	
90	K E V D V F V S M	1	
92	V D V F V S M G Y	1	
93	D V F V S M G Y H	1	
94	V F V S M G Y H K	1	
95	F V S M G Y H K K	1	
102	K K T Y G G Y Q G	1	
110	G R V F L K G G S	1	
112	V F L K G G S D S	1	
115	K G G S D S D A S	1	
117	G S D S D A S L V	1	
119	D S D A S L V I T	1	
122	A S L V I T D L T	1	
131	L E D Y G R Y K C	1	
133	D Y G R Y K C E V	1	
138	K C E V I E G L E	1	
139	C E V I E G L E D	1	
149	T V V V A L D L Q	1	
150	V V V A L D L Q G	1	
157	Q G V V F P Y F P	1	
158	G V V F P Y F P R	1	
170	Y N L N F H E A Q	1	
175	H E A Q Q A C L D	1	
184	Q D A V I A S F D	1	
192	D Q L Y D A W R G	1	
199	R G G L D W C N A	1	
207	A G W L S D G S V	1	
208	G W L S D G S V Q	1	
210	L S D G S V Q Y P	1	
212	D G S V Q Y P I T	1	
213	G S V Q Y P I T K	1	
225	P C G G Q N T V P	1	
226	C G G Q N T V P G	1	
228	G Q N T V P G V R	1	

TABLE XXIX 151P3D4 v.1: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
230	N T V P G V R N Y	1	
237	N Y G F W D K D K	1	
240	F W D K D K S R Y	1	
244	D K S R Y D V F C	1	
247	R Y D V F C F T S	1	
250	V F C F T S N F N	1	
268	T K L T Y D E A V	1	
270	L T Y D E A V Q A	1	
273	D E A V Q A C L N	1	
280	L N D G A Q I A K	1	
281	N D G A Q I A K V	1	
282	D G A Q I A K V G	1	
288	K V G Q I F A A W	1	
289	V G Q I F A A W K	1	
292	I F A A W K I L G	1	
296	W K I L G Y D R C	1	
300	G Y D R C D A G W	1	
303	R C D A G W L A D	1	
306	A G W L A D G S V	1	
307	G W L A D G S V R	1	
312	G S V R Y P I S R	1	
314	V R Y P I S R P R	1	
323	R R C S P T E A A	1	
324	R C S P T E A A V	1	
327	P T E A A V R F V	1	
344	L Y G V Y C F R A	1	
346	G V Y C F R A Y N	1	

TABLE XXIX 151P3D4 v.2: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
107	F C R N K L K Y L	28	
109	R N K L K Y L A F	28	
158	S E A Y K K V C L	24	
185	E E K R K E K A E	24	
80	E K Q R K D K V L	23	
194	I H Y R K N K Q L	23	
391	G G K Q K D K E R	23	
3	E H T T K T F P L	22	
187	K R K E K A E I H	22	
26	G Q K M K Q D K K	21	
29	M K Q D K K V D L	21	
30	K Q D K K V D L L	21	
82	Q R K D K V L L G	21	
212	N M K K K I D K Y	21	
262	S S A H R P P A L	21	
395	K D K E R K A E N	21	
125	N P S R R P Y H F	20	
183	T L E E K R K E K	20	
196	Y R K N K Q L M R	20	
228	S P R G L G F I F	20	
336	C Q G Q K H N V L	20	

TABLE XXIX 151P3D4 v.2: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
344	L A R G K P Q R K	20	
350	Q R K P K S E N N	20	
393	K Q K D K E R K A	20	
362	V E N G R P A D L	19	
79	D E K Q R K D K V	18	
242	L A A T R A T R I	18	
308	S P Y G P R N P L	18	
389	G L G G K Q K D K	18	
38	L V P T K V T G I	17	
81	K Q R K D K V L L	17	
88	L L G R K A V V V	17	
111	K L K Y L A F L H	17	
159	E A Y K K V C L S	17	
209	A E K N M K K K I	17	
328	G L K K P A R H C	17	
348	K P Q R K P K S E	17	
352	K P K S E N N S W	17	
378	A L W K A I E S L	17	
234	F I F K T I A P L	16	
377	G A L W K A I E S	16	
8	T F P L R A L H I	15	
50	G A K D F G H V Q	15	
87	V L L G R K A V V	15	
117	F L H K R M N T N	15	
186	E K R K E K A E I	15	
193	E I H Y R K N K Q	15	
226	G G S P R G L G F	15	
252	H P G G R T P R A	15	
284	W L P L R T P W T	15	
231	G L G F I F K T I	14	
269	A L S A R A P V P	14	
271	S A R A P V P A A	14	
277	P A A S P A A W L	14	
289	T P W T R P S S C	14	
316	L P N P R H S P S	14	
382	A I E S L E E G L	14	
400	K A E N G P H L L	14	
1	M L E H T T K T F	13	
13	A L H I V V E S I	13	
39	V P T K V T G I I	13	
62	S Y K L A Y S N D	13	
90	G R K A V V V S C	13	
172	E V G W K Y Q A V	13	
174	G W K Y Q A V T A	13	
207	K Q A E K N M K K	13	
210	E K N M K K K I D	13	
257	T P R A G S S A H	13	
311	G P R N P L P N P	13	
326	G G G L K K P A R	13	
338	G Q K H N V L A R	13	
398	E R K A E N G P H	13	
10	P L R A L H I V V	12	
20	S I R D H S G Q K	12	

TABLE XXIX 151P3D4 v.2: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
24	H S G Q K M K Q D	12	
46	I I T Q G A K D F	12	
57	V Q F V G S Y K L	12	
60	V G S Y K L A Y S	12	
77	Y Q D E K Q R K D	12	
104	S G S F C R N K L	12	
138	R I F W R Q E K A	12	
141	W R Q E K A D G G	12	
217	I D K Y T E S P G	12	
233	G F I F K T I A P	12	
286	P L R T P W T R P	12	
318	N P R H S P S G G	12	
399	R K A E N G P H L	12	
6	T K T F P L R A L	11	
28	K M K Q D K K V D	11	
32	D K K V D L L V P	11	
40	P T K V T G I I T	11	
84	K D K V L L G R K	11	
105	G S F C R N K L K	11	
118	L H K R M N T N P	11	
161	Y K K V C L S G A	11	
189	K E K A E I H Y R	11	
203	M R L Q K Q A E K	11	
205	L Q K Q A E K N M	11	
213	M K K K I D K Y T	11	
215	K K I D K Y T E S	11	
235	I F K T I A P L A	11	
321	H S P S G G G G L	11	
327	G G L K K P A R H	11	
346	R G K P Q R K P K	11	
371	A G S G Y C G A L	11	
5	T T K T F P L R A	10	
31	Q D K K V D L L V	10	
48	T Q G A K D F G H	10	
110	N K L K Y L A F L	10	
116	A F L H K R M N T	10	
143	Q E K A D G G S C	10	
160	A Y K K V C L S G	10	
176	K Y Q A V T A T L	10	
197	R K N K Q L M R L	10	
198	K N K Q L M R L Q	10	
211	K N M K K K I D K	10	
214	K K K I D K Y T E	10	
224	P G G G S P R G L	10	
279	A S P A A W L P L	10	
299	T S S S T Y D S L	10	
329	L K K P A R H C Q	10	
332	P A R H C Q G Q K	10	
379	L W K A I E S L E	10	
385	S L E E G L G G K	10	
396	D K E R K A E N G	10	
18	V E S I R D H S G	9	
134	Q V P S R I F W R	9	

TABLE XXIX 151P3D4 v.2: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
245	T R A T R I G H P	9	
255	G R T P R A G S S	9	
309	P Y G P R N P L P	9	
342	N V L A R G K P Q	9	
347	G K P Q R K P K S	9	
36	D L L V P T K V T	8	
64	K L A Y S N D G E	8	
89	L G R K A V V V S	8	
99	E G I N I S G S F	8	
124	T N P S R R P Y H	8	
127	S R R P Y H F Q V	8	
132	H F Q V P S R I F	8	
156	H A S E A Y K K V	8	
169	A P H E V G W K Y	8	
184	L E E K R K E K A	8	
200	K Q L M R L Q K Q	8	
202	L M R L Q K Q A E	8	
223	S P G G G S P R G	8	
267	P P A L S A R A P	8	
276	V P A A S P A A W	8	
280	S P A A W L P L R	8	
306	S L S P Y G P R N	8	
322	S P S G G G G L K	8	
330	K K P A R H C Q G	8	
375	Y C G A L W K A I	8	
9	F P L R A L H I V	7	
12	R A L H I V V E S	7	
37	L L V P T K V T G	7	
51	A K D F G H V Q F	7	
93	A V V V S C E G I	7	
95	V V S C E G I N I	7	
114	Y L A F L H K R M	7	
119	H K R M N T N P S	7	
129	R P Y H F Q V P S	7	
135	V P S R I F W R Q	7	
140	F W R Q E K A D G	7	
152	C P Q G H A S E A	7	
165	C L S G A P H E V	7	
195	H Y R K N K Q L M	7	
201	Q L M R L Q K Q A	7	
227	G S P R G L G F I	7	
240	A P L A A T R A T	7	
254	G G R T P R A G S	7	
343	V L A R G K P Q R	7	
349	P Q R K P K S E N	7	
364	N G R P A D L A G	7	
381	K A I E S L E E G	7	
15	H I V V E S I R D	6	
92	K A V V V S C E G	6	
126	P S R R P Y H F Q	6	
131	Y H F Q V P S R I	6	
136	P S R I F W R Q E	6	
168	G A P H E V G W K	6	

TABLE XXIX 151P3D4 v.2: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
181	T A T L E E K R K	6	
204	R L Q K Q A E K N	6	
239	I A P L A A T R A	6	
241	P L A A T R A T R	6	
244	A T R A T R I G H	6	
247	A T R I G H P G G	6	
263	S A H R P P A L S	6	
264	A H R P P A L S A	6	
266	R P P A L S A R A	6	
274	A P V P A A S P A	6	
285	L P L R T P W T R	6	
291	W T R P S S C P T	6	
293	R P S S C P T S S	6	
297	C P T S S S T Y D	6	
314	N P L P N P R H S	6	
315	P L P N P R H S P	6	
331	K P A R H C Q G Q	6	
366	R P A D L A G S G	6	
369	D L A G S G Y C G	6	
397	K E R K A E N G P	6	
45	G I I T Q G A K D	5	
65	L A Y S N D G E H	5	
100	G I N I S G S F C	5	
115	L A F L H K R M N	5	
178	Q A V T A T L E E	5	
208	Q A E K N M K K K	5	
273	R A P V P A A S P	5	
282	A A W L P L R T P	5	
367	P A D L A G S G Y	5	
16	I V V E S I R D H	4	
96	V S C E G I N I S	4	
102	N I S G S F C R N	4	
145	K A D G G S C C P	4	
190	E K A E I H Y R K	4	
191	K A E I H Y R K N	4	
216	K I D K Y T E S P	4	
238	T I A P L A A T R	4	
243	A A T R A T R I G	4	
246	R A T R I G H P G	4	
249	R I G H P G G R T	4	
259	R A G S S A H R P	4	
268	P A L S A R A P V	4	
278	A A S P A A W L P	4	
281	P A A W L P L R T	4	
356	E N N S W Y V E N	4	
359	S W Y V E N G R P	4	
370	L A G S G Y C G A	4	
384	E S L E E G L G G	4	
387	E E G L G G K Q K	4	
11	L R A L H I V V E	3	
54	F G H V Q F V G S	3	
73	H W T V Y Q D E K	3	
86	K V L L G R K A V	3	

TABLE XXIX 151P3D4 v.2: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
97	S C E G I N I S G	3	
137	S R I F W R Q E K	3	
139	I F W R Q E K A D	3	
150	S C C P Q G H A S	3	
167	S G A P H E V G W	3	
301	S S T Y D S L S P	3	
324	S G G G G L K K P	3	
353	P K S E N N S W Y	3	
19	E S I R D H S G Q	2	
25	S G Q K M K Q D K	2	
34	K V D L L V P T K	2	
35	V D L L V P T K V	2	
55	G H V Q F V G S Y	2	
59	F V G S Y K L A Y	2	
68	S N D G E H W T V	2	
69	N D G E H W T V Y	2	
71	G E H W T V Y Q D	2	
72	E H W T V Y Q D E	2	
91	R K A V V V S C E	2	
106	S F C R N K L K Y	2	
144	E K A D G G S C C	2	
170	P H E V G W K Y Q	2	
175	W K Y Q A V T A T	2	
182	A T L E E K R K E	2	
219	K Y T E S P G G G	2	
222	E S P G G G S P R	2	
236	F K T I A P L A A	2	
265	H R P P A L S A R	2	
295	S S C P T S S S T	2	
296	S C P T S S S T Y	2	
300	S S S T Y D S L S	2	
302	S T Y D S L S P Y	2	
313	R N P L P N P R H	2	
325	G G G G L K K P A	2	
337	Q G Q K H N V L A	2	
341	H N V L A R G K P	2	
355	S E N N S W Y V E	2	
360	W Y V E N G R P A	2	
363	E N G R P A D L A	2	
372	G S G Y C G A L W	2	
373	S G Y C G A L W K	2	
383	I E S L E E G L G	2	
388	E G L G G K Q K D	2	
394	Q K D K E R K A E	2	
4	H T T K T F P L R	1	
14	L H I V V E S I R	1	
17	V V E S I R D H S	1	
21	I R D H S G Q K M	1	
22	R D H S G Q K M K	1	
27	Q K M K Q D K K V	1	
33	K K V D L L V P T	1	
41	T K V T G I I T Q	1	
42	K V T G I I T Q G	1	

TABLE XXIX 151P3D4 v.2: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
43	V T G I I T Q G A	1	
44	T G I I T Q G A K	1	
47	I T Q G A K D F G	1	
52	K D F G H V Q F V	1	
56	H V Q F V G S Y K	1	
58	Q F V G S Y K L A	1	
61	G S Y K L A Y S N	1	
70	D G E H W T V Y Q	1	
74	W T V Y Q D E K Q	1	
75	T V Y Q D E K Q R	1	
76	V Y Q D E K Q R K	1	
78	Q D E K Q R K D K	1	
85	D K V L L G R K A	1	
94	V V V S C E G I N	1	
98	C E G I N I S G S	1	
101	I N I S G S F C R	1	
103	I S G S F C R N K	1	
112	L K Y L A F L H K	1	
120	K R M N T N P S R	1	
128	R R P Y H F Q V P	1	
130	P Y H F Q V P S R	1	
133	F Q V P S R I F W	1	
148	G G S C C P Q G H	1	
149	G S C C P Q G H A	1	
153	P Q G H A S E A Y	1	
155	G H A S E A Y K K	1	
157	A S E A Y K K V C	1	
162	K K V C L S G A P	1	
163	K V C L S G A P H	1	
164	V C L S G A P H E	1	
171	H E V G W K Y Q A	1	
173	V G W K Y Q A V T	1	
177	Y Q A V T A T L E	1	
179	A V T A T L E E K	1	
180	V T A T L E E K R	1	
192	A E I H Y R K N K	1	
199	N K Q L M R L Q K	1	
225	G G G S P R G L G	1	
229	P R G L G F I F K	1	
230	R G L G F I F K T	1	
237	K T I A P L A A T	1	
250	I G H P G G R T P	1	
251	G H P G G R T P R	1	
253	P G G R T P R A G	1	
261	G S S A H R P P A	1	
270	L S A R A P V P A	1	
272	A R A P V P A A S	1	
275	P V P A A S P A A	1	
304	Y D S L S P Y G P	1	
307	L S P Y G P R N P	1	
334	R H C Q G Q K H N	1	
335	H C Q G Q K H N V	1	
340	K H N V L A R G K	1	

TABLE XXIX 151P3D4 v.2: HLA Peptide Scoring Results B*08 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
357	N N S W Y V E N G	1	
358	N S W Y V E N G R	1	
361	Y V E N G R P A D	1	
365	G R P A D L A G S	1	
374	G Y C G A L W K A	1	
376	C G A L W K A I E	1	
380	W K A I E S L E E	1	
392	G K Q K D K E R K	1	

TABLE XXX 151P3D4 v.1: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
51	S H R G G N V T L	25	
16	D H L S D N Y T L	21	
174	F H E A Q Q A C L	21	
32	I Q A E N G P H L	16	
106	G G Y Q G R V F L	16	
146	E D D T V V V A L	15	
159	V V F P Y F P R L	15	
1	M K S L L L L V L	13	
30	I H I Q A E N G P	13	
33	Q A E N G P H L L	13	
74	I H K I R I K W T	13	
116	G G S D S D A S L	13	
137	Y K C E V I E G L	13	
336	G F P D K K H K L	13	
10	I S I C W A D H L	12	
100	Y H K K T Y G G Y	12	
121	D A S L V I T D L	12	
164	F P R L G R Y N L	12	
262	Y Y L I H P T K L	12	
265	I H P T K L T Y D	12	
272	Y D E A V Q A C L	12	
341	K H K L Y G V Y C	12	
25	D H D R A I H I Q	11	
38	P H L L V E A E Q	11	
105	Y G G Y Q G R V F	11	
123	S L V I T D L T L	11	
148	D T V V V A L D L	11	
194	L Y D A W R G G L	11	
202	L D W C N A G W L	11	
256	N F N G R F Y Y L	11	
301	Y D R C D A G W L	11	
326	S P T E A A V R F	11	
329	E A A V R F V G F	11	
42	V E A E Q A K V F	10	
76	K I R I K W T K L	10	
81	W T K L T S D Y L	10	
87	D Y L K E V D V F	10	
153	A L D L Q G V V F	10	
186	A V I A S F D Q L	10	
291	Q I F A A W K I L	10	

TABLE XXX 151P3D4 v.1: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
90	K E V D V F V S M	9	
253	F T S N F N G R F	9	
55	G N V T L P C K F	8	
62	K F Y R D P T A F	8	
156	L Q G V V F P Y F	8	
243	K D K S R Y D V F	8	
285	Q I A K V G Q I F	8	
342	H K L Y G V Y C F	8	
144	G L E D D T V V V	7	
183	D Q D A V I A S F	7	
232	V P G V R N Y G F	7	
245	K S R Y D V F C F	7	
308	W L A D G S V R Y	7	
317	P I S R P R R R C	7	
318	I S R P R R R C S	7	
43	E A E Q A K V F S	6	
145	L E D D T V V V A	6	
166	R L G R Y N L N F	6	
229	Q N T V P G V R N	6	
230	N T V P G V R N Y	6	
249	D V F C F T S N F	6	
316	Y P I S R P R R R	6	
22	Y T L D H D R A I	5	
35	E N G P H L L V E	5	
89	L K E V D V F V S	5	
130	T L E D Y G R Y K	5	
154	L D L Q G V V F P	5	
209	W L S D G S V Q Y	5	
217	Y P I T K P R E P	5	
219	I T K P R E P C G	5	
328	T E A A V R F V G	5	
71	G S G I H K I R I	4	
85	T S D Y L K E V D	4	
88	Y L K E V D V F V	4	
104	T Y G G Y Q G R V	4	
118	S D S D A S L V I	4	
135	G R Y K C E V I E	4	
143	E G L E D D T V V	4	
162	P Y F P R L G R Y	4	
213	G S V Q Y P I T K	4	
216	Q Y P I T K P R E	4	
224	E P C G G Q N T V	4	
226	C G G Q N T V P G	4	
228	G Q N T V P G V R	4	
240	F W D K D K S R Y	4	
254	T S N F N G R F Y	4	
264	L I H P T K L T Y	4	
271	T Y D E A V Q A C	4	
282	D G A Q I A K V G	4	
283	G A Q I A K V G Q	4	
286	I A K V G Q I F A	4	
292	I F A A W K I L G	4	
309	L A D G S V R Y P	4	

TABLE XXX 151P3D4 v.1: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
313	S V R Y P I S R P	4	
314	V R Y P I S R P R	4	
315	R Y P I S R P R R	4	
324	R C S P T E A A V	4	
327	P T E A A V R F V	4	
345	Y G V Y C F R A Y	4	
17	H L S D N Y T L D	3	
27	D R A I H I Q A E	3	
36	N G P H L L V E A	3	
37	G P H L L V E A E	3	
45	E Q A K V F S H R	3	
46	Q A K V F S H R G	3	
50	F S H R G G N V T	3	
52	H R G G N V T L P	3	
54	G G N V T L P C K	3	
57	V T L P C K F Y R	3	
58	T L P C K F Y R D	3	
59	L P C K F Y R D P	3	
64	Y R D P T A F G S	3	
72	S G I H K I R I K	3	
73	G I H K I R I K W	3	
77	I R I K W T K L T	3	
84	L T S D Y L K E V	3	
91	E V D V F V S M G	3	
107	G Y Q G R V F L K	3	
120	S D A S L V I T D	3	
129	L T L E D Y G R Y	3	
134	Y G R Y K C E V I	3	
140	E V I E G L E D D	3	
142	I E G L E D D T V	3	
152	V A L D L Q G V V	3	
160	V F P Y F P R L G	3	
163	Y F P R L G R Y N	3	
180	A C L D Q D A V I	3	
181	C L D Q D A V I A	3	
182	L D Q D A V I A S	3	
188	I A S F D Q L Y D	3	
193	Q L Y D A W R G G	3	
200	G G L D W C N A G	3	
208	G W L S D G S V Q	3	
212	D G S V Q Y P I T	3	
218	P I T K P R E P C	3	
222	P R E P C G G Q N	3	
225	P C G G Q N T V P	3	
227	G G Q N T V P G V	3	
231	T V P G V R N Y G	3	
241	W D K D K S R Y D	3	
244	D K S R Y D V F C	3	
270	L T Y D E A V Q A	3	
287	A K V G Q I F A A	3	
296	W K I L G Y D R C	3	
297	K I L G Y D R C D	3	
298	I L G Y D R C D A	3	

TABLE XXX 151P3D4 v.1: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
307	G W L A D G S V R	3	
311	D G S V R Y P I S	3	
332	V R F V G F P D K	3	
335	V G F P D K K H K	3	
340	K K H K L Y G V Y	3	
344	L Y G V Y C F R A	3	
2	K S L L L L V L I	2	
5	L L L V L I S I C	2	
12	I C W A D H L S D	2	
13	C W A D H L S D N	2	
21	N Y T L D H D R A	2	
23	T L D H D R A I H	2	
34	A E N G P H L L V	2	
40	L L V E A E Q A K	2	
47	A K V F S H R G G	2	
61	C K F Y R D P T A	2	
63	F Y R D P T A F G	2	
67	P T A F G S G I H	2	
68	T A F G S G I H K	2	
69	A F G S G I H K I	2	
70	F G S G I H K I R	2	
75	H K I R I K W T K	2	
78	R I K W T K L T S	2	
79	I K W T K L T S D	2	
86	S D Y L K E V D V	2	
93	D V F V S M G Y H	2	
95	F V S M G Y H K K	2	
97	S M G Y H K K T Y	2	
99	G Y H K K T Y G G	2	
103	K T Y G G Y Q G R	2	
110	G R V F L K G G S	2	
112	V F L K G G S D S	2	
113	F L K G G S D S D	2	
119	D S D A S L V I T	2	
125	V I T D L T L E D	2	
126	I T D L T L E D Y	2	
131	L E D Y G R Y K C	2	
132	E D Y G R Y K C E	2	
133	D Y G R Y K C E V	2	
136	R Y K C E V I E G	2	
138	K C E V I E G L E	2	
141	V I E G L E D D T	2	
147	D D T V V V A L D	2	
149	T V V V A L D L Q	2	
155	D L Q G V V F P Y	2	
157	Q G V V F P Y F P	2	
158	G V V F P Y F P R	2	
161	F P Y F P R L G R	2	
169	R Y N L N F H E A	2	
170	Y N L N F H E A Q	2	
173	N F H E A Q Q A C	2	
175	H E A Q Q A C L D	2	
176	E A Q Q A C L D Q	2	

TABLE XXX 151P3D4 v.1: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
184	Q D A V I A S F D	2	
190	S F D Q L Y D A W	2	
192	D Q L Y D A W R G	2	
195	Y D A W R G G L D	2	
197	A W R G G L D W C	2	
205	C N A G W L S D G	2	
210	L S D G S V Q Y P	2	
214	S V Q Y P I T K P	2	
215	V Q Y P I T K P R	2	
220	T K P R E P C G G	2	
221	K P R E P C G G Q	2	
238	Y G F W D K D K S	2	
239	G F W D K D K S R	2	
242	D K D K S R Y D V	2	
247	R Y D V F C F T S	2	
255	S N F N G R F Y Y	2	
261	F Y Y L I H P T K	2	
263	Y L I H P T K L T	2	
268	T K L T Y D E A V	2	
269	K L T Y D E A V Q	2	
273	D E A V Q A C L N	2	
274	E A V Q A C L N D	2	
277	Q A C L N D G A Q	2	
279	C L N D G A Q I A	2	
280	L N D G A Q I A K	2	
288	K V G Q I F A A W	2	
293	F A A W K I L G Y	2	
299	L G Y D R C D A G	2	
303	R C D A G W L A D	2	
304	C D A G W L A D G	2	
312	G S V R Y P I S R	2	
321	P R R R C S P T E	2	
322	R R R C S P T E A	2	
323	R R C S P T E A A	2	
325	C S P T E A A V R	2	
333	R F V G F P D K K	2	
338	P D K K H K L Y G	2	
346	G V Y C F R A Y N	2	
3	S L L L L V L I S	1	
7	L V L I S I C W A	1	
8	V L I S I C W A D	1	
9	L I S I C W A D H	1	
24	L D H D R A I H I	1	
28	R A I H I Q A E N	1	
39	H L L V E A E Q A	1	
41	L V E A E Q A K V	1	
44	A E Q A K V F S H	1	
48	K V F S H R G G N	1	
49	V F S H R G G N V	1	
56	N V T L P C K F Y	1	
60	P C K F Y R D P T	1	
80	K W T K L T S D Y	1	
82	T K L T S D Y L K	1	

TABLE XXX 151P3D4 v.1: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
96	V S M G Y H K K T	1	
98	M G Y H K K T Y G	1	
102	K K T Y G G Y Q G	1	
108	Y Q G R V F L K G	1	
109	Q G R V F L K G G	1	
114	L K G G S D S D A	1	
115	K G G S D S D A S	1	
117	G S D S D A S L V	1	
122	A S L V I T D L T	1	
127	T D L T L E D Y G	1	
139	C E V I E G L E D	1	
151	V V A L D L Q G V	1	
165	P R L G R Y N L N	1	
167	L G R Y N L N F H	1	
168	G R Y N L N F H E	1	
178	Q Q A C L D Q D A	1	
179	Q A C L D Q D A V	1	
187	V I A S F D Q L Y	1	
189	A S F D Q L Y D A	1	
196	D A W R G G L D W	1	
198	W R G G L D W C N	1	
201	G L D W C N A G W	1	
204	W C N A G W L S D	1	
223	R E P C G G Q N T	1	
233	P G V R N Y G F W	1	
234	G V R N Y G F W D	1	
235	V R N Y G F W D K	1	
236	R N Y G F W D K D	1	
246	S R Y D V F C F T	1	
248	Y D V F C F T S N	1	
252	C F T S N F N G R	1	
259	G R F Y Y L I H P	1	
260	R F Y Y L I H P T	1	
266	H P T K L T Y D E	1	
267	P T K L T Y D E A	1	
276	V Q A C L N D G A	1	
281	N D G A Q I A K V	1	
284	A Q I A K V G Q I	1	
290	G Q I F A A W K I	1	
294	A A W K I L G Y D	1	
300	G Y D R C D A G W	1	
302	D R C D A G W L A	1	
310	A D G S V R Y P I	1	
319	S R P R R R C S P	1	
330	A A V R F V G F P	1	
334	F V G F P D K K H	1	
337	F P D K K H K L Y	1	
343	K L Y G V Y C F R	1	

TABLE XXX 151P3D4 v.2: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
194	I H Y R K N K Q L	22	
3	E H T T K T F P L	21	
6	T K T F P L R A L	15	
131	Y H F Q V P S R I	15	
29	M K Q D K K V D L	14	
81	K Q R K D K V L L	14	
158	S E A Y K K V C L	14	
224	P G G G S P R G L	14	
251	G H P G G R T P R	14	
262	S S A H R P P A L	14	
399	R K A E N G P H L	14	
23	D H S G Q K M K Q	13	
55	G H V Q F V G S Y	13	
80	E K Q R K D K V L	13	
170	P H E V G W K Y Q	13	
197	R K N K Q L M R L	13	
264	A H R P P A L S A	13	
308	S P Y G P R N P L	13	
320	R H S P S G G G G	13	
336	C Q G Q K H N V L	13	
340	K H N V L A R G K	13	
371	A G S G Y C G A L	13	
400	K A E N G P H L L	13	
30	K Q D K K V D L L	12	
57	V Q F V G S Y K L	12	
104	S G S F C R N K L	12	
155	G H A S E A Y K K	12	
234	F I F K T I A P L	12	
277	P A A S P A A W L	12	
299	T S S S T Y D S L	12	
334	R H C Q G Q K H N	12	
362	V E N G R P A D L	12	
378	A L W K A I E S L	12	
14	L H I V V E S I R	11	
72	E H W T V Y Q D E	11	
110	N K L K Y L A F L	11	
176	K Y Q A V T A T L	11	
321	H S P S G G G G L	11	
382	A I E S L E E G L	11	
46	I I T Q G A K D F	10	
107	F C R N K L K Y L	10	
114	Y L A F L H K R M	10	
118	L H K R M N T N P	10	
132	H F Q V P S R I F	10	
226	G G S P R G L G F	10	
279	A S P A A W L P L	10	
51	A K D F G H V Q F	9	
195	H Y R K N K Q L M	9	
1	M L E H T T K T F	8	
21	I R D H S G Q K M	8	
125	N P S R R P Y H F	8	
250	I G H P G G R T P	8	
99	E G I N I S G S F	7	

TABLE XXX 151P3D4 v.2: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
109	R N K L K Y L A F	7	
205	L Q K Q A E K N M	7	
228	S P R G L G F I F	7	
11	L R A L H I V V E	6	
16	I V V E S I R D H	6	
37	L L V P T K V T G	6	
89	L G R K A V V V S	6	
306	S L S P Y G P R N	6	
314	N P L P N P R H S	6	
361	Y V E N G R P A D	6	
122	M N T N P S R R P	5	
123	N T N P S R R P Y	5	
167	S G A P H E V G W	5	
183	T L E E K R K E K	5	
190	E K A E I H Y R K	5	
221	T E S P G G G S P	5	
223	S P G G G S P R G	5	
238	T I A P L A A T R	5	
272	A R A P V P A A S	5	
327	G G L K K P A R H	5	
328	G L K K P A R H C	5	
392	G K Q K D K E R K	5	
5	T T K T F P L R A	4	
12	R A L H I V V E S	4	
28	K M K Q D K K V D	4	
36	D L L V P T K V T	4	
41	T K V T G I I T Q	4	
47	I T Q G A K D F G	4	
50	G A K D F G H V Q	4	
76	V Y Q D E K Q R K	4	
77	Y Q D E K Q R K D	4	
87	V L L G R K A V V	4	
88	L L G R K A V V V	4	
90	G R K A V V V S C	4	
102	N I S G S F C R N	4	
103	I S G S F C R N K	4	
121	R M N T N P S R R	4	
144	E K A D G G S C C	4	
157	A S E A Y K K V C	4	
165	C L S G A P H E V	4	
174	G W K Y Q A V T A	4	
182	A T L E E K R K E	4	
186	E K R K E K A E I	4	
198	K N K Q L M R L Q	4	
208	Q A E K N M K K K	4	
239	I A P L A A T R A	4	
252	H P G G R T P R A	4	
253	P G G R T P R A G	4	
261	G S S A H R P P A	4	
267	P P A L S A R A P	4	
269	A L S A R A P V P	4	
270	L S A R A P V P A	4	
271	S A R A P V P A A	4	

TABLE XXX 151P3D4 v.2: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
281	P A A W L P L R T	4	
282	A A W L P L R T P	4	
287	L R T P W T R P S	4	
307	L S P Y G P R N P	4	
313	R N P L P N P R H	4	
326	G G G L K K P A R	4	
338	G Q K H N V L A R	4	
343	V L A R G K P Q R	4	
344	L A R G K P Q R K	4	
345	A R G K P Q R K P	4	
347	G K P Q R K P K S	4	
349	P Q R K P K S E N	4	
356	E N N S W Y V E N	4	
360	W Y V E N G R P A	4	
388	E G L G G K Q K D	4	
7	K T F P L R A L H	3	
15	H I V V E S I R D	3	
32	D K K V D L L V P	3	
33	K K V D L L V P T	3	
34	K V D L L V P T K	3	
54	F G H V Q F V G S	3	
67	Y S N D G E H W T	3	
69	N D G E H W T V Y	3	
70	D G E H W T V Y Q	3	
78	Q D E K Q R K D K	3	
84	K D K V L L G R K	3	
86	K V L L G R K A V	3	
91	R K A V V V S C E	3	
96	V S C E G I N I S	3	
101	I N I S G S F C R	3	
115	L A F L H K R M N	3	
117	F L H K R M N T N	3	
124	T N P S R R P Y H	3	
133	F Q V P S R I F W	3	
135	V P S R I F W R Q	3	
139	I F W R Q E K A D	3	
148	G G S C C P Q G H	3	
150	S C C P Q G H A S	3	
159	E A Y K K V C L S	3	
166	L S G A P H E V G	3	
173	V G W K Y Q A V T	3	
175	W K Y Q A V T A T	3	
177	Y Q A V T A T L E	3	
181	T A T L E E K R K	3	
184	L E E K R K E K A	3	
191	K A E I H Y R K N	3	
220	Y T E S P G G G S	3	
222	E S P G G G S P R	3	
225	G G G S P R G L G	3	
235	I F K T I A P L A	3	
240	A P L A A T R A T	3	
241	P L A A T R A T R	3	
242	L A A T R A T R I	3	

TABLE XXX 151P3D4 v.2: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
245	T R A T R I G H P	3	
248	T R I G H P G G R	3	
249	R I G H P G G R T	3	
254	G G R T P R A G S	3	
255	G R T P R A G S S	3	
257	T P R A G S S A H	3	
260	A G S S A H R P P	3	
265	H R P P A L S A R	3	
276	V P A A S P A A W	3	
278	A A S P A A W L P	3	
283	A W L P L R T P W	3	
286	P L R T P W T R P	3	
292	T R P S S C P T S	3	
304	Y D S L S P Y G P	3	
309	P Y G P R N P L P	3	
310	Y G P R N P L P N	3	
311	G P R N P L P N P	3	
312	P R N P L P N P R	3	
322	S P S G G G G L K	3	
325	G G G G L K K P A	3	
329	L K K P A R H C Q	3	
337	Q G Q K H N V L A	3	
346	R G K P Q R K P K	3	
353	P K S E N N S W Y	3	
359	S W Y V E N G R P	3	
364	N G R P A D L A G	3	
383	I E S L E E G L G	3	
385	S L E E G L G G K	3	
391	G G K Q K D K E R	3	
393	K Q K D K E R K A	3	
394	Q K D K E R K A E	3	
395	K D K E R K A E N	3	
4	H T T K T F P L R	2	
10	P L R A L H I V V	2	
17	V V E S I R D H S	2	
24	H S G Q K M K Q D	2	
25	S G Q K M K Q D K	2	
42	K V T G I I T Q G	2	
44	T G I I T Q G A K	2	
49	Q G A K D F G H V	2	
52	K D F G H V Q F V	2	
53	D F G H V Q F V G	2	
59	F V G S Y K L A Y	2	
61	G S Y K L A Y S N	2	
65	L A Y S N D G E H	2	
68	S N D G E H W T V	2	
71	G E H W T V Y Q D	2	
73	H W T V Y Q D E K	2	
75	T V Y Q D E K Q R	2	
79	D E K Q R K D K V	2	
82	Q R K D K V L L G	2	
85	D K V L L G R K A	2	
92	K A V V V S C E G	2	

TABLE XXX 151P3D4 v.2: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
97	S C E G I N I S G	2	
98	C E G I N I S G S	2	
106	S F C R N K L K Y	2	
108	C R N K L K Y L A	2	
127	S R R P Y H F Q V	2	
128	R R P Y H F Q V P	2	
129	R P Y H F Q V P S	2	
130	P Y H F Q V P S R	2	
136	P S R I F W R Q E	2	
137	S R I F W R Q E K	2	
140	F W R Q E K A D G	2	
142	R Q E K A D G G S	2	
145	K A D G G S C C P	2	
149	G S C C P Q G H A	2	
151	C C P Q G H A S E	2	
152	C P Q G H A S E A	2	
156	H A S E A Y K K V	2	
161	Y K K V C L S G A	2	
164	V C L S G A P H E	2	
168	G A P H E V G W K	2	
171	H E V G W K Y Q A	2	
172	E V G W K Y Q A V	2	
185	E E K R K E K A E	2	
188	R K E K A E I H Y	2	
193	E I H Y R K N K Q	2	
202	L M R L Q K Q A E	2	
203	M R L Q K Q A E K	2	
207	K Q A E K N M K K	2	
210	E K N M K K K I D	2	
211	K N M K K K I D K	2	
212	N M K K K I D K Y	2	
214	K K K I D K Y T E	2	
215	K K I D K Y T E S	2	
217	I D K Y T E S P G	2	
219	K Y T E S P G G G	2	
227	G S P R G L G F I	2	
230	R G L G F I F K T	2	
231	G L G F I F K T I	2	
233	G F I F K T I A P	2	
236	F K T I A P L A A	2	
237	K T I A P L A A T	2	
243	A A T R A T R I G	2	
247	A T R I G H P G G	2	
258	P R A G S S A H R	2	
259	R A G S S A H R P	2	
263	S A H R P P A L S	2	
266	R P P A L S A R A	2	
273	R A P V P A A S P	2	
274	A P V P A A S P A	2	
275	P V P A A S P A A	2	
280	S P A A W L P L R	2	
285	L P L R T P W T R	2	
288	R T P W T R P S S	2	

TABLE XXX 151P3D4 v.2: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
289	T P W T R P S S C	2	
291	W T R P S S C P T	2	
293	R P S S C P T S S	2	
294	P S S C P T S S S	2	
295	S S C P T S S S T	2	
303	T Y D S L S P Y G	2	
315	P L P N P R H S P	2	
316	L P N P R H S P S	2	
323	P S G G G G L K K	2	
324	S G G G G L K K P	2	
335	H C Q G Q K H N V	2	
339	Q K H N V L A R G	2	
350	Q R K P K S E N N	2	
354	K S E N N S W Y V	2	
355	S E N N S W Y V E	2	
357	N N S W Y V E N G	2	
363	E N G R P A D L A	2	
366	R P A D L A G S G	2	
369	D L A G S G Y C G	2	
374	G Y C G A L W K A	2	
375	Y C G A L W K A I	2	
376	C G A L W K A I E	2	
377	G A L W K A I E S	2	
380	W K A I E S L E E	2	
381	K A I E S L E E G	2	
384	E S L E E G L G G	2	
386	L E E G L G G K Q	2	
387	E E G L G G K Q K	2	
389	G L G G K Q K D K	2	
390	L G G K Q K D K E	2	
2	L E H T T K T F P	1	
8	T F P L R A L H I	1	
13	A L H I V V E S I	1	
18	V E S I R D H S G	1	
19	E S I R D H S G Q	1	
20	S I R D H S G Q K	1	
22	R D H S G Q K M K	1	
26	G Q K M K Q D K K	1	
27	Q K M K Q D K K V	1	
31	Q D K K V D L L V	1	
35	V D L L V P T K V	1	
38	L V P T K V T G I	1	
39	V P T K V T G I I	1	
40	P T K V T G I I T	1	
45	G I I T Q G A K D	1	
48	T Q G A K D F G H	1	
58	Q F V G S Y K L A	1	
60	V G S Y K L A Y S	1	
63	Y K L A Y S N D G	1	
64	K L A Y S N D G E	1	
66	A Y S N D G E H W	1	
83	R K D K V L L G R	1	
93	A V V V S C E G I	1	

TABLE XXX 151P3D4 v.2: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
95	V V S C E G I N I	1	
100	G I N I S G S F C	1	
105	G S F C R N K L K	1	
116	A F L H K R M N T	1	
119	H K R M N T N P S	1	
120	K R M N T N P S R	1	
126	P S R R P Y H F Q	1	
134	Q V P S R I F W R	1	
141	W R Q E K A D G G	1	
146	A D G G S C C P Q	1	
147	D G G S C C P Q G	1	
153	P Q G H A S E A Y	1	
160	A Y K K V C L S G	1	
162	K K V C L S G A P	1	
169	A P H E V G W K Y	1	
178	Q A V T A T L E E	1	
179	A V T A T L E E K	1	
180	V T A T L E E K R	1	
187	K R K E K A E I H	1	
189	K E K A E I H Y R	1	
192	A E I H Y R K N K	1	
196	Y R K N K Q L M R	1	
199	N K Q L M R L Q K	1	
204	R L Q K Q A E K N	1	
206	Q K Q A E K N M K	1	
209	A E K N M K K K I	1	
213	M K K K I D K Y T	1	
216	K I D K Y T E S P	1	
218	D K Y T E S P G G	1	
229	P R G L G F I F K	1	
232	L G F I F K T I A	1	
244	A T R A T R I G H	1	
268	P A L S A R A P V	1	
284	W L P L R T P W T	1	
290	P W T R P S S C P	1	
296	S C P T S S S T Y	1	
298	P T S S S T Y D S	1	
300	S S S T Y D S L S	1	
302	S T Y D S L S P Y	1	
305	D S L S P Y G P R	1	
317	P N P R H S P S G	1	
318	N P R H S P S G G	1	
319	P R H S P S G G G	1	
331	K P A R H C Q G Q	1	
341	H N V L A R G K P	1	
348	K P Q R K P K S E	1	
351	R K P K S E N N S	1	
365	G R P A D L A G S	1	
368	A D L A G S G Y C	1	
370	L A G S G Y C G A	1	
372	G S G Y C G A L W	1	
373	S G Y C G A L W K	1	
396	D K E R K A E N G	1	

TABLE XXX 151P3D4 v.2: HLA Peptide Scoring Results B*1510 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
397	K E R K A E N G P	1	
398	E R K A E N G P H	1	

TABLE XXXI 151P3D4 v.1: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
332	V R F V G F P D K	26	
314	V R Y P I S R P R	25	
235	V R N Y G F W D K	23	
106	G G Y Q G R V F L	20	
333	R F V G F P D K K	19	
103	K T Y G G Y Q G R	18	
135	G R Y K C E V I E	18	
166	R L G R Y N L N F	18	
213	G S V Q Y P I T K	18	
259	G R F Y Y L I H P	18	
315	R Y P I S R P R R	18	
322	R R R C S P T E A	18	
51	S H R G G N V T L	17	
55	G N V T L P C K F	17	
68	T A F G S G I H K	17	
76	K I R I K W T K L	17	
87	D Y L K E V D V F	17	
116	G G S D S D A S L	17	
121	D A S L V I T D L	17	
159	V V F P Y F P R L	17	
168	G R Y N L N F H E	17	
307	G W L A D G S V R	17	
336	G F P D K K H K L	17	
343	K L Y G V Y C F R	17	
62	K F Y R D P T A F	16	
72	S G I H K I R I K	16	
75	H K I R I K W T K	16	
107	G Y Q G R V F L K	16	
110	G R V F L K G G S	16	
164	F P R L G R Y N L	16	
183	D Q D A V I A S F	16	
239	G F W D K D K S R	16	
249	D V F C F T S N F	16	
261	F Y Y L I H P T K	16	
262	Y Y L I H P T K L	16	
312	G S V R Y P I S R	16	
342	H K L Y G V Y C F	16	
1	M K S L L L L V L	15	
16	D H L S D N Y T L	15	
52	H R G G N V T L P	15	
54	G G N V T L P C K	15	
77	I R I K W T K L T	15	
82	T K L T S D Y L K	15	
137	Y K C E V I E G L	15	
158	G V V F P Y F P R	15	
162	P Y F P R L G R Y	15	

TABLE XXXI 151P3D4 v.1: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
165	P R L G R Y N L N	15	
186	A V I A S F D Q L	15	
198	W R G G L D W C N	15	
228	G Q N T V P G V R	15	
230	N T V P G V R N Y	15	
280	L N D G A Q I A K	15	
290	G Q I F A A W K I	15	
323	R R C S P T E A A	15	
326	S P T E A A V R F	15	
335	V G F P D K K H K	15	
2	K S L L L L V L I	14	
10	I S I C W A D H L	14	
20	D N Y T L D H D R	14	
45	E Q A K V F S H R	14	
57	V T L P C K F Y R	14	
69	A F G S G I H K I	14	
80	K W T K L T S D Y	14	
90	K E V D V F V S M	14	
95	F V S M G Y H K K	14	
123	S L V I T D L T L	14	
128	D L T L E D Y G R	14	
148	D T V V V A L D L	14	
153	A L D L Q G V V F	14	
161	F P Y F P R L G R	14	
215	V Q Y P I T K P R	14	
240	F W D K D K S R Y	14	
272	Y D E A V Q A C L	14	
308	W L A D G S V R Y	14	
316	Y P I S R P R R R	14	
325	C S P T E A A V R	14	
340	K K H K L Y G V Y	14	
4	L L L L V L I S I	13	
27	D R A I H I Q A E	13	
32	I Q A E N G P H L	13	
42	V E A E Q A K V F	13	
70	F G S G I H K I R	13	
71	G S G I H K I R I	13	
129	L T L E D Y G R Y	13	
146	E D D T V V V A L	13	
174	F H E A Q Q A C L	13	
191	F D Q L Y D A W R	13	
209	W L S D G S V Q Y	13	
243	K D K S R Y D V F	13	
245	K S R Y D V F C F	13	
246	S R Y D V F C F T	13	
253	F T S N F N G R F	13	
255	S N F N G R F Y Y	13	
256	N F N G R F Y Y L	13	
285	Q I A K V G Q I F	13	
291	Q I F A A W K I L	13	
293	F A A W K I L G Y	13	
295	A W K I L G Y D R	13	
321	P R R R C S P T E	13	

TABLE XXXI 151P3D4 v.1: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
14	W A D H L S D N Y	12	
33	Q A E N G P H L L	12	
40	L L V E A E Q A K	12	
44	A E Q A K V F S H	12	
64	Y R D P T A F G S	12	
81	W T K L T S D Y L	12	
92	V D V F V S M G Y	12	
93	D V F V S M G Y H	12	
94	V F V S M G Y H K	12	
155	D L Q G V V F P Y	12	
156	L Q G V V F P Y F	12	
180	A C L D Q D A V I	12	
222	P R E P C G G Q N	12	
232	V P G V R N Y G F	12	
264	L I H P T K L T Y	12	
284	A Q I A K V G Q I	12	
289	V G Q I F A A W K	12	
334	F V G F P D K K H	12	
28	R A I H I Q A E N	11	
67	P T A F G S G I H	11	
105	Y G G Y Q G R V F	11	
126	I T D L T L E D Y	11	
202	L D W C N A G W L	11	
237	N Y G F W D K D K	11	
252	C F T S N F N G R	11	
278	A C L N D G A Q I	11	
301	Y D R C D A G W L	11	
302	D R C D A G W L A	11	
319	S R P R R R C S P	11	
329	E A A V R F V G F	11	
337	F P D K K H K L Y	11	
31	H I Q A E N G P H	10	
56	N V T L P C K F Y	10	
97	S M G Y H K K T Y	10	
100	Y H K K T Y G G Y	10	
111	R V F L K G G S D	10	
130	T L E D Y G R Y K	10	
167	L G R Y N L N F H	10	
194	L Y D A W R G G L	10	
211	S D G S V Q Y P I	10	
236	R N Y G F W D K D	10	
260	R F Y Y L I H P T	10	
9	L I S I C W A D H	9	
18	L S D N Y T L D H	9	
22	Y T L D H D R A I	9	
23	T L D H D R A I H	9	
73	G I H K I R I K W	9	
118	S D S D A S L V I	9	
187	V I A S F D Q L Y	9	
258	N G R F Y Y L I H	9	
310	A D G S V R Y P I	9	
345	Y G V Y C F R A Y	9	
24	L D H D R A I H I	8	

TABLE XXXI 151P3D4 v.1: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
134	Y G R Y K C E V I	8	
136	R Y K C E V I E G	8	
154	L D L Q G V V F P	8	
214	S V Q Y P I T K P	8	
223	R E P C G G Q N T	8	
224	E P C G G Q N T V	8	
254	T S N F N G R F Y	8	
5	L L L V L I S I C	7	
66	D P T A F G S G I	7	
78	R I K W T K L T S	7	
99	G Y H K K T Y G G	7	
112	V F L K G G S D S	7	
143	E G L E D D T V V	7	
199	R G G L D W C N A	7	
208	G W L S D G S V Q	7	
251	F C F T S N F N G	7	
257	F N G R F Y Y L I	7	
287	A K V G Q I F A A	7	
296	W K I L G Y D R C	7	
297	K I L G Y D R C D	7	
303	R C D A G W L A D	7	
313	S V R Y P I S R P	7	
3	S L L L L V L I S	6	
7	L V L I S I C W A	6	
30	I H I Q A E N G P	6	
37	G P H L L V E A E	6	
38	P H L L V E A E Q	6	
41	L V E A E Q A K V	6	
53	R G G N V T L P C	6	
61	C K F Y R D P T A	6	
79	I K W T K L T S D	6	
98	M G Y H K K T Y G	6	
102	K K T Y G G Y Q G	6	
104	T Y G G Y Q G R V	6	
113	F L K G G S D S D	6	
140	E V I E G L E D D	6	
152	V A L D L Q G V V	6	
169	R Y N L N F H E A	6	
172	L N F H E A Q Q A	6	
189	A S F D Q L Y D A	6	
192	D Q L Y D A W R G	6	
197	A W R G G L D W C	6	
200	G G L D W C N A G	6	
225	P C G G Q N T V P	6	
238	Y G F W D K D K S	6	
270	L T Y D E A V Q A	6	
274	E A V Q A C L N D	6	
281	N D G A Q I A K V	6	
286	I A K V G Q I F A	6	
288	K V G Q I F A A W	6	
324	R C S P T E A A V	6	
346	G V Y C F R A Y N	6	
6	L L V L I S I C W	5	

TABLE XXXI 151P3D4 v.1: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
15	A D H L S D N Y T	5	
34	A E N G P H L L V	5	
39	H L L V E A E Q A	5	
48	K V F S H R G G N	5	
65	R D P T A F G S G	5	
83	K L T S D Y L K E	5	
86	S D Y L K E V D V	5	
114	L K G G S D S D A	5	
117	G S D S D A S L V	5	
124	L V I T D L T L E	5	
131	L E D Y G R Y K C	5	
142	I E G L E D D T V	5	
144	G L E D D T V V V	5	
150	V V V A L D L Q G	5	
201	G L D W C N A G W	5	
207	A G W L S D G S V	5	
227	G G Q N T V P G V	5	
247	R Y D V F C F T S	5	
265	I H P T K L T Y D	5	
282	D G A Q I A K V G	5	
283	G A Q I A K V G Q	5	
294	A A W K I L G Y D	5	
300	G Y D R C D A G W	5	
320	R P R R R C S P T	5	
8	V L I S I C W A D	4	
29	A I H I Q A E N G	4	
35	E N G P H L L V E	4	
36	N G P H L L V E A	4	
43	E A E Q A K V F S	4	
50	F S H R G G N V T	4	
58	T L P C K F Y R D	4	
74	I H K I R I K W T	4	
88	Y L K E V D V F V	4	
96	V S M G Y H K K T	4	
108	Y Q G R V F L K G	4	
120	S D A S L V I T D	4	
122	A S L V I T D L T	4	
132	E D Y G R Y K C E	4	
139	C E V I E G L E D	4	
181	C L D Q D A V I A	4	
188	I A S F D Q L Y D	4	
204	W C N A G W L S D	4	
205	C N A G W L S D G	4	
210	L S D G S V Q Y P	4	
216	Q Y P I T K P R E	4	
217	Y P I T K P R E P	4	
221	K P R E P C G G Q	4	
229	Q N T V P G V R N	4	
231	T V P G V R N Y G	4	
242	D K D K S R Y D V	4	
248	Y D V F C F T S N	4	
266	H P T K L T Y D E	4	
269	K L T Y D E A V Q	4	

TABLE XXXI 151P3D4 v.1: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
304	C D A G W L A D G	4	
306	A G W L A D G S V	4	
309	L A D G S V R Y P	4	
338	P D K K H K L Y G	4	
341	K H K L Y G V Y C	4	
12	I C W A D H L S D	3	
21	N Y T L D H D R A	3	
25	D H D R A I H I Q	3	
26	H D R A I H I Q A	3	
46	Q A K V F S H R G	3	
47	A K V F S H R G G	3	
85	T S D Y L K E V D	3	
115	K G G S D S D A S	3	
119	D S D A S L V I T	3	
125	V I T D L T L E D	3	
127	T D L T L E D Y G	3	
138	K C E V I E G L E	3	
141	V I E G L E D D T	3	
145	L E D D T V V V A	3	
147	D D T V V V A L D	3	
173	N F H E A Q Q A C	3	
175	H E A Q Q A C L D	3	
176	E A Q Q A C L D Q	3	
177	A Q Q A C L D Q D	3	
179	Q A C L D Q D A V	3	
184	Q D A V I A S F D	3	
190	S F D Q L Y D A W	3	
196	D A W R G G L D W	3	
218	P I T K P R E P C	3	
219	I T K P R E P C G	3	
226	C G G Q N T V P G	3	
234	G V R N Y G F W D	3	
263	Y L I H P T K L T	3	
268	T K L T Y D E A V	3	
275	A V Q A C L N D G	3	
279	C L N D G A Q I A	3	
292	I F A A W K I L G	3	
317	P I S R P R R R C	3	
330	A A V R F V G F P	3	
339	D K K H K L Y G V	3	
13	C W A D H L S D N	2	
17	H L S D N Y T L D	2	
49	V F S H R G G N V	2	
59	L P C K F Y R D P	2	
63	F Y R D P T A F G	2	
84	L T S D Y L K E V	2	
89	L K E V D V F V S	2	
91	E V D V F V S M G	2	
133	D Y G R Y K C E V	2	
149	T V V V A L D L Q	2	
151	V V A L D L Q G V	2	
157	Q G V V F P Y F P	2	
170	Y N L N F H E A Q	2	

TABLE XXXI 151P3D4 v.1: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
171	N	L	N	F	H	E	A	Q	Q	2	
178	Q	Q	A	C	L	D	Q	D	A	2	
182	L	D	Q	D	A	V	I	A	S	2	
185	D	A	V	I	A	S	F	D	Q	2	
193	Q	L	Y	D	A	W	R	G	G	2	
206	N	A	G	W	L	S	D	G	S	2	
241	W	D	K	D	K	S	R	Y	D	2	
244	D	K	S	R	Y	D	V	F	C	2	
250	V	F	C	F	T	S	N	F	N	2	
267	P	T	K	L	T	Y	D	E	A	2	
271	T	Y	D	E	A	V	Q	A	C	2	
276	V	Q	A	C	L	N	D	G	A	2	
277	Q	A	C	L	N	D	G	A	Q	2	
299	L	G	Y	D	R	C	D	A	G	2	
305	D	A	G	W	L	A	D	G	S	2	
318	I	S	R	P	R	R	R	C	S	2	
328	T	E	A	A	V	R	F	V	G	2	
331	A	V	R	F	V	G	F	P	D	2	
344	L	Y	G	V	Y	C	F	R	A	2	
11	S	I	C	W	A	D	H	L	S	1	
19	S	D	N	Y	T	L	D	H	D	1	
109	Q	G	R	V	F	L	K	G	G	1	
163	Y	F	P	R	L	G	R	Y	N	1	
203	D	W	C	N	A	G	W	L	S	1	
212	D	G	S	V	Q	Y	P	I	T	1	
220	T	K	P	R	E	P	C	G	G	1	
233	P	G	V	R	N	Y	G	F	W	1	
273	D	E	A	V	Q	A	C	L	N	1	
298	I	L	G	Y	D	R	C	D	A	1	
311	D	G	S	V	R	Y	P	I	S	1	
327	P	T	E	A	A	V	R	F	V	1	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
203	M	R	L	Q	K	Q	A	E	K	29	
120	K	R	M	N	T	N	P	S	R	25	
258	P	R	A	G	S	S	A	H	R	25	
196	Y	R	K	N	K	Q	L	M	R	24	
229	P	R	G	L	G	F	I	F	K	24	
248	T	R	I	G	H	P	G	G	R	24	
137	S	R	I	F	W	R	Q	E	K	23	
187	K	R	K	E	K	A	E	I	H	23	
265	H	R	P	P	A	L	S	A	R	23	
312	P	R	N	P	L	P	N	P	R	23	
21	I	R	D	H	S	G	Q	K	M	22	
333	A	R	H	C	Q	G	Q	K	H	21	
197	R	K	N	K	Q	L	M	R	L	20	
398	E	R	K	A	E	N	G	P	H	20	
57	V	Q	F	V	G	S	Y	K	L	19	
83	R	K	D	K	V	L	L	G	R	19	
234	F	I	F	K	T	I	A	P	L	19	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	score	SEQ. ID NO.
251	G	H	P	G	G	R	T	P	R	19	
327	G	G	L	K	K	P	A	R	H	19	
22	R	D	H	S	G	Q	K	M	K	18	
26	G	Q	K	M	K	Q	D	K	K	18	
155	G	H	A	S	E	A	Y	K	K	18	
207	K	Q	A	E	K	N	M	K	K	18	
313	R	N	P	L	P	N	P	R	H	18	
345	A	R	G	K	P	Q	R	K	P	18	
389	G	L	G	G	K	Q	K	D	K	18	
391	G	G	K	Q	K	D	K	E	R	18	
392	G	K	Q	K	D	K	E	R	K	18	
34	K	V	D	L	L	V	P	T	K	17	
90	G	R	K	A	V	V	V	S	C	17	
105	G	S	F	C	R	N	K	L	K	17	
109	R	N	K	L	K	Y	L	A	F	17	
113	K	Y	L	A	F	L	H	K	R	17	
121	R	M	N	T	N	P	S	R	R	17	
211	K	N	M	K	K	K	I	D	K	17	
323	P	S	G	G	G	G	L	K	K	17	
326	G	G	G	L	K	K	P	A	R	17	
378	A	L	W	K	A	I	E	S	L	17	
7	K	T	F	P	L	R	A	L	H	16	
11	L	R	A	L	H	I	V	V	E	16	
30	K	Q	D	K	K	V	D	L	L	16	
46	I	I	T	Q	G	A	K	D	F	16	
55	G	H	V	Q	F	V	G	S	Y	16	
81	K	Q	R	K	D	K	V	L	L	16	
84	K	D	K	V	L	L	G	R	K	16	
101	I	N	I	S	G	S	F	C	R	16	
110	N	K	L	K	Y	L	A	F	L	16	
189	K	E	K	A	E	I	H	Y	R	16	
194	I	H	Y	R	K	N	K	Q	L	16	
212	N	M	K	K	K	I	D	K	Y	16	
255	G	R	T	P	R	A	G	S	S	16	
308	S	P	Y	G	P	R	N	P	L	16	
373	S	G	Y	C	G	A	L	W	K	16	
399	R	K	A	E	N	G	P	H	L	16	
16	I	V	V	E	S	I	R	D	H	15	
51	A	K	D	F	G	H	V	Q	F	15	
75	T	V	Y	Q	D	E	K	Q	R	15	
99	E	G	I	N	I	S	G	S	F	15	
108	C	R	N	K	L	K	Y	L	A	15	
128	R	R	P	Y	H	F	Q	V	P	15	
131	Y	H	F	Q	V	P	S	R	I	15	
168	G	A	P	H	E	V	G	W	K	15	
176	K	Y	Q	A	V	T	A	T	L	15	
188	R	K	E	K	A	E	I	H	Y	15	
190	E	K	A	E	I	H	Y	R	K	15	
192	A	E	I	H	Y	R	K	N	K	15	
222	E	S	P	G	G	G	S	P	R	15	
226	G	G	S	P	R	G	L	G	F	15	
238	T	I	A	P	L	A	A	T	R	15	
336	C	Q	G	Q	K	H	N	V	L	15	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
338	G Q K H N V L A R	15	
343	V L A R G K P Q R	15	
344	L A R G K P Q R K	15	
346	R G K P Q R K P K	15	
350	Q R K P K S E N N	15	
365	G R P A D L A G S	15	
14	L H I V V E S I R	14	
44	T G I I T Q G A K	14	
76	V Y Q D E K Q R K	14	
112	L K Y L A F L H K	14	
169	A P H E V G W K Y	14	
181	T A T L E E K R K	14	
208	Q A E K N M K K K	14	
272	A R A P V P A A S	14	
285	L P L R T P W T R	14	
322	S P S G G G G L K	14	
340	K H N V L A R G K	14	
385	S L E E G L G G K	14	
387	E E G L G G K Q K	14	
400	K A E N G P H L L	14	
4	H T T K T F P L R	13	
25	S G Q K M K Q D K	13	
29	M K Q D K K V D L	13	
73	H W T V Y Q D E K	13	
80	E K Q R K D K V L	13	
82	Q R K D K V L L G	13	
103	I S G S F C R N K	13	
104	S G S F C R N K L	13	
130	P Y H F Q V P S R	13	
134	Q V P S R I F W R	13	
141	W R Q E K A D G G	13	
158	S E A Y K K V C L	13	
163	K V C L S G A P H	13	
179	A V T A T L E E K	13	
180	V T A T L E E K R	13	
183	T L E E K R K E K	13	
199	N K Q L M R L Q K	13	
206	Q K Q A E K N M K	13	
224	P G G G S P R G L	13	
228	S P R G L G F I F	13	
230	R G L G F I F K T	13	
245	T R A T R I G H P	13	
277	P A A S P A A W L	13	
292	T R P S S C P T S	13	
302	S T Y D S L S P Y	13	
305	D S L S P Y G P R	13	
332	P A R H C Q G Q K	13	
362	V E N G R P A D L	13	
371	A G S G Y C G A L	13	
6	T K T F P L R A L	12	
20	S I R D H S G Q K	12	
56	H V Q F V G S Y K	12	
65	L A Y S N D G E H	12	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
69	N D G E H W T V Y	12	
78	Q D E K Q R K D K	12	
106	S F C R N K L K Y	12	
107	F C R N K L K Y L	12	
111	K L K Y L A F L H	12	
127	S R R P Y H F Q V	12	
132	H F Q V P S R I F	12	
154	Q G H A S E A Y K	12	
186	E K R K E K A E I	12	
205	L Q K Q A E K N M	12	
227	G S P R G L G F I	12	
241	P L A A T R A T R	12	
257	T P R A G S S A H	12	
279	A S P A A W L P L	12	
280	S P A A W L P L R	12	
296	S C P T S S S T Y	12	
319	P R H S P S G G G	12	
321	H S P S G G G G L	12	
358	N S W Y V E N G R	12	
382	A I E S L E E G L	12	
1	M L E H T T K T F	11	
3	E H T T K T F P L	11	
42	K V T G I I T Q G	11	
61	G S Y K L A Y S N	11	
114	Y L A F L H K R M	11	
125	N P S R R P Y H F	11	
138	R I F W R Q E K A	11	
148	G G S C C P Q G H	11	
195	H Y R K N K Q L M	11	
231	G L G F I F K T I	11	
242	L A A T R A T R I	11	
262	S S A H R P P A L	11	
287	L R T P W T R P S	11	
299	T S S S T Y D S L	11	
353	P K S E N N S W Y	11	
12	R A L H I V V E S	10	
13	A L H I V V E S I	10	
38	L V P T K V T G I	10	
48	T Q G A K D F G H	10	
59	F V G S Y K L A Y	10	
95	V V S C E G I N I	10	
123	N T N P S R R P Y	10	
209	A E K N M K K K I	10	
244	A T R A T R I G H	10	
334	R H C Q G Q K H N	10	
351	R K P K S E N N S	10	
367	P A D L A G S G Y	10	
8	T F P L R A L H I	9	
39	V P T K V T G I I	9	
93	A V V V S C E G I	9	
124	T N P S R R P Y H	9	
129	R P Y H F Q V P S	9	
153	P Q G H A S E A Y	9	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
204	R L Q K Q A E K N	9	
266	R P P A L S A R A	9	
347	G K P Q R K P K S	9	
374	G Y C G A L W K A	9	
377	G A L W K A I E S	9	
388	E G L G G K Q K D	9	
35	V D L L V P T K V	8	
41	T K V T G I I T Q	8	
45	G I I T Q G A K D	8	
52	K D F G H V Q F V	8	
182	A T L E E K R K E	8	
215	K K I D K Y T E S	8	
223	S P G G G S P R G	8	
259	R A G S S A H R P	8	
273	R A P V P A A S P	8	
311	G P R N P L P N P	8	
381	K A I E S L E E G	8	
86	K V L L G R K A V	7	
87	V L L G R K A V V	7	
91	R K A V V V S C E	7	
96	V S C E G I N I S	7	
116	A F L H K R M N T	7	
142	R Q E K A D G G S	7	
145	K A D G G S C C P	7	
175	W K Y Q A V T A T	7	
200	K Q L M R L Q K Q	7	
233	G F I F K T I A P	7	
237	K T I A P L A A T	7	
239	I A P L A A T R A	7	
249	R I G H P G G R T	7	
283	A W L P L R T P W	7	
293	R P S S C P T S S	7	
324	S G G G G L K K P	7	
325	G G G G L K K P A	7	
328	G L K K P A R H C	7	
366	R P A D L A G S G	7	
375	Y C G A L W K A I	7	
15	H I V V E S I R D	6	
23	D H S G Q K M K Q	6	
28	K M K Q D K K V D	6	
33	K K V D L L V P T	6	
71	G E H W T V Y Q D	6	
77	Y Q D E K Q R K D	6	
92	K A V V V S C E G	6	
97	S C E G I N I S G	6	
149	G S C C P Q G H A	6	
151	C C P Q G H A S E	6	
159	E A Y K K V C L S	6	
160	A Y K K V C L S G	6	
164	V C L S G A P H E	6	
171	H E V G W K Y Q A	6	
173	V G W K Y Q A V T	6	
174	G W K Y Q A V T A	6	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
232	L G F I F K T I A	6	
256	R T P R A G S S A	6	
264	A H R P P A L S A	6	
288	R T P W T R P S S	6	
320	R H S P S G G G G	6	
349	P Q R K P K S E N	6	
352	K P K S E N N S W	6	
359	S W Y V E N G R P	6	
368	A D L A G S G Y C	6	
395	K D K E R K A E N	6	
27	Q K M K Q D K K V	5	
31	Q D K K V D L L V	5	
37	L L V P T K V T G	5	
68	S N D G E H W T V	5	
79	D E K Q R K D K V	5	
85	D K V L L G R K A	5	
89	L G R K A V V V S	5	
100	G I N I S G S F C	5	
102	N I S G S F C R N	5	
115	L A F L H K R M N	5	
118	L H K R M N T N P	5	
140	F W R Q E K A D G	5	
152	C P Q G H A S E A	5	
162	K K V C L S G A P	5	
184	L E E K R K E K A	5	
198	K N K Q L M R L Q	5	
214	K K K I D K Y T E	5	
216	K I D K Y T E S P	5	
218	D K Y T E S P G G	5	
246	R A T R I G H P G	5	
250	I G H P G G R T P	5	
252	H P G G R T P R A	5	
254	G G R T P R A G S	5	
274	A P V P A A S P A	5	
282	A A W L P L R T P	5	
286	P L R T P W T R P	5	
335	H C Q G Q K H N V	5	
339	Q K H N V L A R G	5	
384	E S L E E G L G G	5	
386	L E E G L G G K Q	5	
390	L G G K Q K D K E	5	
393	K Q K D K E R K A	5	
397	K E R K A E N G P	5	
24	H S G Q K M K Q D	4	
36	D L L V P T K V T	4	
47	I T Q G A K D F G	4	
50	G A K D F G H V Q	4	
53	D F G H V Q F V G	4	
58	Q F V G S Y K L A	4	
62	S Y K L A Y S N D	4	
63	Y K L A Y S N D G	4	
64	K L A Y S N D G E	4	
74	W T V Y Q D E K Q	4	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
88	L L G R K A V V V	4	
98	C E G I N I S G S	4	
117	F L H K R M N T N	4	
122	M N T N P S R R P	4	
133	F Q V P S R I F W	4	
135	V P S R I F W R Q	4	
146	A D G G S C C P Q	4	
191	K A E I H Y R K N	4	
193	E I H Y R K N K Q	4	
201	Q L M R L Q K Q A	4	
213	M K K K I D K Y T	4	
219	K Y T E S P G G G	4	
221	T E S P G G G S P	4	
225	G G G S P R G L G	4	
235	I F K T I A P L A	4	
247	A T R I G H P G G	4	
261	G S S A H R P P A	4	
269	A L S A R A P V P	4	
278	A A S P A A W L P	4	
281	P A A W L P L R T	4	
295	S S C P T S S S T	4	
297	C P T S S S T Y D	4	
306	S L S P Y G P R N	4	
307	L S P Y G P R N P	4	
337	Q G Q K H N V L A	4	
341	H N V L A R G K P	4	
348	K P Q R K P K S E	4	
354	K S E N N S W Y V	4	
369	D L A G S G Y C G	4	
372	G S G Y C G A L W	4	
380	W K A I E S L E E	4	
396	D K E R K A E N G	4	
2	L E H T T K T F P	3	
5	T T K T F P L R A	3	
9	F P L R A L H I V	3	
10	P L R A L H I V V	3	
19	E S I R D H S G Q	3	
32	D K K V D L L V P	3	
60	V G S Y K L A Y S	3	
144	E K A D G G S C C	3	
156	H A S E A Y K K V	3	
157	A S E A Y K K V C	3	
165	C L S G A P H E V	3	
177	Y Q A V T A T L E	3	
178	Q A V T A T L E E	3	
240	A P L A A T R A T	3	
267	P P A L S A R A P	3	
268	P A L S A R A P V	3	
271	S A R A P V P A A	3	
290	P W T R P S S C P	3	
291	W T R P S S C P T	3	
294	P S S C P T S S S	3	
301	S S T Y D S L S P	3	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
303	T Y D S L S P Y G	3	
304	Y D S L S P Y G P	3	
309	P Y G P R N P L P	3	
314	N P L P N P R H S	3	
317	P N P R H S P S G	3	
330	K K P A R H C Q G	3	
355	S E N N S W Y V E	3	
357	N N S W Y V E N G	3	
361	Y V E N G R P A D	3	
364	N G R P A D L A G	3	
376	C G A L W K A I E	3	
383	I E S L E E G L G	3	
394	Q K D K E R K A E	3	
18	V E S I R D H S G	2	
49	Q G A K D F G H V	2	
67	Y S N D G E H W T	2	
147	D G G S C C P Q G	2	
161	Y K K V C L S G A	2	
166	L S G A P H E V G	2	
167	S G A P H E V G W	2	
170	P H E V G W K Y Q	2	
202	L M R L Q K Q A E	2	
210	E K N M K K K I D	2	
217	I D K Y T E S P G	2	
263	S A H R P P A L S	2	
275	P V P A A S P A A	2	
276	V P A A S P A A W	2	
284	W L P L R T P W T	2	
289	T P W T R P S S C	2	
298	P T S S S T Y D S	2	
300	S S S T Y D S L S	2	
315	P L P N P R H S P	2	
316	L P N P R H S P S	2	
318	N P R H S P S G G	2	
331	K P A R H C Q G Q	2	
342	N V L A R G K P Q	2	
356	E N N S W Y V E N	2	
360	W Y V E N G R P A	2	
363	E N G R P A D L A	2	
370	L A G S G Y C G A	2	
379	L W K A I E S L E	2	
17	V V E S I R D H S	1	
40	P T K V T G I I T	1	
43	V T G I I T Q G A	1	
54	F G H V Q F V G S	1	
66	A Y S N D G E H W	1	
70	D G E H W T V Y Q	1	
72	E H W T V Y Q D E	1	
94	V V V S C E G I N	1	
119	H K R M N T N P S	1	
126	P S R R P Y H F Q	1	
136	P S R I F W R Q E	1	
139	I F W R Q E K A D	1	

TABLE XXXI 151P3D4 v.2: HLA Peptide Scoring Results B*2705 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
143	Q E K A D G G S C	1	
150	S C C P Q G H A S	1	
172	E V G W K Y Q A V	1	
185	E E K R K E K A E	1	
220	Y T E S P G G G S	1	
236	F K T I A P L A A	1	
243	A A T R A T R I G	1	
260	A G S S A H R P P	1	
270	L S A R A P V P A	1	
310	Y G P R N P L P N	1	
329	L K K P A R H C Q	1	

TABLE XXXII 151P3D4 v.1: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
106	G G Y Q G R V F L	16	
135	G R Y K C E V I E	16	
16	D H L S D N Y T L	15	
159	V V F P Y F P R L	15	
168	G R Y N L N F H E	15	
259	G R F Y Y L I H P	15	
323	R R C S P T E A A	15	
110	G R V F L K G G S	14	
117	G S D S D A S L V	14	
166	R L G R Y N L N F	14	
314	V R Y P I S R P R	14	
322	R R R C S P T E A	14	
2	K S L L L L V L I	13	
10	I S I C W A D H L	13	
62	K F Y R D P T A F	13	
116	G G S D S D A S L	13	
144	G L E D D T V V V	13	
148	D T V V V A L D L	13	
186	A V I A S F D Q L	13	
227	G G Q N T V P G V	13	
278	A C L N D G A Q I	13	
290	G Q I F A A W K I	13	
324	R C S P T E A A V	13	
332	V R F V G F P D K	13	
336	G F P D K K H K L	13	
32	I Q A E N G P H L	12	
55	G N V T L P C K F	12	
64	Y R D P T A F G S	12	
71	G S G I H K I R I	12	
76	K I R I K W T K L	12	
77	I R I K W T K L T	12	
90	K E V D V F V S M	12	
123	S L V I T D L T L	12	
146	E D D T V V V A L	12	
164	F P R L G R Y N L	12	
165	P R L G R Y N L N	12	
222	P R E P C G G Q N	12	

TABLE XXXII 151P3D4 v.1: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
245	K S R Y D V F C F	12	
246	S R Y D V F C F T	12	
262	Y Y L I H P T K L	12	
284	A Q I A K V G Q I	12	
291	Q I F A A W K I L	12	
301	Y D R C D A G W L	12	
326	S P T E A A V R F	12	
342	H K L Y G V Y C F	12	
1	M K S L L L L V L	11	
51	S H R G G N V T L	11	
52	H R G G N V T L P	11	
86	S D Y L K E V D V	11	
87	D Y L K E V D V F	11	
143	E G L E D D T V V	11	
180	A C L D Q D A V I	11	
202	L D W C N A G W L	11	
243	K D K S R Y D V F	11	
249	D V F C F T S N F	11	
256	N F N G R F Y Y L	11	
310	A D G S V R Y P I	11	
321	P R R R C S P T E	11	
4	L L L L V L I S I	10	
22	Y T L D H D R A I	10	
27	D R A I H I Q A E	10	
33	Q A E N G P H L L	10	
34	A E N G P H L L V	10	
69	A F G S G I H K I	10	
81	W T K L T S D Y L	10	
121	D A S L V I T D L	10	
137	Y K C E V I E G L	10	
152	V A L D L Q G V V	10	
153	A L D L Q G V V F	10	
174	F H E A Q Q A C L	10	
194	L Y D A W R G G L	10	
198	W R G G L D W C N	10	
211	S D G S V Q Y P I	10	
235	V R N Y G F W D K	10	
268	T K L T Y D E A V	10	
272	Y D E A V Q A C L	10	
302	D R C D A G W L A	10	
319	S R P R R R C S P	10	
24	L D H D R A I H I	9	
42	V E A E Q A K V F	9	
49	V F S H R G G N V	9	
66	D P T A F G S G I	9	
88	Y L K E V D V F V	9	
104	T Y G G Y Q G R V	9	
118	S D S D A S L V I	9	
142	I E G L E D D T V	9	
151	V V A L D L Q G V	9	
156	L Q G V V F P Y F	9	
179	Q A C L D Q D A V	9	
207	A G W L S D G S V	9	

TABLE XXXII 151P3D4 v.1: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
232	V P G V R N Y G F	9	
242	D K D K S R Y D V	9	
253	F T S N F N G R F	9	
257	F N G R F Y Y L I	9	
306	A G W L A D G S V	9	
327	P T E A A V R F V	9	
329	E A A V R F V G F	9	
339	D K K H K L Y G V	9	
41	L V E A E Q A K V	8	
84	L T S D Y L K E V	8	
105	Y G G Y Q G R V F	8	
133	D Y G R Y K C E V	8	
134	Y G R Y K C E V I	8	
183	D Q D A V I A S F	8	
224	E P C G G Q N T V	8	
281	N D G A Q I A K V	8	
285	Q I A K V G Q I F	8	
208	G W L S D G S V Q	7	
28	R A I H I Q A E N	6	
83	K L T S D Y L K E	6	
111	R V F L K G G S D	6	
199	R G G L D W C N A	6	
236	R N Y G F W D K D	6	
260	R F Y Y L I H P T	6	
307	G W L A D G S V R	6	
315	R Y P I S R P R R	6	
48	K V F S H R G G N	5	
53	R G G N V T L P C	5	
78	R I K W T K L T S	5	
102	K K T Y G G Y Q G	5	
136	R Y K C E V I E G	5	
192	D Q L Y D A W R G	5	
200	G G L D W C N A G	5	
223	R E P C G G Q N T	5	
270	L T Y D E A V Q A	5	
303	R C D A G W L A D	5	
333	R F V G F P D K K	5	
346	G V Y C F R A Y N	5	
3	S L L L L V L I S	4	
37	G P H L L V E A E	4	
39	H L L V E A E Q A	4	
54	G G N V T L P C K	4	
65	R D P T A F G S G	4	
73	G I H K I R I K W	4	
99	G Y H K K T Y G G	4	
103	K T Y G G Y Q G R	4	
107	G Y Q G R V F L K	4	
115	K G G S D S D A S	4	
122	A S L V I T D L T	4	
129	L T L E D Y G R Y	4	
154	L D L Q G V V F P	4	
158	G V V F P Y F P R	4	
162	P Y F P R L G R Y	4	

TABLE XXXII 151P3D4 v.1: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
169	R Y N L N F H E A	4	
172	L N F H E A Q Q A	4	
189	A S F D Q L Y D A	4	
213	G S V Q Y P I T K	4	
215	V Q Y P I T K P R	4	
230	N T V P G V R N Y	4	
247	R Y D V F C F T S	4	
261	F Y Y L I H P T K	4	
269	K L T Y D E A V Q	4	
283	G A Q I A K V G Q	4	
297	K I L G Y D R C D	4	
312	G S V R Y P I S R	4	
320	R P R R R C S P T	4	
335	V G F P D K K H K	4	
343	K L Y G V Y C F R	4	
8	V L I S I C W A D	3	
12	I C W A D H L S D	3	
21	N Y T L D H D R A	3	
29	A I H I Q A E N G	3	
57	V T L P C K F Y R	3	
61	C K F Y R D P T A	3	
80	K W T K L T S D Y	3	
82	T K L T S D Y L K	3	
94	V F V S M G Y H K	3	
138	K C E V I E G L E	3	
150	V V V A L D L Q G	3	
161	F P Y F P R L G R	3	
181	C L D Q D A V I A	3	
188	I A S F D Q L Y D	3	
201	G L D W C N A G W	3	
219	I T K P R E P C G	3	
228	G Q N T V P G V R	3	
229	Q N T V P G V R N	3	
234	G V R N Y G F W D	3	
238	Y G F W D K D K S	3	
239	G F W D K D K S R	3	
251	F C F T S N F N G	3	
274	E A V Q A C L N D	3	
288	K V G Q I F A A W	3	
300	G Y D R C D A G W	3	
316	Y P I S R P R R R	3	
330	A A V R F V G F P	3	
341	K H K L Y G V Y C	3	
5	L L L V L I S I C	2	
6	L L V L I S I C W	2	
7	L V L I S I C W A	2	
20	D N Y T L D H D R	2	
26	H D R A I H I Q A	2	
30	I H I Q A E N G P	2	
35	E N G P H L L V E	2	
38	P H L L V E A E Q	2	
44	A E Q A K V F S H	2	
47	A K V F S H R G G	2	

TABLE XXXII 151P3D4 v.1: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
58	T L P C K F Y R D	2	
68	T A F G S G I H K	2	
75	H K I R I K W T K	2	
89	L K E V D V F V S	2	
93	D V F V S M G Y H	2	
98	M G Y H K K T Y G	2	
112	V F L K G G S D S	2	
120	S D A S L V I T D	2	
124	L V I T D L T L E	2	
125	V I T D L T L E D	2	
127	T D L T L E D Y G	2	
128	D L T L E D Y G R	2	
132	E D Y G R Y K C E	2	
139	C E V I E G L E D	2	
145	L E D D T V V V A	2	
147	D D T V V V A L D	2	
157	Q G V V F P Y F P	2	
170	Y N L N F H E A Q	2	
177	A Q Q A C L D Q D	2	
184	Q D A V I A S F D	2	
193	Q L Y D A W R G G	2	
209	W L S D G S V Q Y	2	
216	Q Y P I T K P R E	2	
221	K P R E P C G G Q	2	
240	F W D K D K S R Y	2	
252	C F T S N F N G R	2	
255	S N F N G R F Y Y	2	
264	L I H P T K L T Y	2	
266	H P T K L T Y D E	2	
282	D G A Q I A K V G	2	
287	A K V G Q I F A A	2	
294	A A W K I L G Y D	2	
295	A W K I L G Y D R	2	
296	W K I L G Y D R C	2	
298	I L G Y D R C D A	2	
299	L G Y D R C D A G	2	
308	W L A D G S V R Y	2	
318	I S R P R R R C S	2	
340	K K H K L Y G V Y	2	
14	W A D H L S D N Y	1	
15	A D H L S D N Y T	1	
18	L S D N Y T L D H	1	
23	T L D H D R A I H	1	
36	N G P H L L V E A	1	
40	L L V E A E Q A K	1	
43	E A E Q A K V F S	1	
46	Q A K V F S H R G	1	
56	N V T L P C K F Y	1	
70	F G S G I H K I R	1	
72	S G I H K I R I K	1	
74	I H K I R I K W T	1	
79	I K W T K L T S D	1	
91	E V D V F V S M G	1	

TABLE XXXII 151P3D4 v.1: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
92	V D V F V S M G Y	1	
108	Y Q G R V F L K G	1	
119	D S D A S L V I T	1	
126	I T D L T L E D Y	1	
131	L E D Y G R Y K C	1	
140	E V I E G L E D D	1	
149	T V V V A L D L Q	1	
155	D L Q G V V F P Y	1	
171	N L N F H E A Q Q	1	
175	H E A Q Q A C L D	1	
176	E A Q Q A C L D Q	1	
182	L D Q D A V I A S	1	
185	D A V I A S F D Q	1	
187	V I A S F D Q L Y	1	
196	D A W R G G L D W	1	
197	A W R G G L D W C	1	
204	W C N A G W L S D	1	
210	L S D G S V Q Y P	1	
212	D G S V Q Y P I T	1	
217	Y P I T K P R E P	1	
218	P I T K P R E P C	1	
226	C G G Q N T V P G	1	
233	P G V R N Y G F W	1	
244	D K S R Y D V F C	1	
248	Y D V F C F T S N	1	
258	N G R F Y Y L I H	1	
263	Y L I H P T K L T	1	
265	I H P T K L T Y D	1	
271	T Y D E A V Q A C	1	
273	D E A V Q A C L N	1	
275	A V Q A C L N D G	1	
279	C L N D G A Q I A	1	
286	I A K V G Q I F A	1	
289	V G Q I F A A W K	1	
292	I F A A W K I L G	1	
293	F A A W K I L G Y	1	
305	D A G W L A D G S	1	
309	L A D G S V R Y P	1	
311	D G S V R Y P I S	1	
313	S V R Y P I S R P	1	
317	P I S R P R R R C	1	
325	C S P T E A A V R	1	
331	A V R F V G F P D	1	
338	P D K K H K L Y G	1	
344	L Y G V Y C F R A	1	
345	Y G V Y C F R A Y	1	

TABLE XXXII 151P3D4 v.2: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
127	S R R P Y H F Q V	20	
21	I R D H S G Q K M	19	

TABLE XXXII 151P3D4 v.2: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
255	G R T P R A G S S	16	
90	G R K A V V V S C	15	
197	R K N K Q L M R L	15	
399	R K A E N G P H L	15	
81	K Q R K D K V L L	14	
128	R R P Y H F Q V P	14	
194	I H Y R K N K Q L	14	
365	G R P A D L A G S	14	
30	K Q D K K V D L L	13	
52	K D F G H V Q F V	13	
57	V Q F V G S Y K L	13	
109	R N K L K Y L A F	13	
120	K R M N T N P S R	13	
187	K R K E K A E I H	13	
226	G G S P R G L G F	13	
82	Q R K D K V L L G	12	
86	K V L L G R K A V	12	
110	N K L K Y L A F L	12	
176	K Y Q A V T A T L	12	
203	M R L Q K Q A E K	12	
231	G L G F I F K T I	12	
234	F I F K T I A P L	12	
272	A R A P V P A A S	12	
277	P A A S P A A W L	12	
279	A S P A A W L P L	12	
287	L R T P W T R P S	12	
292	T R P S S C P T S	12	
308	S P Y G P R N P L	12	
350	Q R K P K S E N N	12	
382	A I E S L E E G L	12	
400	K A E N G P H L L	12	
3	E H T T K T F P L	11	
6	T K T F P L R A L	11	
11	L R A L H I V V E	11	
29	M K Q D K K V D L	11	
46	I I T Q G A K D F	11	
51	A K D F G H V Q F	11	
108	C R N K L K Y L A	11	
131	Y H F Q V P S R I	11	
137	S R I F W R Q E K	11	
141	W R Q E K A D G G	11	
158	S E A Y K K V C L	11	
196	Y R K N K Q L M R	11	
227	G S P R G L G F I	11	
248	T R I G H P G G R	11	
262	S S A H R P P A L	11	
265	H R P P A L S A R	11	
268	P A L S A R A P V	11	
299	T S S S T Y D S L	11	
312	P R N P L P N P R	11	
319	P R H S P S G G G	11	
321	H S P S G G G G L	11	
333	A R H C Q G Q K H	11	

TABLE XXXII 151P3D4 v.2: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
345	A R G K P Q R K P	11	
371	A G S G Y C G A L	11	
378	A L W K A I E S L	11	
8	T F P L R A L H I	10	
9	F P L R A L H I V	10	
13	A L H I V V E S I	10	
35	V D L L V P T K V	10	
80	E K Q R K D K V L	10	
87	V L L G R K A V V	10	
88	L L G R K A V V V	10	
93	A V V V S C E G I	10	
99	E G I N I S G S F	10	
104	S G S F C R N K L	10	
107	F C R N K L K Y L	10	
224	P G G G S P R G L	10	
229	P R G L G F I F K	10	
242	L A A T R A T R I	10	
245	T R A T R I G H P	10	
258	P R A G S S A H R	10	
336	C Q G Q K H N V L	10	
354	K S E N N S W Y V	10	
362	V E N G R P A D L	10	
398	E R K A E N G P H	10	
12	R A L H I V V E S	9	
31	Q D K K V D L L V	9	
38	L V P T K V T G I	9	
39	V P T K V T G I I	9	
49	Q G A K D F G H V	9	
95	V V S C E G I N I	9	
114	Y L A F L H K R M	9	
125	N P S R R P Y H F	9	
205	L Q K Q A E K N M	9	
209	A E K N M K K K I	9	
335	H C Q G Q K H N V	9	
1	M L E H T T K T F	8	
10	P L R A L H I V V	8	
27	Q K M K Q D K K V	8	
68	S N D G E H W T V	8	
79	D E K Q R K D K V	8	
132	H F Q V P S R I F	8	
156	H A S E A Y K K V	8	
165	C L S G A P H E V	8	
172	E V G W K Y Q A V	8	
186	E K R K E K A E I	8	
195	H Y R K N K Q L M	8	
228	S P R G L G F I F	8	
375	Y C G A L W K A I	8	
61	G S Y K L A Y S N	7	
129	R P Y H F Q V P S	7	
259	R A G S S A H R P	7	
71	G E H W T V Y Q D	6	
138	R I F W R Q E K A	6	
155	G H A S E A Y K K	6	

TABLE XXXII 151P3D4 v.2: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
230	R G L G F I F K T	6	
246	R A T R I G H P G	6	
313	R N P L P N P R H	6	
327	G G L K K P A R H	6	
377	G A L W K A I E S	6	
7	K T F P L R A L H	5	
22	R D H S G Q K M K	5	
42	K V T G I I T Q G	5	
55	G H V Q F V G S Y	5	
83	R K D K V L L G R	5	
91	R K A V V V S C E	5	
105	G S F C R N K L K	5	
121	R M N T N P S R R	5	
164	V C L S G A P H E	5	
174	G W K Y Q A V T A	5	
204	R L Q K Q A E K N	5	
249	R I G H P G G R T	5	
266	R P P A L S A R A	5	
273	R A P V P A A S P	5	
288	R T P W T R P S S	5	
293	R P S S C P T S S	5	
311	G P R N P L P N P	5	
320	R H S P S G G G G	5	
338	G Q K H N V L A R	5	
346	R G K P Q R K P K	5	
351	R K P K S E N N S	5	
366	R P A D L A G S G	5	
392	G K Q K D K E R K	5	
33	K K V D L L V P T	4	
34	K V D L L V P T K	4	
45	G I I T Q G A K D	4	
75	T V Y Q D E K Q R	4	
113	K Y L A F L H K R	4	
116	A F L H K R M N T	4	
142	R Q E K A D G G S	4	
168	G A P H E V G W K	4	
188	R K E K A E I H Y	4	
200	K Q L M R L Q K Q	4	
214	K K K I D K Y T E	4	
225	G G G S P R G L G	4	
233	G F I F K T I A P	4	
235	I F K T I A P L A	4	
256	R T P R A G S S A	4	
261	G S S A H R P P A	4	
264	A H R P P A L S A	4	
274	A P V P A A S P A	4	
283	A W L P L R T P W	4	
326	G G G L K K P A R	4	
328	G L K K P A R H C	4	
334	R H C Q G Q K H N	4	
347	G K P Q R K P K S	4	
373	S G Y C G A L W K	4	
26	G Q K M K Q D K K	3	

TABLE XXXII 151P3D4 v.2: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
28	K M K Q D K K V D	3	
37	L L V P T K V T G	3	
50	G A K D F G H V Q	3	
65	L A Y S N D G E H	3	
84	K D K V L L G R K	3	
92	K A V V V S C E G	3	
100	G I N I S G S F C	3	
101	I N I S G S F C R	3	
103	I S G S F C R N K	3	
111	K L K Y L A F L H	3	
112	L K Y L A F L H K	3	
147	D G G S C C P Q G	3	
148	G G S C C P Q G H	3	
149	G S C C P Q G H A	3	
159	E A Y K K V C L S	3	
162	K K V C L S G A P	3	
171	H E V G W K Y Q A	3	
175	W K Y Q A V T A T	3	
182	A T L E E K R K E	3	
190	E K A E I H Y R K	3	
192	A E I H Y R K N K	3	
215	K K I D K Y T E S	3	
218	D K Y T E S P G G	3	
219	K Y T E S P G G G	3	
237	K T I A P L A A T	3	
239	I A P L A A T R A	3	
240	A P L A A T R A T	3	
251	G H P G G R T P R	3	
254	G G R T P R A G S	3	
269	A L S A R A P V P	3	
278	A A S P A A W L P	3	
301	S S T Y D S L S P	3	
305	D S L S P Y G P R	3	
306	S L S P Y G P R N	3	
314	N P L P N P R H S	3	
325	G G G G L K K P A	3	
330	K K P A R H C Q G	3	
340	K H N V L A R G K	3	
352	K P K S E N N S W	3	
359	S W Y V E N G R P	3	
368	A D L A G S G Y C	3	
372	G S G Y C G A L W	3	
374	G Y C G A L W K A	3	
381	K A I E S L E E G	3	
384	E S L E E G L G G	3	
389	G L G G K Q K D K	3	
391	G G K Q K D K E R	3	
4	H T T K T F P L R	2	
5	T T K T F P L R A	2	
15	H I V V E S I R D	2	
16	I V V E S I R D H	2	
17	V V E S I R D H S	2	
19	E S I R D H S G Q	2	

TABLE XXXII 151P3D4 v.2: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
32	D K K V D L L V P	2	
36	D L L V P T K V T	2	
59	F V G S Y K L A Y	2	
63	Y K L A Y S N D G	2	
64	K L A Y S N D G E	2	
66	A Y S N D G E H W	2	
89	L G R K A V V V S	2	
94	V V V S C E G I N	2	
115	L A F L H K R M N	2	
122	M N T N P S R R P	2	
124	T N P S R R P Y H	2	
130	P Y H F Q V P S R	2	
133	F Q V P S R I F W	2	
135	V P S R I F W R Q	2	
145	K A D G G S C C P	2	
160	A Y K K V C L S G	2	
163	K V C L S G A P H	2	
167	S G A P H E V G W	2	
178	Q A V T A T L E E	2	
179	A V T A T L E E K	2	
181	T A T L E E K R K	2	
189	K E K A E I H Y R	2	
191	K A E I H Y R K N	2	
198	K N K Q L M R L Q	2	
199	N K Q L M R L Q K	2	
207	K Q A E K N M K K	2	
211	K N M K K K I D K	2	
216	K I D K Y T E S P	2	
223	S P G G G S P R G	2	
232	L G F I F K T I A	2	
236	F K T I A P L A A	2	
238	T I A P L A A T R	2	
243	A A T R A T R I G	2	
247	A T R I G H P G G	2	
250	I G H P G G R T P	2	
252	H P G G R T P R A	2	
260	A G S S A H R P P	2	
271	S A R A P V P A A	2	
281	P A A W L P L R T	2	
285	L P L R T P W T R	2	
297	C P T S S S T Y D	2	
298	P T S S S T Y D S	2	
302	S T Y D S L S P Y	2	
303	T Y D S L S P Y G	2	
309	P Y G P R N P L P	2	
331	K P A R H C Q G Q	2	
342	N V L A R G K P Q	2	
343	V L A R G K P Q R	2	
348	K P Q R K P K S E	2	
356	E N N S W Y V E N	2	
357	N N S W Y V E N G	2	
364	N G R P A D L A G	2	
388	E G L G G K Q K D	2	

TABLE XXXII 151P3D4 v.2: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
393	K Q K D K E R K A	2	
395	K D K E R K A E N	2	
396	D K E R K A E N G	2	
397	K E R K A E N G P	2	
14	L H I V V E S I R	1	
20	S I R D H S G Q K	1	
24	H S G Q K M K Q D	1	
41	T K V T G I I T Q	1	
43	V T G I I T Q G A	1	
44	T G I I T Q G A K	1	
47	I T Q G A K D F G	1	
54	F G H V Q F V G S	1	
58	Q F V G S Y K L A	1	
62	S Y K L A Y S N D	1	
70	D G E H W T V Y Q	1	
73	H W T V Y Q D E K	1	
74	W T V Y Q D E K Q	1	
76	V Y Q D E K Q R K	1	
85	D K V L L G R K A	1	
97	S C E G I N I S G	1	
102	N I S G S F C R N	1	
106	S F C R N K L K Y	1	
118	L H K R M N T N P	1	
123	N T N P S R R P Y	1	
134	Q V P S R I F W R	1	
136	P S R I F W R Q E	1	
139	I F W R Q E K A D	1	
143	Q E K A D G G S C	1	
146	A D G G S C C P Q	1	
150	S C C P Q G H A S	1	
152	C P Q G H A S E A	1	
157	A S E A Y K K V C	1	
169	A P H E V G W K Y	1	
177	Y Q A V T A T L E	1	
201	Q L M R L Q K Q A	1	
213	M K K K I D K Y T	1	
217	I D K Y T E S P G	1	
220	Y T E S P G G G S	1	
221	T E S P G G G S P	1	
244	A T R A T R I G H	1	
267	P P A L S A R A P	1	
270	L S A R A P V P A	1	
275	P V P A A S P A A	1	
280	S P A A W L P L R	1	
282	A A W L P L R T P	1	
284	W L P L R T P W T	1	
286	P L R T P W T R P	1	
290	P W T R P S S C P	1	
291	W T R P S S C P T	1	
295	S S C P T S S S T	1	
304	Y D S L S P Y G P	1	
307	L S P Y G P R N P	1	
310	Y G P R N P L P N	1	

TABLE XXXII 151P3D4 v.2: HLA Peptide Scoring Results B*2709 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
316	L P N P R H S P S	1	
317	P N P R H S P S G	1	
323	P S G G G G L K K	1	
329	L K K P A R H C Q	1	
332	P A R H C Q G Q K	1	
337	Q G Q K H N V L A	1	
339	Q K H N V L A R G	1	
341	H N V L A R G K P	1	
344	L A R G K P Q R K	1	
355	S E N N S W Y V E	1	
360	W Y V E N G R P A	1	
361	Y V E N G R P A D	1	
363	E N G R P A D L A	1	
369	D L A G S G Y C G	1	
370	L A G S G Y C G A	1	
379	L W K A I E S L E	1	
380	W K A I E S L E E	1	
383	I E S L E E G L G	1	
387	E E G L G G K Q K	1	

TABLE XXXIII 151P3D4 v.1: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
42	V E A E Q A K V F	24	
146	E D D T V V V A L	18	
186	A V I A S F D Q L	18	
153	A L D L Q G V V F	17	
162	P Y F P R L G R Y	17	
34	A E N G P H L L V	16	
69	A F G S G I H K I	16	
159	V V F P Y F P R L	16	
230	N T V P G V R N Y	16	
284	A Q I A K V G Q I	16	
1	M K S L L L L V L	15	
62	K F Y R D P T A F	15	
121	D A S L V I T D L	15	
145	L E D D T V V V A	15	
255	S N F N G R F Y Y	15	
264	L I H P T K L T Y	15	
288	K V G Q I F A A W	15	
329	E A A V R F V G F	15	
2	K S L L L L V L I	14	
10	I S I C W A D H L	14	
33	Q A E N G P H L L	14	
44	A E Q A K V F S H	14	
51	S H R G G N V T L	14	
56	N V T L P C K F Y	14	
73	G I H K I R I K W	14	
90	K E V D V F V S M	14	
97	S M G Y H K K T Y	14	
180	A C L D Q D A V I	14	
183	D Q D A V I A S F	14	

TABLE XXXIII 151P3D4 v.1: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
190	S F D Q L Y D A W	14	
209	W L S D G S V Q Y	14	
256	N F N G R F Y Y L	14	
278	A C L N D G A Q I	14	
291	Q I F A A W K I L	14	
293	F A A W K I L G Y	14	
336	G F P D K K H K L	14	
337	F P D K K H K L Y	14	
345	Y G V Y C F R A Y	14	
6	L L V L I S I C W	13	
22	Y T L D H D R A I	13	
55	G N V T L P C K F	13	
87	D Y L K E V D V F	13	
118	S D S D A S L V I	13	
123	S L V I T D L T L	13	
126	I T D L T L E D Y	13	
131	L E D Y G R Y K C	13	
137	Y K C E V I E G L	13	
243	K D K S R Y D V F	13	
249	D V F C F T S N F	13	
262	Y Y L I H P T K L	13	
290	G Q I F A A W K I	13	
326	S P T E A A V R F	13	
4	L L L L V L I S I	12	
16	D H L S D N Y T L	12	
24	L D H D R A I H I	12	
76	K I R I K W T K L	12	
80	K W T K L T S D Y	12	
105	Y G G Y Q G R V F	12	
106	G G Y Q G R V F L	12	
116	G G S D S D A S L	12	
142	I E G L E D D T V	12	
148	D T V V V A L D L	12	
155	D L Q G V V F P Y	12	
164	F P R L G R Y N L	12	
166	R L G R Y N L N F	12	
175	H E A Q Q A C L D	12	
194	L Y D A W R G G L	12	
196	D A W R G G L D W	12	
202	L D W C N A G W L	12	
233	P G V R N Y G F W	12	
245	K S R Y D V F C F	12	
253	F T S N F N G R F	12	
254	T S N F N G R F Y	12	
273	D E A V Q A C L N	12	
300	G Y D R C D A G W	12	
308	W L A D G S V R Y	12	
310	A D G S V R Y P I	12	
328	T E A A V R F V G	12	
340	K K H K L Y G V Y	12	
342	H K L Y G V Y C F	12	
14	W A D H L S D N Y	11	
32	I Q A E N G P H L	11	

TABLE XXXIII 151P3D4 v.1: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
81	W T K L T S D Y L	11	
129	L T L E D Y G R Y	11	
139	C E V I E G L E D	11	
156	L Q G V V F P Y F	11	
187	V I A S F D Q L Y	11	
201	G L D W C N A G W	11	
223	R E P C G G Q N T	11	
232	V P G V R N Y G F	11	
240	F W D K D K S R Y	11	
301	Y D R C D A G W L	11	
92	V D V F V S M G Y	10	
100	Y H K K T Y G G Y	10	
174	F H E A Q Q A C L	10	
257	F N G R F Y Y L I	10	
272	Y D E A V Q A C L	10	
285	Q I A K V G Q I F	10	
71	G S G I H K I R I	9	
134	Y G R Y K C E V I	9	
211	S D G S V Q Y P I	9	
287	A K V G Q I F A A	9	
35	E N G P H L L V E	8	
66	D P T A F G S G I	8	
72	S G I H K I R I K	8	
77	I R I K W T K L T	7	
122	A S L V I T D L T	7	
189	A S F D Q L Y D A	7	
215	V Q Y P I T K P R	7	
263	Y L I H P T K L T	7	
335	V G F P D K K H K	7	
8	V L I S I C W A D	6	
25	D H D R A I H I Q	6	
74	I H K I R I K W T	6	
75	H K I R I K W T K	6	
124	L V I T D L T L E	6	
132	E D Y G R Y K C E	6	
140	E V I E G L E D D	6	
217	Y P I T K P R E P	6	
316	Y P I S R P R R R	6	
318	I S R P R R R C S	6	
324	R C S P T E A A V	6	
3	S L L L L V L I S	5	
15	A D H L S D N Y T	5	
27	D R A I H I Q A E	5	
64	Y R D P T A F G S	5	
70	F G S G I H K I R	5	
84	L T S D Y L K E V	5	
96	V S M G Y H K K T	5	
165	P R L G R Y N L N	5	
177	A Q Q A C L D Q D	5	
182	L D Q D A V I A S	5	
197	A W R G G L D W C	5	
200	G G L D W C N A G	5	
214	S V Q Y P I T K P	5	

TABLE XXXIII 151P3D4 v.1: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
224	E P C G G Q N T V	5	
275	A V Q A C L N D G	5	
280	L N D G A Q I A K	5	
281	N D G A Q I A K V	5	
282	D G A Q I A K V G	5	
294	A A W K I L G Y D	5	
314	V R Y P I S R P R	5	
319	S R P R R R C S P	5	
330	A A V R F V G F P	5	
5	L L L V L I S I C	4	
7	L V L I S I C W A	4	
17	H L S D N Y T L D	4	
18	L S D N Y T L D H	4	
28	R A I H I Q A E N	4	
29	A I H I Q A E N G	4	
30	I H I Q A E N G P	4	
36	N G P H L L V E A	4	
37	G P H L L V E A E	4	
47	A K V F S H R G G	4	
48	K V F S H R G G N	4	
52	H R G G N V T L P	4	
57	V T L P C K F Y R	4	
61	C K F Y R D P T A	4	
68	T A F G S G I H K	4	
91	E V D V F V S M G	4	
107	G Y Q G R V F L K	4	
108	Y Q G R V F L K G	4	
120	S D A S L V I T D	4	
143	E G L E D D T V V	4	
144	G L E D D T V V V	4	
160	V F P Y F P R L G	4	
169	R Y N L N F H E A	4	
170	Y N L N F H E A Q	4	
172	L N F H E A Q Q A	4	
207	A G W L S D G S V	4	
219	I T K P R E P C G	4	
222	P R E P C G G Q N	4	
231	T V P G V R N Y G	4	
259	G R F Y Y L I H P	4	
260	R F Y Y L I H P T	4	
268	T K L T Y D E A V	4	
270	L T Y D E A V Q A	4	
271	T Y D E A V Q A C	4	
277	Q A C L N D G A Q	4	
296	W K I L G Y D R C	4	
297	K I L G Y D R C D	4	
299	L G Y D R C D A G	4	
303	R C D A G W L A D	4	
306	A G W L A D G S V	4	
309	L A D G S V R Y P	4	
313	S V R Y P I S R P	4	
317	P I S R P R R R C	4	
325	C S P T E A A V R	4	

TABLE XXXIII 151P3D4 v.1: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
11	S I C W A D H L S	3	
26	H D R A I H I Q A	3	
39	H L L V E A E Q A	3	
43	E A E Q A K V F S	3	
45	E Q A K V F S H R	3	
50	F S H R G G N V T	3	
53	R G G N V T L P C	3	
65	R D P T A F G S G	3	
82	T K L T S D Y L K	3	
83	K L T S D Y L K E	3	
86	S D Y L K E V D V	3	
95	F V S M G Y H K K	3	
109	Q G R V F L K G G	3	
111	R V F L K G G S D	3	
115	K G G S D S D A S	3	
117	G S D S D A S L V	3	
119	D S D A S L V I T	3	
125	V I T D L T L E D	3	
138	K C E V I E G L E	3	
152	V A L D L Q G V V	3	
154	L D L Q G V V F P	3	
163	Y F P R L G R Y N	3	
167	L G R Y N L N F H	3	
173	N F H E A Q Q A C	3	
176	E A Q Q A C L D Q	3	
179	Q A C L D Q D A V	3	
181	C L D Q D A V I A	3	
210	L S D G S V Q Y P	3	
213	G S V Q Y P I T K	3	
220	T K P R E P C G G	3	
226	C G G Q N T V P G	3	
228	G Q N T V P G V R	3	
237	N Y G F W D K D K	3	
238	Y G F W D K D K S	3	
239	G F W D K D K S R	3	
244	D K S R Y D V F C	3	
246	S R Y D V F C F T	3	
251	F C F T S N F N G	3	
252	C F T S N F N G R	3	
261	F Y Y L I H P T K	3	
265	I H P T K L T Y D	3	
274	E A V Q A C L N D	3	
295	A W K I L G Y D R	3	
312	G S V R Y P I S R	3	
323	R R C S P T E A A	3	
331	A V R F V G F P D	3	
332	V R F V G F P D K	3	
333	R F V G F P D K K	3	
334	F V G F P D K K H	3	
341	K H K L Y G V Y C	3	
13	C W A D H L S D N	2	
19	S D N Y T L D H D	2	
20	D N Y T L D H D R	2	

TABLE XXXIII 151P3D4 v.1: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
21	N Y T L D H D R A	2	
23	T L D H D R A I H	2	
38	P H L L V E A E Q	2	
40	L L V E A E Q A K	2	
49	V F S H R G G N V	2	
58	T L P C K F Y R D	2	
63	F Y R D P T A F G	2	
78	R I K W T K L T S	2	
79	I K W T K L T S D	2	
85	T S D Y L K E V D	2	
89	L K E V D V F V S	2	
93	D V F V S M G Y H	2	
102	K K T Y G G Y Q G	2	
103	K T Y G G Y Q G R	2	
127	T D L T L E D Y G	2	
130	T L E D Y G R Y K	2	
136	R Y K C E V I E G	2	
147	D D T V V V A L D	2	
149	T V V V A L D L Q	2	
150	V V V A L D L Q G	2	
151	V V A L D L Q G V	2	
161	F P Y F P R L G R	2	
171	N L N F H E A Q Q	2	
184	Q D A V I A S F D	2	
188	I A S F D Q L Y D	2	
192	D Q L Y D A W R G	2	
193	Q L Y D A W R G G	2	
195	Y D A W R G G L D	2	
203	D W C N A G W L S	2	
205	C N A G W L S D G	2	
208	G W L S D G S V Q	2	
225	P C G G Q N T V P	2	
227	G G Q N T V P G V	2	
236	R N Y G F W D K D	2	
241	W D K D K S R Y D	2	
242	D K D K S R Y D V	2	
247	R Y D V F C F T S	2	
258	N G R F Y Y L I H	2	
269	K L T Y D E A V Q	2	
279	C L N D G A Q I A	2	
292	I F A A W K I L G	2	
302	D R C D A G W L A	2	
304	C D A G W L A D G	2	
307	G W L A D G S V R	2	
311	D G S V R Y P I S	2	
315	R Y P I S R P R R	2	
320	R P R R R C S P T	2	
321	P R R R C S P T E	2	
327	P T E A A V R F V	2	
343	K L Y G V Y C F R	2	
9	L I S I C W A D H	1	
12	I C W A D H L S D	1	
41	L V E A E Q A K V	1	

TABLE XXXIII 151P3D4 v.1: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
46	Q A K V F S H R G	1	
54	G G N V T L P C K	1	
59	L P C K F Y R D P	1	
60	P C K F Y R D P T	1	
88	Y L K E V D V F V	1	
99	G Y H K K T Y G G	1	
101	H K K T Y G G Y Q	1	
104	T Y G G Y Q G R V	1	
112	V F L K G G S D S	1	
113	F L K G G S D S D	1	
114	L K G G S D S D A	1	
128	D L T L E D Y G R	1	
133	D Y G R Y K C E V	1	
135	G R Y K C E V I E	1	
141	V I E G L E D D T	1	
157	Q G V V F P Y F P	1	
168	G R Y N L N F H E	1	
191	F D Q L Y D A W R	1	
198	W R G G L D W C N	1	
199	R G G L D W C N A	1	
204	W C N A G W L S D	1	
206	N A G W L S D G S	1	
212	D G S V Q Y P I T	1	
216	Q Y P I T K P R E	1	
218	P I T K P R E P C	1	
221	K P R E P C G G Q	1	
229	Q N T V P G V R N	1	
234	G V R N Y G F W D	1	
235	V R N Y G F W D K	1	
248	Y D V F C F T S N	1	
250	V F C F T S N F N	1	
266	H P T K L T Y D E	1	
267	P T K L T Y D E A	1	
283	G A Q I A K V G Q	1	
286	I A K V G Q I F A	1	
289	V G Q I F A A W K	1	
298	I L G Y D R C D A	1	
305	D A G W L A D G S	1	
322	R R R C S P T E A	1	
338	P D K K H K L Y G	1	
339	D K K H K L Y G V	1	
346	G V Y C F R A Y N	1	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
209	A E K N M K K K I	25	
362	V E N G R P A D L	23	
158	S E A Y K K V C L	22	
192	A E I H Y R K N K	19	
283	A W L P L R T P W	18	
99	E G I N I S G S F	17	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
185	E E K R K E K A E	17	
371	A G S G Y C G A L	17	
51	A K D F G H V Q F	16	
80	E K Q R K D K V L	16	
123	N T N P S R R P Y	16	
226	G G S P R G L G F	16	
378	A L W K A I E S L	16	
387	E E G L G G K Q K	16	
66	A Y S N D G E H W	15	
104	S G S F C R N K L	15	
106	S F C R N K L K Y	15	
125	N P S R R P Y H F	15	
133	F Q V P S R I F W	15	
167	S G A P H E V G W	15	
189	K E K A E I H Y R	15	
212	N M K K K I D K Y	15	
234	F I F K T I A P L	15	
262	S S A H R P P A L	15	
279	A S P A A W L P L	15	
400	K A E N G P H L L	15	
1	M L E H T T K T F	14	
3	E H T T K T F P L	14	
6	T K T F P L R A L	14	
30	K Q D K K V D L L	14	
98	C E G I N I S G S	14	
107	F C R N K L K Y L	14	
109	R N K L K Y L A F	14	
169	A P H E V G W K Y	14	
194	I H Y R K N K Q L	14	
221	T E S P G G G S P	14	
296	S C P T S S S T Y	14	
308	S P Y G P R N P L	14	
8	T F P L R A L H I	13	
18	V E S I R D H S G	13	
46	I I T Q G A K D F	13	
57	V Q F V G S Y K L	13	
59	F V G S Y K L A Y	13	
81	K Q R K D K V L L	13	
110	N K L K Y L A F L	13	
176	K Y Q A V T A T L	13	
224	P G G G S P R G L	13	
231	G L G F I F K T I	13	
276	V P A A S P A A W	13	
302	S T Y D S L S P Y	13	
355	S E N N S W Y V E	13	
382	A I E S L E E G L	13	
383	I E S L E E G L G	13	
13	A L H I V V E S I	12	
29	M K Q D K K V D L	12	
69	N D G E H W T V Y	12	
71	G E H W T V Y Q D	12	
79	D E K Q R K D K V	12	
153	P Q G H A S E A Y	12	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
171	H E V G W K Y Q A	12	
184	L E E K R K E K A	12	
228	S P R G L G F I F	12	
336	C Q G Q K H N V L	12	
352	K P K S E N N S W	12	
353	P K S E N N S W Y	12	
367	P A D L A G S G Y	12	
375	Y C G A L W K A I	12	
386	L E E G L G G K Q	12	
397	K E R K A E N G P	12	
2	L E H T T K T F P	11	
38	L V P T K V T G I	11	
55	G H V Q F V G S Y	11	
93	A V V V S C E G I	11	
131	Y H F Q V P S R I	11	
132	H F Q V P S R I F	11	
188	R K E K A E I H Y	11	
197	R K N K Q L M R L	11	
227	G S P R G L G F I	11	
242	L A A T R A T R I	11	
277	P A A S P A A W L	11	
299	T S S S T Y D S L	11	
321	H S P S G G G G L	11	
372	G S G Y C G A L W	11	
399	R K A E N G P H L	11	
95	V V S C E G I N I	10	
143	Q E K A D G G S C	10	
186	E K R K E K A E I	10	
39	V P T K V T G I I	9	
272	A R A P V P A A S	9	
278	A A S P A A W L P	9	
7	K T F P L R A L H	8	
86	K V L L G R K A V	8	
240	A P L A A T R A T	8	
264	A H R P P A L S A	8	
314	N P L P N P R H S	8	
42	K V T G I I T Q G	7	
150	S C C P Q G H A S	7	
233	G F I F K T I A P	7	
237	K T I A P L A A T	7	
265	H R P P A L S A R	7	
269	A L S A R A P V P	7	
274	A P V P A A S P A	7	
282	A A W L P L R T P	7	
364	N G R P A D L A G	7	
11	L R A L H I V V E	6	
19	E S I R D H S G Q	6	
41	T K V T G I I T Q	6	
105	G S F C R N K L K	6	
157	A S E A Y K K V C	6	
182	A T L E E K R K E	6	
230	R G L G F I F K T	6	
243	A A T R A T R I G	6	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
324	S G G G G L K K P	6	
346	R G K P Q R K P K	6	
394	Q K D K E R K A E	6	
34	K V D L L V P T K	5	
36	D L L V P T K V T	5	
37	L L V P T K V T G	5	
44	T G I I T Q G A K	5	
45	G I I T Q G A K D	5	
52	K D F G H V Q F V	5	
113	K Y L A F L H K R	5	
116	A F L H K R M N T	5	
127	S R R P Y H F Q V	5	
134	Q V P S R I F W R	5	
137	S R I F W R Q E K	5	
139	I F W R Q E K A D	5	
193	E I H Y R K N K Q	5	
199	N K Q L M R L Q K	5	
200	K Q L M R L Q K Q	5	
201	Q L M R L Q K Q A	5	
215	K K I D K Y T E S	5	
238	T I A P L A A T R	5	
244	A T R A T R I G H	5	
245	T R A T R I G H P	5	
248	T R I G H P G G R	5	
250	I G H P G G R T P	5	
253	P G G R T P R A G	5	
255	G R T P R A G S S	5	
260	A G S S A H R P P	5	
267	P P A L S A R A P	5	
287	L R T P W T R P S	5	
306	S L S P Y G P R N	5	
309	P Y G P R N P L P	5	
310	Y G P R N P L P N	5	
312	P R N P L P N P R	5	
329	L K K P A R H C Q	5	
338	G Q K H N V L A R	5	
342	N V L A R G K P Q	5	
345	A R G K P Q R K P	5	
348	K P Q R K P K S E	5	
363	E N G R P A D L A	5	
381	K A I E S L E E G	5	
388	E G L G G K Q K D	5	
9	F P L R A L H I V	4	
12	R A L H I V V E S	4	
16	I V V E S I R D H	4	
27	Q K M K Q D K K V	4	
28	K M K Q D K K V D	4	
33	K K V D L L V P T	4	
35	V D L L V P T K V	4	
58	Q F V G S Y K L A	4	
68	S N D G E H W T V	4	
82	Q R K D K V L L G	4	
87	V L L G R K A V V	4	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
88	L L G R K A V V V	4	
96	V S C E G I N I S	4	
97	S C E G I N I S G	4	
102	N I S G S F C R N	4	
115	L A F L H K R M N	4	
135	V P S R I F W R Q	4	
138	R I F W R Q E K A	4	
146	A D G G S C C P Q	4	
156	H A S E A Y K K V	4	
159	E A Y K K V C L S	4	
160	A Y K K V C L S G	4	
165	C L S G A P H E V	4	
172	E V G W K Y Q A V	4	
179	A V T A T L E E K	4	
208	Q A E K N M K K K	4	
210	E K N M K K K I D	4	
222	E S P G G G S P R	4	
235	I F K T I A P L A	4	
236	F K T I A P L A A	4	
263	S A H R P P A L S	4	
271	S A R A P V P A A	4	
284	W L P L R T P W T	4	
285	L P L R T P W T R	4	
295	S S C P T S S S T	4	
300	S S S T Y D S L S	4	
315	P L P N P R H S P	4	
316	L P N P R H S P S	4	
320	R H S P S G G G G	4	
322	S P S G G G G L K	4	
330	K K P A R H C Q G	4	
333	A R H C Q G Q K H	4	
361	Y V E N G R P A D	4	
368	A D L A G S G Y C	4	
384	E S L E E G L G G	4	
393	K Q K D K E R K A	4	
5	T T K T F P L R A	3	
14	L H I V V E S I R	3	
20	S I R D H S G Q K	3	
23	D H S G Q K M K Q	3	
24	H S G Q K M K Q D	3	
32	D K K V D L L V P	3	
50	G A K D F G H V Q	3	
72	E H W T V Y Q D E	3	
75	T V Y Q D E K Q R	3	
77	Y Q D E K Q R K D	3	
78	Q D E K Q R K D K	3	
83	R K D K V L L G R	3	
85	D K V L L G R K A	3	
89	L G R K A V V V S	3	
101	I N I S G S F C R	3	
111	K L K Y L A F L H	3	
112	L K Y L A F L H K	3	
117	F L H K R M N T N	3	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
119	H K R M N T N P S	3	
120	K R M N T N P S R	3	
121	R M N T N P S R R	3	
124	T N P S R R P Y H	3	
128	R R P Y H F Q V P	3	
144	E K A D G G S C C	3	
145	K A D G G S C C P	3	
162	K K V C L S G A P	3	
174	G W K Y Q A V T A	3	
175	W K Y Q A V T A T	3	
178	Q A V T A T L E E	3	
181	T A T L E E K R K	3	
183	T L E E K R K E K	3	
190	E K A E I H Y R K	3	
191	K A E I H Y R K N	3	
198	K N K Q L M R L Q	3	
202	L M R L Q K Q A E	3	
211	K N M K K K I D K	3	
213	M K K K I D K Y T	3	
216	K I D K Y T E S P	3	
229	P R G L G F I F K	3	
239	I A P L A A T R A	3	
246	R A T R I G H P G	3	
247	A T R I G H P G G	3	
251	G H P G G R T P R	3	
252	H P G G R T P R A	3	
270	L S A R A P V P A	3	
275	P V P A A S P A A	3	
280	S P A A W L P L R	3	
289	T P W T R P S S C	3	
291	W T R P S S C P T	3	
304	Y D S L S P Y G P	3	
307	L S P Y G P R N P	3	
323	P S G G G G L K K	3	
325	G G G G L K K P A	3	
326	G G G L K K P A R	3	
340	K H N V L A R G K	3	
341	H N V L A R G K P	3	
347	G K P Q R K P K S	3	
350	Q R K P K S E N N	3	
354	K S E N N S W Y V	3	
356	E N N S W Y V E N	3	
357	N N S W Y V E N G	3	
373	S G Y C G A L W K	3	
374	G Y C G A L W K A	3	
377	G A L W K A I E S	3	
389	G L G G K Q K D K	3	
4	H T T K T F P L R	2	
10	P L R A L H I V V	2	
17	V V E S I R D H S	2	
21	I R D H S G Q K M	2	
22	R D H S G Q K M K	2	
31	Q D K K V D L L V	2	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
43	V T G I I T Q G A	2	
54	F G H V Q F V G S	2	
60	V G S Y K L A Y S	2	
62	S Y K L A Y S N D	2	
63	Y K L A Y S N D G	2	
67	Y S N D G E H W T	2	
70	D G E H W T V Y Q	2	
84	K D K V L L G R K	2	
90	G R K A V V V S C	2	
114	Y L A F L H K R M	2	
122	M N T N P S R R P	2	
126	P S R R P Y H F Q	2	
136	P S R I F W R Q E	2	
148	G G S C C P Q G H	2	
152	C P Q G H A S E A	2	
155	G H A S E A Y K K	2	
163	K V C L S G A P H	2	
164	V C L S G A P H E	2	
168	G A P H E V G W K	2	
170	P H E V G W K Y Q	2	
177	Y Q A V T A T L E	2	
180	V T A T L E E K R	2	
187	K R K E K A E I H	2	
195	H Y R K N K Q L M	2	
196	Y R K N K Q L M R	2	
204	R L Q K Q A E K N	2	
205	L Q K Q A E K N M	2	
207	K Q A E K N M K K	2	
214	K K K I D K Y T E	2	
219	K Y T E S P G G G	2	
223	S P G G G S P R G	2	
225	G G G S P R G L G	2	
232	L G F I F K T I A	2	
241	P L A A T R A T R	2	
254	G G R T P R A G S	2	
256	R T P R A G S S A	2	
257	T P R A G S S A H	2	
259	R A G S S A H R P	2	
261	G S S A H R P P A	2	
268	P A L S A R A P V	2	
273	R A P V P A A S P	2	
281	P A A W L P L R T	2	
288	R T P W T R P S S	2	
292	T R P S S C P T S	2	
293	R P S S C P T S S	2	
294	P S S C P T S S S	2	
298	P T S S S T Y D S	2	
301	S S T Y D S L S P	2	
311	G P R N P L P N P	2	
313	R N P L P N P R H	2	
317	P N P R H S P S G	2	
318	N P R H S P S G G	2	
327	G G L K K P A R H	2	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
328	G L K K P A R H C	2	
331	K P A R H C Q G Q	2	
334	R H C Q G Q K H N	2	
335	H C Q G Q K H N V	2	
337	Q G Q K H N V L A	2	
339	Q K H N V L A R G	2	
343	V L A R G K P Q R	2	
344	L A R G K P Q R K	2	
351	R K P K S E N N S	2	
358	N S W Y V E N G R	2	
360	W Y V E N G R P A	2	
365	G R P A D L A G S	2	
366	R P A D L A G S G	2	
379	L W K A I E S L E	2	
385	S L E E G L G G K	2	
391	G G K Q K D K E R	2	
395	K D K E R K A E N	2	
396	D K E R K A E N G	2	
398	E R K A E N G P H	2	
15	H I V V E S I R D	1	
25	S G Q K M K Q D K	1	
26	G Q K M K Q D K K	1	
40	P T K V T G I I T	1	
47	I T Q G A K D F G	1	
49	Q G A K D F G H V	1	
53	D F G H V Q F V G	1	
61	G S Y K L A Y S N	1	
64	K L A Y S N D G E	1	
65	L A Y S N D G E H	1	
74	W T V Y Q D E K Q	1	
76	V Y Q D E K Q R K	1	
91	R K A V V V S C E	1	
92	K A V V V S C E G	1	
103	I S G S F C R N K	1	
108	C R N K L K Y L A	1	
118	L H K R M N T N P	1	
129	R P Y H F Q V P S	1	
130	P Y H F Q V P S R	1	
141	W R Q E K A D G G	1	
147	D G G S C C P Q G	1	
151	C C P Q G H A S E	1	
161	Y K K V C L S G A	1	
166	L S G A P H E V G	1	
173	V G W K Y Q A V T	1	
203	M R L Q K Q A E K	1	
206	Q K Q A E K N M K	1	
218	D K Y T E S P G G	1	
258	P R A G S S A H R	1	
266	R P P A L S A R A	1	
286	P L R T P W T R P	1	
290	P W T R P S S C P	1	
303	T Y D S L S P Y G	1	
305	D S L S P Y G P R	1	

TABLE XXXIII 151P3D4 v.2: HLA Peptide Scoring Results B*4402 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
332	P A R H C Q G Q K	1	
359	S W Y V E N G R P	1	
369	D L A G S G Y C G	1	
376	C G A L W K A I E	1	
380	W K A I E S L E E	1	
390	L G G K Q K D K E	1	

TABLE XXXIV 151P3D4 v.1: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
66	D P T A F G S G I	25	
152	V A L D L Q G V V	25	
121	D A S L V I T D L	24	
134	Y G R Y K C E V I	22	
143	E G L E D D T V V	22	
224	E P C G G Q N T V	22	
4	L L L L V L I S I	18	
179	Q A C L D Q D A V	18	
33	Q A E N G P H L L	17	
106	G G Y Q G R V F L	17	
164	F P R L G R Y N L	17	
227	G G Q N T V P G V	17	
309	L A D G S V R Y P	17	
22	Y T L D H D R A I	16	
24	L D H D R A I H I	16	
68	T A F G S G I H K	16	
161	F P Y F P R L G R	16	
180	A C L D Q D A V I	16	
196	D A W R G G L D W	16	
207	A G W L S D G S V	16	
217	Y P I T K P R E P	16	
16	D H L S D N Y T L	15	
88	Y L K E V D V F V	15	
118	S D S D A S L V I	15	
282	D G A Q I A K V G	15	
305	D A G W L A D G S	15	
306	A G W L A D G S V	15	
316	Y P I S R P R R R	15	
326	S P T E A A V R F	15	
2	K S L L L L V L I	14	
59	L P C K F Y R D P	14	
84	L T S D Y L K E V	14	
86	S D Y L K E V D V	14	
116	G G S D S D A S L	14	
148	D T V V V A L D L	14	
185	D A V I A S F D Q	14	
242	D K D K S R Y D V	14	
262	Y Y L I H P T K L	14	
284	A Q I A K V G Q I	14	
293	F A A W K I L G Y	14	
337	F P D K K H K L Y	14	
339	D K K H K L Y G V	14	

TABLE XXXIV 151P3D4 v.1: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
41	L V E A E Q A K V	13	
69	A F G S G I H K I	13	
98	M G Y H K K T Y G	13	
133	D Y G R Y K C E V	13	
137	Y K C E V I E G L	13	
144	G L E D D T V V V	13	
188	I A S F D Q L Y D	13	
268	T K L T Y D E A V	13	
281	N D G A Q I A K V	13	
286	I A K V G Q I F A	13	
290	G Q I F A A W K I	13	
294	A A W K I L G Y D	13	
299	L G Y D R C D A G	13	
1	M K S L L L L V L	12	
37	G P H L L V E A E	12	
71	G S G I H K I R I	12	
87	D Y L K E V D V F	12	
104	T Y G G Y Q G R V	12	
105	Y G G Y Q G R V F	12	
142	I E G L E D D T V	12	
146	E D D T V V V A L	12	
211	S D G S V Q Y P I	12	
221	K P R E P C G G Q	12	
232	V P G V R N Y G F	12	
278	A C L N D G A Q I	12	
310	A D G S V R Y P I	12	
327	P T E A A V R F V	12	
329	E A A V R F V G F	12	
330	A A V R F V G F P	12	
32	I Q A E N G P H L	11	
43	E A E Q A K V F S	11	
46	Q A K V F S H R G	11	
51	S H R G G N V T L	11	
159	V V F P Y F P R L	11	
176	E A Q Q A C L D Q	11	
206	N A G W L S D G S	11	
238	Y G F W D K D K S	11	
257	F N G R F Y Y L I	11	
266	H P T K L T Y D E	11	
272	Y D E A V Q A C L	11	
274	E A V Q A C L N D	11	
283	G A Q I A K V G Q	11	
336	G F P D K K H K L	11	
10	I S I C W A D H L	10	
14	W A D H L S D N Y	10	
28	R A I H I Q A E N	10	
34	A E N G P H L L V	10	
36	N G P H L L V E A	10	
76	K I R I K W T K L	10	
123	S L V I T D L T L	10	
145	L E D D T V V V A	10	
151	V V A L D L Q G V	10	
167	L G R Y N L N F H	10	

TABLE XXXIV 151P3D4 v.1: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
200	G G L D W C N A G	10	
202	L D W C N A G W L	10	
212	D G S V Q Y P I T	10	
277	Q A C L N D G A Q	10	
311	D G S V R Y P I S	10	
320	R P R R R C S P T	10	
335	V G F P D K K H K	10	
345	Y G V Y C F R A Y	10	
20	D N Y T L D H D R	9	
49	V F S H R G G N V	9	
53	R G G N V T L P C	9	
70	F G S G I H K I R	9	
72	S G I H K I R I K	9	
117	G S D S D A S L V	9	
155	D L Q G V V F P Y	9	
186	A V I A S F D Q L	9	
194	L Y D A W R G G L	9	
256	N F N G R F Y Y L	9	
258	N G R F Y Y L I H	9	
270	L T Y D E A V Q A	9	
291	Q I F A A W K I L	9	
301	Y D R C D A G W L	9	
324	R C S P T E A A V	9	
42	V E A E Q A K V F	8	
54	G G N V T L P C K	8	
108	Y Q G R V F L K G	8	
109	Q G R V F L K G G	8	
119	D S D A S L V I T	8	
147	D D T V V V A L D	8	
174	F H E A Q Q A C L	8	
183	D Q D A V I A S F	8	
192	D Q L Y D A W R G	8	
246	S R Y D V F C F T	8	
289	V G Q I F A A W K	8	
79	I K W T K L T S D	7	
81	W T K L T S D Y L	7	
89	L K E V D V F V S	7	
129	L T L E D Y G R Y	7	
154	L D L Q G V V F P	7	
157	Q G V V F P Y F P	7	
226	C G G Q N T V P G	7	
228	G Q N T V P G V R	7	
236	R N Y G F W D K D	7	
261	F Y Y L I H P T K	7	
265	I H P T K L T Y D	7	
328	T E A A V R F V G	7	
343	K L Y G V Y C F R	7	
7	L V L I S I C W A	6	
62	K F Y R D P T A F	6	
93	D V F V S M G Y H	6	
96	V S M G Y H K K T	6	
115	K G G S D S D A S	6	
132	E D Y G R Y K C E	6	

TABLE XXXIV 151P3D4 v.1: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
135	G R Y K C E V I E	6	
168	G R Y N L N F H E	6	
182	L D Q D A V I A S	6	
193	Q L Y D A W R G G	6	
199	R G G L D W C N A	6	
210	L S D G S V Q Y P	6	
215	V Q Y P I T K P R	6	
225	P C G G Q N T V P	6	
231	T V P G V R N Y G	6	
233	P G V R N Y G F W	6	
244	D K S R Y D V F C	6	
264	L I H P T K L T Y	6	
307	G W L A D G S V R	6	
314	V R Y P I S R P R	6	
325	C S P T E A A V R	6	
3	S L L L L V L I S	5	
5	L L L V L I S I C	5	
12	I C W A D H L S D	5	
25	D H D R A I H I Q	5	
27	D R A I H I Q A E	5	
35	E N G P H L L V E	5	
45	E Q A K V F S H R	5	
50	F S H R G G N V T	5	
58	T L P C K F Y R D	5	
82	T K L T S D Y L K	5	
90	K E V D V F V S M	5	
103	K T Y G G Y Q G R	5	
120	S D A S L V I T D	5	
124	L V I T D L T L E	5	
156	L Q G V V F P Y F	5	
208	G W L S D G S V Q	5	
213	G S V Q Y P I T K	5	
249	D V F C F T S N F	5	
251	F C F T S N F N G	5	
259	G R F Y Y L I H P	5	
260	R F Y Y L I H P T	5	
271	T Y D E A V Q A C	5	
273	D E A V Q A C L N	5	
297	K I L G Y D R C D	5	
302	D R C D A G W L A	5	
18	L S D N Y T L D H	4	
38	P H L L V E A E Q	4	
40	L L V E A E Q A K	4	
44	A E Q A K V F S H	4	
52	H R G G N V T L P	4	
55	G N V T L P C K F	4	
64	Y R D P T A F G S	4	
73	G I H K I R I K W	4	
74	I H K I R I K W T	4	
77	I R I K W T K L T	4	
78	R I K W T K L T S	4	
85	T S D Y L K E V D	4	
100	Y H K K T Y G G Y	4	

TABLE XXXIV 151P3D4 v.1: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
112	V F L K G G S D S	4	
114	L K G G S D S D A	4	
126	I T D L T L E D Y	4	
127	T D L T L E D Y G	4	
128	D L T L E D Y G R	4	
130	T L E D Y G R Y K	4	
131	L E D Y G R Y K C	4	
153	A L D L Q G V V F	4	
160	V F P Y F P R L G	4	
163	Y F P R L G R Y N	4	
165	P R L G R Y N L N	4	
170	Y N L N F H E A Q	4	
172	L N F H E A Q Q A	4	
203	D W C N A G W L S	4	
214	S V Q Y P I T K P	4	
230	N T V P G V R N Y	4	
239	G F W D K D K S R	4	
248	Y D V F C F T S N	4	
280	L N D G A Q I A K	4	
292	I F A A W K I L G	4	
333	R F V G F P D K K	4	
334	F V G F P D K K H	4	
340	K K H K L Y G V Y	4	
342	H K L Y G V Y C F	4	
344	L Y G V Y C F R A	4	
346	G V Y C F R A Y N	4	
6	L L V L I S I C W	3	
19	S D N Y T L D H D	3	
30	I H I Q A E N G P	3	
39	H L L V E A E Q A	3	
57	V T L P C K F Y R	3	
61	C K F Y R D P T A	3	
65	R D P T A F G S G	3	
83	K L T S D Y L K E	3	
92	V D V F V S M G Y	3	
94	V F V S M G Y H K	3	
95	F V S M G Y H K K	3	
97	S M G Y H K K T Y	3	
107	G Y Q G R V F L K	3	
125	V I T D L T L E D	3	
136	R Y K C E V I E G	3	
140	E V I E G L E D D	3	
150	V V V A L D L Q G	3	
162	P Y F P R L G R Y	3	
166	R L G R Y N L N F	3	
173	N F H E A Q Q A C	3	
189	A S F D Q L Y D A	3	
216	Q Y P I T K P R E	3	
220	T K P R E P C G G	3	
240	F W D K D K S R Y	3	
241	W D K D K S R Y D	3	
243	K D K S R Y D V F	3	
250	V F C F T S N F N	3	

TABLE XXXIV 151P3D4 v.1: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
253	F T S N F N G R F	3	
263	Y L I H P T K L T	3	
269	K L T Y D E A V Q	3	
275	A V Q A C L N D G	3	
285	Q I A K V G Q I F	3	
308	W L A D G S V R Y	3	
312	G S V R Y P I S R	3	
315	R Y P I S R P R R	3	
318	I S R P R R R C S	3	
322	R R R C S P T E A	3	
332	V R F V G F P D K	3	
9	L I S I C W A D H	2	
13	C W A D H L S D N	2	
15	A D H L S D N Y T	2	
17	H L S D N Y T L D	2	
21	N Y T L D H D R A	2	
26	H D R A I H I Q A	2	
31	H I Q A E N G P H	2	
47	A K V F S H R G G	2	
56	N V T L P C K F Y	2	
63	F Y R D P T A F G	2	
75	H K I R I K W T K	2	
91	E V D V F V S M G	2	
99	G Y H K K T Y G G	2	
101	H K K T Y G G Y Q	2	
111	R V F L K G G S D	2	
113	F L K G G S D S D	2	
122	A S L V I T D L T	2	
141	V I E G L E D D T	2	
149	T V V V A L D L Q	2	
177	A Q Q A C L D Q D	2	
181	C L D Q D A V I A	2	
191	F D Q L Y D A W R	2	
195	Y D A W R G G L D	2	
197	A W R G G L D W C	2	
204	W C N A G W L S D	2	
205	C N A G W L S D G	2	
209	W L S D G S V Q Y	2	
219	I T K P R E P C G	2	
229	Q N T V P G V R N	2	
235	V R N Y G F W D K	2	
237	N Y G F W D K D K	2	
245	K S R Y D V F C F	2	
247	R Y D V F C F T S	2	
252	C F T S N F N G R	2	
254	T S N F N G R F Y	2	
276	V Q A C L N D G A	2	
279	C L N D G A Q I A	2	
287	A K V G Q I F A A	2	
298	I L G Y D R C D A	2	
303	R C D A G W L A D	2	
304	C D A G W L A D G	2	
313	S V R Y P I S R P	2	

TABLE XXXIV 151P3D4 v.1: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
317	P I S R P R R R C	2	
321	P R R R C S P T E	2	
331	A V R F V G F P D	2	
338	P D K K H K L Y G	2	
341	K H K L Y G V Y C	2	
8	V L I S I C W A D	1	
23	T L D H D R A I H	1	
29	A I H I Q A E N G	1	
48	K V F S H R G G N	1	
60	P C K F Y R D P T	1	
80	K W T K L T S D Y	1	
139	C E V I E G L E D	1	
169	R Y N L N F H E A	1	
171	N L N F H E A Q Q	1	
175	H E A Q Q A C L D	1	
184	Q D A V I A S F D	1	
187	V I A S F D Q L Y	1	
198	W R G G L D W C N	1	
201	G L D W C N A G W	1	
218	P I T K P R E P C	1	
223	R E P C G G Q N T	1	
234	G V R N Y G F W D	1	
255	S N F N G R F Y Y	1	
267	P T K L T Y D E A	1	
288	K V G Q I F A A W	1	
296	W K I L G Y D R C	1	
319	S R P R R R C S P	1	

TABLE XXXIV 151P3D4 v.2: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
242	L A A T R A T R I	26	
39	V P T K V T G I I	24	
156	H A S E A Y K K V	23	
9	F P L R A L H I V	22	
308	S P Y G P R N P L	22	
268	P A L S A R A P V	20	
38	L V P T K V T G I	18	
159	E A Y K K V C L S	18	
285	L P L R T P W T R	18	
35	V D L L V P T K V	17	
49	Q G A K D F G H V	17	
131	Y H F Q V P S R I	17	
277	P A A S P A A W L	17	
400	K A E N G P H L L	17	
65	L A Y S N D G E H	16	
88	L L G R K A V V V	16	
169	A P H E V G W K Y	16	
224	P G G G S P R G L	16	
239	I A P L A A T R A	16	
314	N P L P N P R H S	16	
344	L A R G K P Q R K	16	

TABLE XXXIV 151P3D4 v.2: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
8	T F P L R A L H I	15	
12	R A L H I V V E S	15	
87	V L L G R K A V V	15	
89	L G R K A V V V S	15	
104	S G S F C R N K L	15	
129	R P Y H F Q V P S	15	
194	I H Y R K N K Q L	15	
282	A A W L P L R T P	15	
377	G A L W K A I E S	15	
13	A L H I V V E S I	14	
50	G A K D F G H V Q	14	
79	D E K Q R K D K V	14	
115	L A F L H K R M N	14	
208	Q A E K N M K K K	14	
209	A E K N M K K K I	14	
231	G L G F I F K T I	14	
240	A P L A A T R A T	14	
276	V P A A S P A A W	14	
289	T P W T R P S S C	14	
371	A G S G Y C G A L	14	
375	Y C G A L W K A I	14	
381	K A I E S L E E G	14	
10	P L R A L H I V V	13	
125	N P S R R P Y H F	13	
135	V P S R I F W R Q	13	
168	G A P H E V G W K	13	
173	V G W K Y Q A V T	13	
181	T A T L E E K R K	13	
191	K A E I H Y R K N	13	
259	R A G S S A H R P	13	
266	R P P A L S A R A	13	
267	P P A L S A R A P	13	
271	S A R A P V P A A	13	
281	P A A W L P L R T	13	
318	N P R H S P S G G	13	
348	K P Q R K P K S E	13	
27	Q K M K Q D K K V	12	
31	Q D K K V D L L V	12	
52	K D F G H V Q F V	12	
92	K A V V V S C E G	12	
95	V V S C E G I N I	12	
110	N K L K Y L A F L	12	
152	C P Q G H A S E A	12	
178	Q A V T A T L E E	12	
223	S P G G G S P R G	12	
227	G S P R G L G F I	12	
230	R G L G F I F K T	12	
252	H P G G R T P R A	12	
257	T P R A G S S A H	12	
273	R A P V P A A S P	12	
280	S P A A W L P L R	12	
293	R P S S C P T S S	12	
297	C P T S S S T Y D	12	

TABLE XXXIV 151P3D4 v.2: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
316	L P N P R H S P S	12	
327	G G L K K P A R H	12	
352	K P K S E N N S W	12	
366	R P A D L A G S G	12	
370	L A G S G Y C G A	12	
373	S G Y C G A L W K	12	
68	S N D G E H W T V	11	
70	D G E H W T V Y Q	11	
80	E K Q R K D K V L	11	
86	K V L L G R K A V	11	
93	A V V V S C E G I	11	
145	K A D G G S C C P	11	
176	K Y Q A V T A T L	11	
186	E K R K E K A E I	11	
228	S P R G L G F I F	11	
234	F I F K T I A P L	11	
243	A A T R A T R I G	11	
250	I G H P G G R T P	11	
263	S A H R P P A L S	11	
274	A P V P A A S P A	11	
278	A A S P A A W L P	11	
310	Y G P R N P L P N	11	
311	G P R N P L P N P	11	
322	S P S G G G G L K	11	
324	S G G G G L K K P	11	
336	C Q G Q K H N V L	11	
388	E G L G G K Q K D	11	
390	L G G K Q K D K E	11	
29	M K Q D K K V D L	10	
30	K Q D K K V D L L	10	
36	D L L V P T K V T	10	
57	V Q F V G S Y K L	10	
107	F C R N K L K Y L	10	
147	D G G S C C P Q G	10	
165	C L S G A P H E V	10	
232	L G F I F K T I A	10	
246	R A T R I G H P G	10	
331	K P A R H C Q G Q	10	
332	P A R H C Q G Q K	10	
367	P A D L A G S G Y	10	
6	T K T F P L R A L	9	
32	D K K V D L L V P	9	
53	D F G H V Q F V G	9	
54	F G H V Q F V G S	9	
60	V G S Y K L A Y S	9	
112	L K Y L A F L H K	9	
127	S R R P Y H F Q V	9	
172	E V G W K Y Q A V	9	
197	R K N K Q L M R L	9	
218	D K Y T E S P G G	9	
253	P G G R T P R A G	9	
279	A S P A A W L P L	9	
335	H C Q G Q K H N V	9	

TABLE XXXIV 151P3D4 v.2: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
337	Q G Q K H N V L A	9	
362	V E N G R P A D L	9	
378	A L W K A I E S L	9	
399	R K A E N G P H L	9	
3	E H T T K T F P L	8	
25	S G Q K M K Q D K	8	
44	T G I I T Q G A K	8	
77	Y Q D E K Q R K D	8	
81	K Q R K D K V L L	8	
154	Q G H A S E A Y K	8	
158	S E A Y K K V C L	8	
299	T S S S T Y D S L	8	
325	G G G G L K K P A	8	
354	K S E N N S W Y V	8	
364	N G R P A D L A G	8	
391	G G K Q K D K E R	8	
11	L R A L H I V V E	7	
16	I V V E S I R D H	7	
23	D H S G Q K M K Q	7	
63	Y K L A Y S N D G	7	
69	N D G E H W T V Y	7	
85	D K V L L G R K A	7	
148	G G S C C P Q G H	7	
167	S G A P H E V G W	7	
175	W K Y Q A V T A T	7	
182	A T L E E K R K E	7	
226	G G S P R G L G F	7	
254	G G R T P R A G S	7	
260	A G S S A H R P P	7	
262	S S A H R P P A L	7	
302	S T Y D S L S P Y	7	
321	H S P S G G G G L	7	
326	G G G L K K P A R	7	
346	R G K P Q R K P K	7	
37	L L V P T K V T G	6	
41	T K V T G I I T Q	6	
61	G S Y K L A Y S N	6	
75	T V Y Q D E K Q R	6	
90	G R K A V V V S C	6	
99	E G I N I S G S F	6	
113	K Y L A F L H K R	6	
157	A S E A Y K K V C	6	
166	L S G A P H E V G	6	
207	K Q A E K N M K K	6	
212	N M K K K I D K Y	6	
225	G G G S P R G L G	6	
305	D S L S P Y G P R	6	
359	S W Y V E N G R P	6	
369	D L A G S G Y C G	6	
376	C G A L W K A I E	6	
382	A I E S L E E G L	6	
396	D K E R K A E N G	6	
1	M L E H T T K T F	5	

TABLE XXXIV 151P3D4 v.2: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
2	L E H T T K T F P	5	
5	T T K T F P L R A	5	
21	I R D H S G Q K M	5	
82	Q R K D K V L L G	5	
83	R K D K V L L G R	5	
96	V S C E G I N I S	5	
102	N I S G S F C R N	5	
117	F L H K R M N T N	5	
118	L H K R M N T N P	5	
128	R R P Y H F Q V P	5	
164	V C L S G A P H E	5	
177	Y Q A V T A T L E	5	
183	T L E E K R K E K	5	
184	L E E K R K E K A	5	
200	K Q L M R L Q K Q	5	
269	A L S A R A P V P	5	
292	T R P S S C P T S	5	
296	S C P T S S S T Y	5	
307	L S P Y G P R N P	5	
342	N V L A R G K P Q	5	
358	N S W Y V E N G R	5	
384	E S L E E G L G G	5	
386	L E E G L G G K Q	5	
393	K Q K D K E R K A	5	
14	L H I V V E S I R	4	
28	K M K Q D K K V D	4	
34	K V D L L V P T K	4	
46	I I T Q G A K D F	4	
72	E H W T V Y Q D E	4	
91	R K A V V V S C E	4	
114	Y L A F L H K R M	4	
139	I F W R Q E K A D	4	
141	W R Q E K A D G G	4	
160	A Y K K V C L S G	4	
174	G W K Y Q A V T A	4	
180	V T A T L E E K R	4	
187	K R K E K A E I H	4	
196	Y R K N K Q L M R	4	
203	M R L Q K Q A E K	4	
204	R L Q K Q A E K N	4	
219	K Y T E S P G G G	4	
235	I F K T I A P L A	4	
238	T I A P L A A T R	4	
241	P L A A T R A T R	4	
245	T R A T R I G H P	4	
270	L S A R A P V P A	4	
304	Y D S L S P Y G P	4	
323	P S G G G G L K K	4	
328	G L K K P A R H C	4	
339	Q K H N V L A R G	4	
345	A R G K P Q R K P	4	
351	R K P K S E N N S	4	
355	S E N N S W Y V E	4	

TABLE XXXIV 151P3D4 v.2: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
357	N N S W Y V E N G	4	
374	G Y C G A L W K A	4	
4	H T T K T F P L R	3	
26	G Q K M K Q D K K	3	
33	K K V D L L V P T	3	
42	K V T G I I T Q G	3	
45	G I I T Q G A K D	3	
47	I T Q G A K D F G	3	
48	T Q G A K D F G H	3	
58	Q F V G S Y K L A	3	
59	F V G S Y K L A Y	3	
67	Y S N D G E H W T	3	
71	G E H W T V Y Q D	3	
76	V Y Q D E K Q R K	3	
97	S C E G I N I S G	3	
103	I S G S F C R N K	3	
105	G S F C R N K L K	3	
106	S F C R N K L K Y	3	
116	A F L H K R M N T	3	
121	R M N T N P S R R	3	
122	M N T N P S R R P	3	
123	N T N P S R R P Y	3	
133	F Q V P S R I F W	3	
138	R I F W R Q E K A	3	
155	G H A S E A Y K K	3	
161	Y K K V C L S G A	3	
179	A V T A T L E E K	3	
188	R K E K A E I H Y	3	
190	E K A E I H Y R K	3	
193	E I H Y R K N K Q	3	
199	N K Q L M R L Q K	3	
205	L Q K Q A E K N M	3	
211	K N M K K K I D K	3	
213	M K K K I D K Y T	3	
215	K K I D K Y T E S	3	
217	I D K Y T E S P G	3	
236	F K T I A P L A A	3	
244	A T R A T R I G H	3	
248	T R I G H P G G R	3	
251	G H P G G R T P R	3	
258	P R A G S S A H R	3	
272	A R A P V P A A S	3	
283	A W L P L R T P W	3	
286	P L R T P W T R P	3	
287	L R T P W T R P S	3	
313	R N P L P N P R H	3	
338	G Q K H N V L A R	3	
347	G K P Q R K P K S	3	
353	P K S E N N S W Y	3	
360	W Y V E N G R P A	3	
365	G R P A D L A G S	3	
368	A D L A G S G Y C	3	
379	L W K A I E S L E	3	

TABLE XXXIV 151P3D4 v.2: HLA Peptide Scoring Results B*5101 9-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9	score	SEQ. ID NO.
385	S L E E G L G G K	3	
389	G L G G K Q K D K	3	
15	H I V V E S I R D	2	
17	V V E S I R D H S	2	
24	H S G Q K M K Q D	2	
40	P T K V T G I I T	2	
55	G H V Q F V G S Y	2	
56	H V Q F V G S Y K	2	
64	K L A Y S N D G E	2	
74	W T V Y Q D E K Q	2	
78	Q D E K Q R K D K	2	
84	K D K V L L G R K	2	
101	I N I S G S F C R	2	
109	R N K L K Y L A F	2	
120	K R M N T N P S R	2	
124	T N P S R R P Y H	2	
130	P Y H F Q V P S R	2	
134	Q V P S R I F W R	2	
146	A D G G S C C P Q	2	
185	E E K R K E K A E	2	
189	K E K A E I H Y R	2	
192	A E I H Y R K N K	2	
202	L M R L Q K Q A E	2	
206	Q K Q A E K N M K	2	
210	E K N M K K K I D	2	
214	K K K I D K Y T E	2	
216	K I D K Y T E S P	2	
220	Y T E S P G G G S	2	
222	E S P G G G S P R	2	
229	P R G L G F I F K	2	
233	G F I F K T I A P	2	
237	K T I A P L A A T	2	
264	A H R P P A L S A	2	
265	H R P P A L S A R	2	
275	P V P A A S P A A	2	
288	R T P W T R P S S	2	
300	S S S T Y D S L S	2	
306	S L S P Y G P R N	2	
312	P R N P L P N P R	2	
329	L K K P A R H C Q	2	
330	K K P A R H C Q G	2	
333	A R H C Q G Q K H	2	
334	R H C Q G Q K H N	2	
340	K H N V L A R G K	2	
341	H N V L A R G K P	2	
361	Y V E N G R P A D	2	
383	I E S L E E G L G	2	
392	G K Q K D K E R K	2	
394	Q K D K E R K A E	2	
395	K D K E R K A E N	2	
397	K E R K A E N G P	2	
398	E R K A E N G P H	2	
7	K T F P L R A L H	1	
18	V E S I R D H S G	1	
20	S I R D H S G Q K	1	
22	R D H S G Q K M K	1	
43	V T G I I T Q G A	1	
51	A K D F G H V Q F	1	
66	A Y S N D G E H W	1	
73	H W T V Y Q D E K	1	
94	V V V S C E G I N	1	
98	C E G I N I S G S	1	
100	G I N I S G S F C	1	
108	C R N K L K Y L A	1	
111	K L K Y L A F L H	1	
119	H K R M N T N P S	1	
132	H F Q V P S R I F	1	
136	P S R I F W R Q E	1	
140	F W R Q E K A D G	1	
142	R Q E K A D G G S	1	
143	Q E K A D G G S C	1	
144	E K A D G G S C C	1	
149	G S C C P Q G H A	1	
151	C C P Q G H A S E	1	
163	K V C L S G A P H	1	
170	P H E V G W K Y Q	1	
171	H E V G W K Y Q A	1	
195	H Y R K N K Q L M	1	
198	K N K Q L M R L Q	1	
201	Q L M R L Q K Q A	1	
221	T E S P G G G S P	1	
249	R I G H P G G R T	1	
255	G R T P R A G S S	1	
256	R T P R A G S S A	1	
261	G S S A H R P P A	1	
284	W L P L R T P W T	1	
291	W T R P S S C P T	1	
295	S S C P T S S S T	1	
298	P T S S S T Y D S	1	
301	S S T Y D S L S P	1	
303	T Y D S L S P Y G	1	
309	P Y G P R N P L P	1	
315	P L P N P R H S P	1	
317	P N P R H S P S G	1	
320	R H S P S G G G G	1	
343	V L A R G K P Q R	1	
349	P Q R K P K S E N	1	
350	Q R K P K S E N N	1	
356	E N N S W Y V E N	1	
363	E N G R P A D L A	1	
380	W K A I E S L E E	1	
387	E E G L G G K Q K	1	

TABLE XXXV 151P3D4 v.1: HLA Peptide Scoring Results A1 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
91	E	V	D	V	F	V	S	M	G	Y	25	
263	Y	L	I	H	P	T	K	L	T	Y	24	
253	F	T	S	N	F	N	G	R	F	Y	23	
96	V	S	M	G	Y	H	K	K	T	Y	21	
117	G	S	D	S	D	A	S	L	V	I	21	
292	I	F	A	A	W	K	I	L	G	Y	21	
254	T	S	N	F	N	G	R	F	Y	Y	20	
64	Y	R	D	P	T	A	F	G	S	G	19	
119	D	S	D	A	S	L	V	I	T	D	19	
33	Q	A	E	N	G	P	H	L	L	V	18	
186	A	V	I	A	S	F	D	Q	L	Y	18	
327	P	T	E	A	A	V	R	F	V	G	18	
344	L	Y	G	V	Y	C	F	R	A	Y	18	
138	K	C	E	V	I	E	G	L	E	D	17	
336	G	F	P	D	K	K	H	K	L	Y	17	
337	F	P	D	K	K	H	K	L	Y	G	17	
125	V	I	T	D	L	T	L	E	D	Y	16	
126	I	T	D	L	T	L	E	D	Y	G	16	
128	D	L	T	L	E	D	Y	G	R	Y	16	
154	L	D	L	Q	G	V	V	F	P	Y	16	
161	F	P	Y	F	P	R	L	G	R	Y	16	
181	C	L	D	Q	D	A	V	I	A	S	16	
229	Q	N	T	V	P	G	V	R	N	Y	16	
339	D	K	K	H	K	L	Y	G	V	Y	16	
13	C	W	A	D	H	L	S	D	N	Y	15	
23	T	L	D	H	D	R	A	I	H	I	15	
55	G	N	V	T	L	P	C	K	F	Y	15	
79	I	K	W	T	K	L	T	S	D	Y	15	
99	G	Y	H	K	K	T	Y	G	G	Y	15	
208	G	W	L	S	D	G	S	V	Q	Y	15	
210	L	S	D	G	S	V	Q	Y	P	I	15	
222	P	R	E	P	C	G	G	Q	N	T	15	
239	G	F	W	D	K	D	K	S	R	Y	15	
307	G	W	L	A	D	G	S	V	R	Y	15	
18	L	S	D	N	Y	T	L	D	H	D	14	
25	D	H	D	R	A	I	H	I	Q	A	14	
57	V	T	L	P	C	K	F	Y	R	D	14	
85	T	S	D	Y	L	K	E	V	D	V	14	
130	T	L	E	D	Y	G	R	Y	K	C	14	
272	Y	D	E	A	V	Q	A	C	L	N	14	
89	L	K	E	V	D	V	F	V	S	M	13	
144	G	L	E	D	D	T	V	V	V	A	13	
146	E	D	D	T	V	V	V	A	L	D	13	
153	A	L	D	L	Q	G	V	V	F	P	13	
174	F	H	E	A	Q	Q	A	C	L	D	13	
194	L	Y	D	A	W	R	G	G	L	D	13	
247	R	Y	D	V	F	C	F	T	S	N	13	
280	L	N	D	G	A	Q	I	A	K	V	13	
107	G	Y	Q	G	R	V	F	L	K	G	12	
141	V	I	E	G	L	E	D	D	T	V	12	
190	S	F	D	Q	L	Y	D	A	W	R	12	
309	L	A	D	G	S	V	R	Y	P	I	12	
2	K	S	L	L	L	L	V	L	I	S	11	
41	L	V	E	A	E	Q	A	K	V	F	11	
43	E	A	E	Q	A	K	V	F	S	H	11	
67	P	T	A	F	G	S	G	I	H	K	11	
122	A	S	L	V	I	T	D	L	T	L	11	
145	L	E	D	D	T	V	V	V	A	L	11	
201	G	L	D	W	C	N	A	G	W	L	11	
230	N	T	V	P	G	V	R	N	Y	G	11	
240	F	W	D	K	D	K	S	R	Y	D	11	
242	D	K	D	K	S	R	Y	D	V	F	11	
14	W	A	D	H	L	S	D	N	Y	T	10	
131	L	E	D	Y	G	R	Y	K	C	E	10	
183	D	Q	D	A	V	I	A	S	F	D	10	
219	I	T	K	P	R	E	P	C	G	G	10	
271	T	Y	D	E	A	V	Q	A	C	L	10	
300	G	Y	D	R	C	D	A	G	W	L	10	
303	R	C	D	A	G	W	L	A	D	G	10	
22	Y	T	L	D	H	D	R	A	I	H	9	
34	A	E	N	G	P	H	L	L	V	E	9	
72	S	G	I	H	K	I	R	I	K	W	9	
195	Y	D	A	W	R	G	G	L	D	W	9	
318	I	S	R	P	R	R	R	C	S	P	9	
11	S	I	C	W	A	D	H	L	S	D	8	
81	W	T	K	L	T	S	D	Y	L	K	8	
82	T	K	L	T	S	D	Y	L	K	E	8	
148	D	T	V	V	V	A	L	D	L	Q	8	
160	V	F	P	Y	F	P	R	L	G	R	8	
165	P	R	L	G	R	Y	N	L	N	F	8	
3	S	L	L	L	L	V	L	I	S	I	7	
17	H	L	S	D	N	Y	T	L	D	H	7	
52	H	R	G	G	N	V	T	L	P	C	7	
84	L	T	S	D	Y	L	K	E	V	D	7	
103	K	T	Y	G	G	Y	Q	G	R	V	7	
129	L	T	L	E	D	Y	G	R	Y	K	7	
159	V	V	F	P	Y	F	P	R	L	G	7	
187	V	I	A	S	F	D	Q	L	Y	D	7	
245	K	S	R	Y	D	V	F	C	F	T	7	
257	F	N	G	R	F	Y	Y	L	I	H	7	
270	L	T	Y	D	E	A	V	Q	A	C	7	
335	V	G	F	P	D	K	K	H	K	L	7	
10	I	S	I	C	W	A	D	H	L	S	6	
50	F	S	H	R	G	G	N	V	T	L	6	
51	S	H	R	G	G	N	V	T	L	P	6	
70	F	G	S	G	I	H	K	I	R	I	6	
77	I	R	I	K	W	T	K	L	T	S	6	
124	L	V	I	T	D	L	T	L	E	D	6	
147	D	D	T	V	V	V	A	L	D	L	6	
149	T	V	V	V	A	L	D	L	Q	G	6	
175	H	E	A	Q	Q	A	C	L	D	Q	6	
203	D	W	C	N	A	G	W	L	S	D	6	
213	G	S	V	Q	Y	P	I	T	K	P	6	
267	P	T	K	L	T	Y	D	E	A	V	6	
273	D	E	A	V	Q	A	C	L	N	D	6	
291	Q	I	F	A	A	W	K	I	L	G	6	

TABLE XXXV 151P3D4 v.1: HLA Peptide Scoring Results A1 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
302	D R C D A G W L A D	6	
314	V R Y P I S R P R R	6	
5	L L L V L I S I C W	5	
88	Y L K E V D V F V S	5	
123	S L V I T D L T L E	5	
135	G R Y K C E V I E G	5	
155	D L Q G V V F P Y F	5	
162	P Y F P R L G R Y N	5	
189	A S F D Q L Y D A W	5	
215	V Q Y P I T K P R E	5	
255	S N F N G R F Y Y L	5	
279	C L N D G A Q I A K	5	
287	A K V G Q I F A A W	5	
301	Y D R C D A G W L A	5	
324	R C S P T E A A V R	5	
35	E N G P H L L V E A	4	
44	A E Q A K V F S H R	4	
71	G S G I H K I R I K	4	
86	S D Y L K E V D V F	4	
137	Y K C E V I E G L E	4	
212	D G S V Q Y P I T K	4	
251	F C F T S N F N G R	4	
258	N G R F Y Y L I H P	4	
262	Y Y L I H P T K L T	4	
264	L I H P T K L T Y D	4	
285	Q I A K V G Q I F A	4	
311	D G S V R Y P I S R	4	
312	G S V R Y P I S R P	4	
325	C S P T E A A V R F	4	
331	A V R F V G F P D K	4	
40	L L V E A E Q A K V	3	
49	V F S H R G G N V T	3	
68	T A F G S G I H K I	3	
94	V F V S M G Y H K K	3	
95	F V S M G Y H K K T	3	
100	Y H K K T Y G G Y Q	3	
104	T Y G G Y Q G R V F	3	
105	Y G G Y Q G R V F L	3	
106	G G Y Q G R V F L K	3	
113	F L K G G S D S D A	3	
152	V A L D L Q G V V F	3	
158	G V V F P Y F P R L	3	
163	Y F P R L G R Y N L	3	
164	F P R L G R Y N L N	3	
168	G R Y N L N F H E A	3	
185	D A V I A S F D Q L	3	
202	L D W C N A G W L S	3	
207	A G W L S D G S V Q	3	
217	Y P I T K P R E P C	3	
224	E P C G G Q N T V P	3	
234	G V R N Y G F W D K	3	
235	V R N Y G F W D K D	3	
256	N F N G R F Y Y L I	3	

TABLE XXXV 151P3D4 v.1: HLA Peptide Scoring Results A1 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
261	F Y Y L I H P T K L	3	
289	V G Q I F A A W K I	3	
306	A G W L A D G S V R	3	
316	Y P I S R P R R R C	3	
326	S P T E A A V R F V	3	
328	T E A A V R F V G F	3	
332	V R F V G F P D K K	3	
333	R F V G F P D K K H	3	
345	Y G V Y C F R A Y N	3	
1	M K S L L L L V L I	2	
8	V L I S I C W A D H	2	
15	A D H L S D N Y T L	2	
16	D H L S D N Y T L D	2	
19	S D N Y T L D H D R	2	
32	I Q A E N G P H L L	2	
47	A K V F S H R G G N	2	
54	G G N V T L P C K F	2	
75	H K I R I K W T K L	2	
76	K I R I K W T K L T	2	
90	K E V D V F V S M G	2	
97	S M G Y H K K T Y G	2	
108	Y Q G R V F L K G G	2	
116	G G S D S D A S L V	2	
118	S D S D A S L V I T	2	
120	S D A S L V I T D L	2	
121	D A S L V I T D L T	2	
134	Y G R Y K C E V I E	2	
151	V V A L D L Q G V V	2	
170	Y N L N F H E A Q Q	2	
193	Q L Y D A W R G G L	2	
197	A W R G G L D W C N	2	
209	W L S D G S V Q Y P	2	
211	S D G S V Q Y P I T	2	
214	S V Q Y P I T K P R	2	
231	T V P G V R N Y G F	2	
237	N Y G F W D K D K S	2	
238	Y G F W D K D K S R	2	
246	S R Y D V F C F T S	2	
248	Y D V F C F T S N F	2	
250	V F C F T S N F N G	2	
275	A V Q A C L N D G A	2	
284	A Q I A K V G Q I F	2	
294	A A W K I L G Y D R	2	
297	K I L G Y D R C D A	2	
308	W L A D G S V R Y P	2	
313	S V R Y P I S R P R	2	
319	S R P R R R C S P T	2	
330	A A V R F V G F P D	2	
343	K L Y G V Y C F R A	2	
4	L L L L V L I S I C	1	
6	L L V L I S I C W A	1	
29	A I H I Q A E N G P	1	
30	I H I Q A E N G P H	1	

TABLE XXXV 151P3D4 v.1: HLA Peptide Scoring Results A1 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
31	H	I	Q	A	E	N	G	P	H	L	1	
36	N	G	P	H	L	L	V	E	A	E	1	
39	H	L	L	V	E	A	E	Q	A	K	1	
42	V	E	A	E	Q	A	K	V	F	S	1	
48	K	V	F	S	H	R	G	G	N	V	1	
58	T	L	P	C	K	F	Y	R	D	P	1	
59	L	P	C	K	F	Y	R	D	P	T	1	
63	F	Y	R	D	P	T	A	F	G	S	1	
65	R	D	P	T	A	F	G	S	G	I	1	
69	A	F	G	S	G	I	H	K	I	R	1	
83	K	L	T	S	D	Y	L	K	E	V	1	
92	V	D	V	F	V	S	M	G	Y	H	1	
93	D	V	F	V	S	M	G	Y	H	K	1	
101	H	K	K	T	Y	G	G	Y	Q	G	1	
110	G	R	V	F	L	K	G	G	S	D	1	
111	R	V	F	L	K	G	G	S	D	S	1	
112	V	F	L	K	G	G	S	D	S	D	1	
114	L	K	G	G	S	D	S	D	A	S	1	
132	E	D	Y	G	R	Y	K	C	E	V	1	
133	D	Y	G	R	Y	K	C	E	V	I	1	
142	I	E	G	L	E	D	D	T	V	V	1	
143	E	G	L	E	D	D	T	V	V	V	1	
150	V	V	V	A	L	D	L	Q	G	V	1	
166	R	L	G	R	Y	N	L	N	F	H	1	
167	L	G	R	Y	N	L	N	F	H	E	1	
171	N	L	N	F	H	E	A	Q	Q	A	1	
177	A	Q	Q	A	C	L	D	Q	D	A	1	
179	Q	A	C	L	D	Q	D	A	V	I	1	
180	A	C	L	D	Q	D	A	V	I	A	1	
191	F	D	Q	L	Y	D	A	W	R	G	1	
198	W	R	G	G	L	D	W	C	N	A	1	
200	G	G	L	D	W	C	N	A	G	W	1	
205	C	N	A	G	W	L	S	D	G	S	1	
221	K	P	R	E	P	C	G	G	Q	N	1	
225	P	C	G	G	Q	N	T	V	P	G	1	
226	C	G	G	Q	N	T	V	P	G	V	1	
227	G	G	Q	N	T	V	P	G	V	R	1	
228	G	Q	N	T	V	P	G	V	R	N	1	
232	V	P	G	V	R	N	Y	G	F	W	1	
233	P	G	V	R	N	Y	G	F	W	D	1	
236	R	N	Y	G	F	W	D	K	D	K	1	
241	W	D	K	D	K	S	R	Y	D	V	1	
244	D	K	S	R	Y	D	V	F	C	F	1	
252	C	F	T	S	N	F	N	G	R	F	1	
268	T	K	L	T	Y	D	E	A	V	Q	1	
269	K	L	T	Y	D	E	A	V	Q	A	1	
276	V	Q	A	C	L	N	D	G	A	Q	1	
277	Q	A	C	L	N	D	G	A	Q	I	1	
278	A	C	L	N	D	G	A	Q	I	A	1	
281	N	D	G	A	Q	I	A	K	V	G	1	
283	G	A	Q	I	A	K	V	G	Q	I	1	
293	F	A	A	W	K	I	L	G	Y	D	1	
295	A	W	K	I	L	G	Y	D	R	C	1	

TABLE XXXV 151P3D4 v.1: HLA Peptide Scoring Results A1 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
298	I	L	G	Y	D	R	C	D	A	G	1	
304	C	D	A	G	W	L	A	D	G	S	1	
310	A	D	G	S	V	R	Y	P	I	S	1	
317	P	I	S	R	P	R	R	R	C	S	1	
329	E	A	A	V	R	F	V	G	F	P	1	
334	F	V	G	F	P	D	K	K	H	K	1	
340	K	K	H	K	L	Y	G	V	Y	C	1	
341	K	H	K	L	Y	G	V	Y	C	F	1	

TABLE XXXV 151P3D4 v.2: HLA Peptide Scoring Results A1 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
68	S	N	D	G	E	H	W	T	V	Y	29	
105	G	S	F	C	R	N	K	L	K	Y	27	
295	S	S	C	P	T	S	S	S	T	Y	25	
58	Q	F	V	G	S	Y	K	L	A	Y	22	
301	S	S	T	Y	D	S	L	S	P	Y	21	
187	K	R	K	E	K	A	E	I	H	Y	19	
220	Y	T	E	S	P	G	G	G	S	P	19	
30	K	Q	D	K	K	V	D	L	L	V	18	
168	G	A	P	H	E	V	G	W	K	Y	18	
54	F	G	H	V	Q	F	V	G	S	Y	17	
211	K	N	M	K	K	K	I	D	K	Y	17	
7	K	T	F	P	L	R	A	L	H	I	16	
122	M	N	T	N	P	S	R	R	P	Y	16	
152	C	P	Q	G	H	A	S	E	A	Y	16	
352	K	P	K	S	E	N	N	S	W	Y	16	
366	R	P	A	D	L	A	G	S	G	Y	16	
385	S	L	E	E	G	L	G	G	K	Q	16	
157	A	S	E	A	Y	K	K	V	C	L	15	
354	K	S	E	N	N	S	W	Y	V	E	15	
77	Y	Q	D	E	K	Q	R	K	D	K	13	
97	S	C	E	G	I	N	I	S	G	S	13	
183	T	L	E	E	K	R	K	E	K	A	13	
382	A	I	E	S	L	E	E	G	L	G	13	
4	H	T	T	K	T	F	P	L	R	A	12	
34	K	V	D	L	L	V	P	T	K	V	12	
51	A	K	D	F	G	H	V	Q	F	V	12	
78	Q	D	E	K	Q	R	K	D	K	V	12	
208	Q	A	E	K	N	M	K	K	K	I	12	
300	S	S	S	T	Y	D	S	L	S	P	12	
322	S	P	S	G	G	G	G	L	K	K	12	
361	Y	V	E	N	G	R	P	A	D	L	12	
386	L	E	E	G	L	G	G	K	Q	K	12	
1	M	L	E	H	T	T	K	T	F	P	11	
17	V	V	E	S	I	R	D	H	S	G	11	
21	I	R	D	H	S	G	Q	K	M	K	11	
70	D	G	E	H	W	T	V	Y	Q	D	11	
123	N	T	N	P	S	R	R	P	Y	H	11	
142	R	Q	E	K	A	D	G	G	S	C	11	
145	K	A	D	G	G	S	C	C	P	Q	11	
191	K	A	E	I	H	Y	R	K	N	K	11	

TABLE XXXV 151P3D4 v.2: HLA Peptide Scoring Results A1 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
278	A	A	S	P	A	A	W	L	P	L	11	
40	P	T	K	V	T	G	I	I	T	Q	10	
83	R	K	D	K	V	L	L	G	R	K	10	
96	V	S	C	E	G	I	N	I	S	G	10	
111	K	L	K	Y	L	A	F	L	H	K	10	
127	S	R	R	P	Y	H	F	Q	V	P	10	
170	P	H	E	V	G	W	K	Y	Q	A	10	
184	L	E	E	K	R	K	E	K	A	E	10	
188	R	K	E	K	A	E	I	H	Y	R	10	
216	K	I	D	K	Y	T	E	S	P	G	10	
228	S	P	R	G	L	G	F	I	F	K	10	
291	W	T	R	P	S	S	C	P	T	S	10	
303	T	Y	D	S	L	S	P	Y	G	P	10	
309	P	Y	G	P	R	N	P	L	P	N	10	
367	P	A	D	L	A	G	S	G	Y	C	10	
372	G	S	G	Y	C	G	A	L	W	K	10	
394	Q	K	D	K	E	R	K	A	E	N	10	
396	D	K	E	R	K	A	E	N	G	P	10	
81	K	Q	R	K	D	K	V	L	L	G	9	
177	Y	Q	A	V	T	A	T	L	E	E	8	
182	A	T	L	E	E	K	R	K	E	K	8	
262	S	S	A	H	R	P	P	A	L	S	8	
263	S	A	H	R	P	P	A	L	S	A	8	
280	S	P	A	A	W	L	P	L	R	T	8	
302	S	T	Y	D	S	L	S	P	Y	G	8	
31	Q	D	K	K	V	D	L	L	V	P	7	
43	V	T	G	I	I	T	Q	G	A	K	7	
47	I	T	Q	G	A	K	D	F	G	H	7	
103	I	S	G	S	F	C	R	N	K	L	7	
167	S	G	A	P	H	E	V	G	W	K	7	
180	V	T	A	T	L	E	E	K	R	K	7	
195	H	Y	R	K	N	K	Q	L	M	R	7	
198	K	N	K	Q	L	M	R	L	Q	K	7	
225	G	G	G	S	P	R	G	L	G	F	7	
244	A	T	R	A	T	R	I	G	H	P	7	
247	A	T	R	I	G	H	P	G	G	R	7	
279	A	S	P	A	A	W	L	P	L	R	7	
306	S	L	S	P	Y	G	P	R	N	P	7	
321	H	S	P	S	G	G	G	G	L	K	7	
323	P	S	G	G	G	G	L	K	K	P	7	
337	Q	G	Q	K	H	N	V	L	A	R	7	
383	I	E	S	L	E	E	G	L	G	G	7	
5	T	T	K	T	F	P	L	R	A	L	6	
9	F	P	L	R	A	L	H	I	V	V	6	
37	L	L	V	P	T	K	V	T	G	I	6	
39	V	P	T	K	V	T	G	I	I	T	6	
67	Y	S	N	D	G	E	H	W	T	V	6	
74	W	T	V	Y	Q	D	E	K	Q	R	6	
82	Q	R	K	D	K	V	L	L	G	R	6	
94	V	V	V	S	C	E	G	I	N	I	6	
108	C	R	N	K	L	K	Y	L	A	F	6	
150	S	C	C	P	Q	G	H	A	S	E	6	
159	E	A	Y	K	K	V	C	L	S	G	6	

TABLE XXXV 151P3D4 v.2: HLA Peptide Scoring Results A1 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
235	I	F	K	T	I	A	P	L	A	A	6	
237	K	T	I	A	P	L	A	A	T	R	6	
243	A	A	T	R	A	T	R	I	G	H	6	
256	R	T	P	R	A	G	S	S	A	H	6	
288	R	T	P	W	T	R	P	S	S	C	6	
298	P	T	S	S	S	T	Y	D	S	L	6	
299	T	S	S	S	T	Y	D	S	L	S	6	
308	S	P	Y	G	P	R	N	P	L	P	6	
346	R	G	K	P	Q	R	K	P	K	S	6	
363	E	N	G	R	P	A	D	L	A	G	6	
379	L	W	K	A	I	E	S	L	E	E	6	
3	E	H	T	T	K	T	F	P	L	R	5	
20	S	I	R	D	H	S	G	Q	K	M	5	
104	S	G	S	F	C	R	N	K	L	K	5	
132	H	F	Q	V	P	S	R	I	F	W	5	
133	F	Q	V	P	S	R	I	F	W	R	5	
136	P	S	R	I	F	W	R	Q	E	K	5	
149	G	S	C	C	P	Q	G	H	A	S	5	
158	S	E	A	Y	K	K	V	C	L	S	5	
221	T	E	S	P	G	G	G	S	P	R	5	
222	E	S	P	G	G	G	S	P	R	G	5	
227	G	S	P	R	G	L	G	F	I	F	5	
250	I	G	H	P	G	G	R	T	P	R	5	
255	G	R	T	P	R	A	G	S	S	A	5	
264	A	H	R	P	P	A	L	S	A	R	5	
270	L	S	A	R	A	P	V	P	A	A	5	
272	A	R	A	P	V	P	A	A	S	P	5	
274	A	P	V	P	A	A	S	P	A	A	5	
283	A	W	L	P	L	R	T	P	W	T	5	
287	L	R	T	P	W	T	R	P	S	S	5	
305	D	S	L	S	P	Y	G	P	R	N	5	
307	L	S	P	Y	G	P	R	N	P	L	5	
312	P	R	N	P	L	P	N	P	R	H	5	
314	N	P	L	P	N	P	R	H	S	P	5	
320	R	H	S	P	S	G	G	G	G	L	5	
358	N	S	W	Y	V	E	N	G	R	P	5	
371	A	G	S	G	Y	C	G	A	L	W	5	
14	L	H	I	V	V	E	S	I	R	D	4	
19	E	S	I	R	D	H	S	G	Q	K	4	
24	H	S	G	Q	K	M	K	Q	D	K	4	
25	S	G	Q	K	M	K	Q	D	K	K	4	
61	G	S	Y	K	L	A	Y	S	N	D	4	
87	V	L	L	G	R	K	A	V	V	V	4	
114	Y	L	A	F	L	H	K	R	M	N	4	
126	P	S	R	R	P	Y	H	F	Q	V	4	
137	S	R	I	F	W	R	Q	E	K	A	4	
166	L	S	G	A	P	H	E	V	G	W	4	
210	E	K	N	M	K	K	K	I	D	K	4	
224	P	G	G	G	S	P	R	G	L	G	4	
226	G	G	S	P	R	G	L	G	F	I	4	
230	R	G	L	G	F	I	F	K	T	I	4	
232	L	G	F	I	F	K	T	I	A	P	4	
238	T	I	A	P	L	A	A	T	R	A	4	

TABLE XXXV 151P3D4 v.2: HLA Peptide Scoring Results A1 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
261	G	S	S	A	H	R	P	P	A	L	4	
265	H	R	P	P	A	L	S	A	R	A	4	
294	P	S	S	C	P	T	S	S	S	T	4	
316	L	P	N	P	R	H	S	P	S	G	4	
329	L	K	K	P	A	R	H	C	Q	G	4	
350	Q	R	K	P	K	S	E	N	N	S	4	
362	V	E	N	G	R	P	A	D	L	A	4	
364	N	G	R	P	A	D	L	A	G	S	4	
373	S	G	Y	C	G	A	L	W	K	A	4	
376	C	G	A	L	W	K	A	I	E	S	4	
378	A	L	W	K	A	I	E	S	L	E	4	
384	E	S	L	E	E	G	L	G	G	K	4	
389	G	L	G	G	K	Q	K	D	K	E	4	
6	T	K	T	F	P	L	R	A	L	H	3	
29	M	K	Q	D	K	K	V	D	L	L	3	
44	T	G	I	I	T	Q	G	A	K	D	3	
48	T	Q	G	A	K	D	F	G	H	V	3	
53	D	F	G	H	V	Q	F	V	G	S	3	
57	V	Q	F	V	G	S	Y	K	L	A	3	
63	Y	K	L	A	Y	S	N	D	G	E	3	
76	V	Y	Q	D	E	K	Q	R	K	D	3	
84	K	D	K	V	L	L	G	R	K	A	3	
88	L	L	G	R	K	A	V	V	V	S	3	
101	I	N	I	S	G	S	F	C	R	N	3	
107	F	C	R	N	K	L	K	Y	L	A	3	
117	F	L	H	K	R	M	N	T	N	P	3	
134	Q	V	P	S	R	I	F	W	R	Q	3	
165	C	L	S	G	A	P	H	E	V	G	3	
179	A	V	T	A	T	L	E	E	K	R	3	
192	A	E	I	H	Y	R	K	N	K	Q	3	
206	Q	K	Q	A	E	K	N	M	K	K	3	
223	S	P	G	G	G	S	P	R	G	L	3	
234	F	I	F	K	T	I	A	P	L	A	3	
324	S	G	G	G	G	L	K	K	P	A	3	
332	P	A	R	H	C	Q	G	Q	K	H	3	
336	C	Q	G	Q	K	H	N	V	L	A	3	
340	K	H	N	V	L	A	R	G	K	P	3	
344	L	A	R	G	K	P	Q	R	K	P	3	
359	S	W	Y	V	E	N	G	R	P	A	3	
10	P	L	R	A	L	H	I	V	V	E	2	
13	A	L	H	I	V	V	E	S	I	R	2	
22	R	D	H	S	G	Q	K	M	K	Q	2	
26	G	Q	K	M	K	Q	D	K	K	V	2	
35	V	D	L	L	V	P	T	K	V	T	2	
49	Q	G	A	K	D	F	G	H	V	Q	2	
52	K	D	F	G	H	V	Q	F	V	G	2	
56	H	V	Q	F	V	G	S	Y	K	L	2	
62	S	Y	K	L	A	Y	S	N	D	G	2	
73	H	W	T	V	Y	Q	D	E	K	Q	2	
80	E	K	Q	R	K	D	K	V	L	L	2	
106	S	F	C	R	N	K	L	K	Y	L	2	
110	N	K	L	K	Y	L	A	F	L	H	2	
112	L	K	Y	L	A	F	L	H	K	R	2	
131	Y	H	F	Q	V	P	S	R	I	F	2	
146	A	D	G	G	S	C	C	P	Q	G	2	
154	Q	G	H	A	S	E	A	Y	K	K	2	
155	G	H	A	S	E	A	Y	K	K	V	2	
161	Y	K	K	V	C	L	S	G	A	P	2	
176	K	Y	Q	A	V	T	A	T	L	E	2	
181	T	A	T	L	E	E	K	R	K	E	2	
190	E	K	A	E	I	H	Y	R	K	N	2	
194	I	H	Y	R	K	N	K	Q	L	M	2	
196	Y	R	K	N	K	Q	L	M	R	L	2	
197	R	K	N	K	Q	L	M	R	L	Q	2	
199	N	K	Q	L	M	R	L	Q	K	Q	2	
203	M	R	L	Q	K	Q	A	E	K	N	2	
207	K	Q	A	E	K	N	M	K	K	K	2	
229	P	R	G	L	G	F	I	F	K	T	2	
240	A	P	L	A	A	T	R	A	T	R	2	
248	T	R	I	G	H	P	G	G	R	T	2	
260	A	G	S	S	A	H	R	P	P	A	2	
269	A	L	S	A	R	A	P	V	P	A	2	
271	S	A	R	A	P	V	P	A	A	S	2	
277	P	A	A	S	P	A	A	W	L	P	2	
282	A	A	W	L	P	L	R	T	P	W	2	
296	S	C	P	T	S	S	S	T	Y	D	2	
304	Y	D	S	L	S	P	Y	G	P	R	2	
310	Y	G	P	R	N	P	L	P	N	P	2	
328	G	L	K	K	P	A	R	H	C	Q	2	
335	H	C	Q	G	Q	K	H	N	V	L	2	
343	V	L	A	R	G	K	P	Q	R	K	2	
345	A	R	G	K	P	Q	R	K	P	K	2	
355	S	E	N	N	S	W	Y	V	E	N	2	
368	A	D	L	A	G	S	G	Y	C	G	2	
369	D	L	A	G	S	G	Y	C	G	A	2	
375	Y	C	G	A	L	W	K	A	I	E	2	
387	E	E	G	L	G	G	K	Q	K	D	2	
392	G	K	Q	K	D	K	E	R	K	A	2	
399	R	K	A	E	N	G	P	H	L	L	2	
11	L	R	A	L	H	I	V	V	E	S	1	
12	R	A	L	H	I	V	V	E	S	I	1	
16	I	V	V	E	S	I	R	D	H	S	1	
18	V	E	S	I	R	D	H	S	G	Q	1	
23	D	H	S	G	Q	K	M	K	Q	D	1	
27	Q	K	M	K	Q	D	K	K	V	D	1	
33	K	K	V	D	L	L	V	P	T	K	1	
36	D	L	L	V	P	T	K	V	T	G	1	
42	K	V	T	G	I	I	T	Q	G	A	1	
55	G	H	V	Q	F	V	G	S	Y	K	1	
59	F	V	G	S	Y	K	L	A	Y	S	1	
60	V	G	S	Y	K	L	A	Y	S	N	1	
64	K	L	A	Y	S	N	D	G	E	H	1	
65	L	A	Y	S	N	D	G	E	H	W	1	
66	A	Y	S	N	D	G	E	H	W	T	1	
79	D	E	K	Q	R	K	D	K	V	L	1	
85	D	K	V	L	L	G	R	K	A	V	1	

TABLE XXXV 151P3D4 v.2: HLA Peptide Scoring Results A1 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
86	K V L L G R K A V V	1	
89	L G R K A V V V S C	1	
90	G R K A V V V S C E	1	
93	A V V V S C E G I N	1	
95	V V S C E G I N I S	1	
99	E G I N I S G S F C	1	
102	N I S G S F C R N K	1	
115	L A F L H K R M N T	1	
116	A F L H K R M N T N	1	
119	H K R M N T N P S R	1	
129	R P Y H F Q V P S R	1	
135	V P S R I F W R Q E	1	
140	F W R Q E K A D G G	1	
143	Q E K A D G G S C C	1	
156	H A S E A Y K K V C	1	
160	A Y K K V C L S G A	1	
162	K K V C L S G A P H	1	
164	V C L S G A P H E V	1	
169	A P H E V G W K Y Q	1	
171	H E V G W K Y Q A V	1	
172	E V G W K Y Q A V T	1	
173	V G W K Y Q A V T A	1	
174	G W K Y Q A V T A T	1	
193	E I H Y R K N K Q L	1	
201	Q L M R L Q K Q A E	1	
204	R L Q K Q A E K N M	1	
205	L Q K Q A E K N M K	1	
209	A E K N M K K K I D	1	
219	K Y T E S P G G G S	1	
231	G L G F I F K T I A	1	
236	F K T I A P L A A T	1	
241	P L A A T R A T R I	1	
245	T R A T R I G H P G	1	
249	R I G H P G G R T P	1	
251	G H P G G R T P R A	1	
252	H P G G R T P R A G	1	
253	P G G R T P R A G S	1	
258	P R A G S S A H R P	1	
267	P P A L S A R A P V	1	
268	P A L S A R A P V P	1	
276	V P A A S P A A W L	1	
284	W L P L R T P W T R	1	
286	P L R T P W T R P S	1	
315	P L P N P R H S P S	1	
319	P R H S P S G G G G	1	
325	G G G G L K K P A R	1	
333	A R H C Q G Q K H N	1	
341	H N V L A R G K P Q	1	
351	R K P K S E N N S W	1	
356	E N N S W Y V E N G	1	
360	W Y V E N G R P A D	1	
374	G Y C G A L W K A I	1	
388	E G L G G K Q K D K	1	

TABLE XXXV 151P3D4 v.2: HLA Peptide Scoring Results A1 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
393	K Q K D K E R K A E	1	
397	K E R K A E N G P H	1	
398	E R K A E N G P H L	1	

TABLE XXXVI 151P3D4 v.1: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
3	S L L L L V L I S I	28	
40	L L V E A E Q A K V	28	
83	K L T S D Y L K E V	25	
193	Q L Y D A W R G G L	23	
68	T A F G S G I H K I	22	
141	V I E G L E D D T V	22	
280	L N D G A Q I A K V	22	
144	G L E D D T V V V A	21	
201	G L D W C N A G W L	21	
6	L L V L I S I C W A	20	
9	L I S I C W A D H L	20	
145	L E D D T V V V A L	20	
150	V V V A L D L Q G V	20	
31	H I Q A E N G P H L	19	
4	L L L L V L I S I C	18	
23	T L D H D R A I H I	18	
103	K T Y G G Y Q G R V	18	
120	S D A S L V I T D L	18	
153	A L D L Q G V V F P	18	
343	K L Y G V Y C F R A	18	
32	I Q A E N G P H L L	17	
88	Y L K E V D V F V S	17	
122	A S L V I T D L T L	17	
151	V V A L D L Q G V V	17	
263	Y L I H P T K L T Y	17	
283	G A Q I A K V G Q I	17	
297	K I L G Y D R C D A	17	
308	W L A D G S V R Y P	17	
309	L A D G S V R Y P I	17	
326	S P T E A A V R F V	17	
335	V G F P D K K H K L	17	
48	K V F S H R G G N V	16	
73	G I H K I R I K W T	16	
113	F L K G G S D S D A	16	
123	S L V I T D L T L E	16	
206	N A G W L S D G S V	16	
226	C G G Q N T V P G V	16	
264	L I H P T K L T Y D	16	
8	V L I S I C W A D H	15	
15	A D H L S D N Y T L	15	
50	F S H R G G N V T L	15	
115	K G G S D S D A S L	15	
158	G V V F P Y F P R L	15	
166	R L G R Y N L N F H	15	
181	C L D Q D A V I A S	15	

TABLE XXXVI 151P3D4 v.1: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
209	W	L	S	D	G	S	V	Q	Y	P	15	
269	K	L	T	Y	D	E	A	V	Q	A	15	
305	D	A	G	W	L	A	D	G	S	V	15	
1	M	K	S	L	L	L	L	V	L	I	14	
5	L	L	L	V	L	I	S	I	C	W	14	
33	Q	A	E	N	G	P	H	L	L	V	14	
75	H	K	I	R	I	K	W	T	K	L	14	
136	R	Y	K	C	E	V	I	E	G	L	14	
171	N	L	N	F	H	E	A	Q	Q	A	14	
173	N	F	H	E	A	Q	Q	A	C	L	14	
179	Q	A	C	L	D	Q	D	A	V	I	14	
188	I	A	S	F	D	Q	L	Y	D	A	14	
255	S	N	F	N	G	R	F	Y	Y	L	14	
261	F	Y	Y	L	I	H	P	T	K	L	14	
271	T	Y	D	E	A	V	Q	A	C	L	14	
277	Q	A	C	L	N	D	G	A	Q	I	14	
285	Q	I	A	K	V	G	Q	I	F	A	14	
286	I	A	K	V	G	Q	I	F	A	A	14	
11	S	I	C	W	A	D	H	L	S	D	13	
39	H	L	L	V	E	A	E	Q	A	K	13	
78	R	I	K	W	T	K	L	T	S	D	13	
87	D	Y	L	K	E	V	D	V	F	V	13	
105	Y	G	G	Y	Q	G	R	V	F	L	13	
118	S	D	S	D	A	S	L	V	I	T	13	
125	V	I	T	D	L	T	L	E	D	Y	13	
130	T	L	E	D	Y	G	R	Y	K	C	13	
143	E	G	L	E	D	D	T	V	V	V	13	
163	Y	F	P	R	L	G	R	Y	N	L	13	
178	Q	Q	A	C	L	D	Q	D	A	V	13	
185	D	A	V	I	A	S	F	D	Q	L	13	
210	L	S	D	G	S	V	Q	Y	P	I	13	
223	R	E	P	C	G	G	Q	N	T	V	13	
270	L	T	Y	D	E	A	V	Q	A	C	13	
279	C	L	N	D	G	A	Q	I	A	K	13	
323	R	R	C	S	P	T	E	A	A	V	13	
17	H	L	S	D	N	Y	T	L	D	H	12	
29	A	I	H	I	Q	A	E	N	G	P	12	
76	K	I	R	I	K	W	T	K	L	T	12	
116	G	G	S	D	S	D	A	S	L	V	12	
132	E	D	Y	G	R	Y	K	C	E	V	12	
142	I	E	G	L	E	D	D	T	V	V	12	
155	D	L	Q	G	V	V	F	P	Y	F	12	
187	V	I	A	S	F	D	Q	L	Y	D	12	
256	N	F	N	G	R	F	Y	Y	L	I	12	
298	I	L	G	Y	D	R	C	D	A	G	12	
338	P	D	K	K	H	K	L	Y	G	V	12	
22	Y	T	L	D	H	D	R	A	I	H	11	
35	E	N	G	P	H	L	L	V	E	A	11	
70	F	G	S	G	I	H	K	I	R	I	11	
85	T	S	D	Y	L	K	E	V	D	V	11	
124	L	V	I	T	D	L	T	L	E	D	11	
180	A	C	L	D	Q	D	A	V	I	A	11	
182	L	D	Q	D	A	V	I	A	S	F	11	

TABLE XXXVI 151P3D4 v.1: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
241	W	D	K	D	K	S	R	Y	D	V	11	
267	P	T	K	L	T	Y	D	E	A	V	11	
275	A	V	Q	A	C	L	N	D	G	A	11	
289	V	G	Q	I	F	A	A	W	K	I	11	
290	G	Q	I	F	A	A	W	K	I	L	11	
293	F	A	A	W	K	I	L	G	Y	D	11	
300	G	Y	D	R	C	D	A	G	W	L	11	
34	A	E	N	G	P	H	L	L	V	E	10	
57	V	T	L	P	C	K	F	Y	R	D	10	
58	T	L	P	C	K	F	Y	R	D	P	10	
80	K	W	T	K	L	T	S	D	Y	L	10	
95	F	V	S	M	G	Y	H	K	K	T	10	
117	G	S	D	S	D	A	S	L	V	I	10	
129	L	T	L	E	D	Y	G	R	Y	K	10	
152	V	A	L	D	L	Q	G	V	V	F	10	
259	G	R	F	Y	Y	L	I	H	P	T	10	
292	I	F	A	A	W	K	I	L	G	Y	10	
7	L	V	L	I	S	I	C	W	A	D	9	
14	W	A	D	H	L	S	D	N	Y	T	9	
65	R	D	P	T	A	F	G	S	G	I	9	
89	L	K	E	V	D	V	F	V	S	M	9	
97	S	M	G	Y	H	K	K	T	Y	G	9	
140	E	V	I	E	G	L	E	D	D	T	9	
147	D	D	T	V	V	V	A	L	D	L	9	
168	G	R	Y	N	L	N	F	H	E	A	9	
291	Q	I	F	A	A	W	K	I	L	G	9	
2	K	S	L	L	L	L	V	L	I	S	8	
21	N	Y	T	L	D	H	D	R	A	I	8	
24	L	D	H	D	R	A	I	H	I	Q	8	
51	S	H	R	G	G	N	V	T	L	P	8	
128	D	L	T	L	E	D	Y	G	R	Y	8	
135	G	R	Y	K	C	E	V	I	E	G	8	
154	L	D	L	Q	G	V	V	F	P	Y	8	
159	V	V	F	P	Y	F	P	R	L	G	8	
186	A	V	I	A	S	F	D	Q	L	Y	8	
196	D	A	W	R	G	G	L	D	W	C	8	
219	I	T	K	P	R	E	P	C	G	G	8	
231	T	V	P	G	V	R	N	Y	G	F	8	
278	A	C	L	N	D	G	A	Q	I	A	8	
294	A	A	W	K	I	L	G	Y	D	R	8	
12	I	C	W	A	D	H	L	S	D	N	7	
42	V	E	A	E	Q	A	K	V	F	S	7	
77	I	R	I	K	W	T	K	L	T	S	7	
84	L	T	S	D	Y	L	K	E	V	D	7	
86	S	D	Y	L	K	E	V	D	V	F	7	
121	D	A	S	L	V	I	T	D	L	T	7	
133	D	Y	G	R	Y	K	C	E	V	I	7	
148	D	T	V	V	V	A	L	D	L	Q	7	
200	G	G	L	D	W	C	N	A	G	W	7	
211	S	D	G	S	V	Q	Y	P	I	T	7	
213	G	S	V	Q	Y	P	I	T	K	P	7	
230	N	T	V	P	G	V	R	N	Y	G	7	
262	Y	Y	L	I	H	P	T	K	L	T	7	

TABLE XXXVI 151P3D4 v.1: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
287	A	K	V	G	Q	I	F	A	A	W	7	
288	K	V	G	Q	I	F	A	A	W	K	7	
299	L	G	Y	D	R	C	D	A	G	W	7	
329	E	A	A	V	R	F	V	G	F	P	7	
18	L	S	D	N	Y	T	L	D	H	D	6	
28	R	A	I	H	I	Q	A	E	N	G	6	
43	E	A	E	Q	A	K	V	F	S	H	6	
49	V	F	S	H	R	G	G	N	V	T	6	
59	L	P	C	K	F	Y	R	D	P	T	6	
64	Y	R	D	P	T	A	F	G	S	G	6	
72	S	G	I	H	K	I	R	I	K	W	6	
90	K	E	V	D	V	F	V	S	M	G	6	
106	G	G	Y	Q	G	R	V	F	L	K	6	
107	G	Y	Q	G	R	V	F	L	K	G	6	
108	Y	Q	G	R	V	F	L	K	G	G	6	
126	I	T	D	L	T	L	E	D	Y	G	6	
170	Y	N	L	N	F	H	E	A	Q	Q	6	
177	A	Q	Q	A	C	L	D	Q	D	A	6	
198	W	R	G	G	L	D	W	C	N	A	6	
246	S	R	Y	D	V	F	C	F	T	S	6	
274	E	A	V	Q	A	C	L	N	D	G	6	
301	Y	D	R	C	D	A	G	W	L	A	6	
303	R	C	D	A	G	W	L	A	D	G	6	
318	I	S	R	P	R	R	R	C	S	P	6	
319	S	R	P	R	R	R	C	S	P	T	6	
330	A	A	V	R	F	V	G	F	P	D	6	
331	A	V	R	F	V	G	F	P	D	K	6	
10	I	S	I	C	W	A	D	H	L	S	5	
26	H	D	R	A	I	H	I	Q	A	E	5	
27	D	R	A	I	H	I	Q	A	E	N	5	
36	N	G	P	H	L	L	V	E	A	E	5	
37	G	P	H	L	L	V	E	A	E	Q	5	
53	R	G	G	N	V	T	L	P	C	K	5	
71	G	S	G	I	H	K	I	R	I	K	5	
82	T	K	L	T	S	D	Y	L	K	E	5	
93	D	V	F	V	S	M	G	Y	H	K	5	
96	V	S	M	G	Y	H	K	K	T	Y	5	
111	R	V	F	L	K	G	G	S	D	S	5	
112	V	F	L	K	G	G	S	D	S	D	5	
114	L	K	G	G	S	D	S	D	A	S	5	
119	D	S	D	A	S	L	V	I	T	D	5	
149	T	V	V	V	A	L	D	L	Q	G	5	
161	F	P	Y	F	P	R	L	G	R	Y	5	
176	E	A	Q	Q	A	C	L	D	Q	D	5	
189	A	S	F	D	Q	L	Y	D	A	W	5	
195	Y	D	A	W	R	G	G	L	D	W	5	
204	W	C	N	A	G	W	L	S	D	G	5	
205	C	N	A	G	W	L	S	D	G	S	5	
208	G	W	L	S	D	G	S	V	Q	Y	5	
215	V	Q	Y	P	I	T	K	P	R	E	5	
218	P	I	T	K	P	R	E	P	C	G	5	
234	G	V	R	N	Y	G	F	W	D	K	5	
249	D	V	F	C	F	T	S	N	F	N	5	

TABLE XXXVI 151P3D4 v.1: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
253	F	T	S	N	F	N	G	R	F	Y	5	
266	H	P	T	K	L	T	Y	D	E	A	5	
304	C	D	A	G	W	L	A	D	G	S	5	
307	G	W	L	A	D	G	S	V	R	Y	5	
312	G	S	V	R	Y	P	I	S	R	P	5	
313	S	V	R	Y	P	I	S	R	P	R	5	
314	V	R	Y	P	I	S	R	P	R	R	5	
317	P	I	S	R	P	R	R	R	C	S	5	
322	R	R	R	C	S	P	T	E	A	A	5	
328	T	E	A	A	V	R	F	V	G	F	5	
341	K	H	K	L	Y	G	V	Y	C	F	5	
20	D	N	Y	T	L	D	H	D	R	A	4	
30	I	H	I	Q	A	E	N	G	P	H	4	
41	L	V	E	A	E	Q	A	K	V	F	4	
46	Q	A	K	V	F	S	H	R	G	G	4	
54	G	G	N	V	T	L	P	C	K	F	4	
62	K	F	Y	R	D	P	T	A	F	G	4	
81	W	T	K	L	T	S	D	Y	L	K	4	
94	V	F	V	S	M	G	Y	H	K	K	4	
127	T	D	L	T	L	E	D	Y	G	R	4	
137	Y	K	C	E	V	I	E	G	L	E	4	
139	C	E	V	I	E	G	L	E	D	D	4	
172	L	N	F	H	E	A	Q	Q	A	C	4	
190	S	F	D	Q	L	Y	D	A	W	R	4	
197	A	W	R	G	G	L	D	W	C	N	4	
214	S	V	Q	Y	P	I	T	K	P	R	4	
217	Y	P	I	T	K	P	R	E	P	C	4	
228	G	Q	N	T	V	P	G	V	R	N	4	
238	Y	G	F	W	D	K	D	K	S	R	4	
245	K	S	R	Y	D	V	F	C	F	T	4	
251	F	C	F	T	S	N	F	N	G	R	4	
268	T	K	L	T	Y	D	E	A	V	Q	4	
276	V	Q	A	C	L	N	D	G	A	Q	4	
282	D	G	A	Q	I	A	K	V	G	Q	4	
284	A	Q	I	A	K	V	G	Q	I	F	4	
316	Y	P	I	S	R	P	R	R	R	C	4	
324	R	C	S	P	T	E	A	A	V	R	4	
332	V	R	F	V	G	F	P	D	K	K	4	
13	C	W	A	D	H	L	S	D	N	Y	3	
19	S	D	N	Y	T	L	D	H	D	R	3	
25	D	H	D	R	A	I	H	I	Q	A	3	
38	P	H	L	L	V	E	A	E	Q	A	3	
52	H	R	G	G	N	V	T	L	P	C	3	
56	N	V	T	L	P	C	K	F	Y	R	3	
63	F	Y	R	D	P	T	A	F	G	S	3	
74	I	H	K	I	R	I	K	W	T	K	3	
79	I	K	W	T	K	L	T	S	D	Y	3	
98	M	G	Y	H	K	K	T	Y	G	G	3	
134	Y	G	R	Y	K	C	E	V	I	E	3	
138	K	C	E	V	I	E	G	L	E	D	3	
146	E	D	D	T	V	V	V	A	L	D	3	
156	L	Q	G	V	V	F	P	Y	F	P	3	
175	H	E	A	Q	Q	A	C	L	D	Q	3	

TABLE XXXVI 151P3D4 v.1: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
202	L	D	W	C	N	A	G	W	L	S	3	
207	A	G	W	L	S	D	G	S	V	Q	3	
221	K	P	R	E	P	C	G	G	Q	N	3	
229	Q	N	T	V	P	G	V	R	N	Y	3	
235	V	R	N	Y	G	F	W	D	K	D	3	
239	G	F	W	D	K	D	K	S	R	Y	3	
244	D	K	S	R	Y	D	V	F	C	F	3	
258	N	G	R	F	Y	Y	L	I	H	P	3	
260	R	F	Y	Y	L	I	H	P	T	K	3	
265	I	H	P	T	K	L	T	Y	D	E	3	
306	A	G	W	L	A	D	G	S	V	R	3	
310	A	D	G	S	V	R	Y	P	I	S	3	
320	R	P	R	R	R	C	S	P	T	E	3	
321	P	R	R	R	C	S	P	T	E	A	3	
333	R	F	V	G	F	P	D	K	K	H	3	
334	F	V	G	F	P	D	K	K	H	K	3	
340	K	K	H	K	L	Y	G	V	Y	C	3	
344	L	Y	G	V	Y	C	F	R	A	Y	3	
345	Y	G	V	Y	C	F	R	A	Y	N	3	
44	A	E	Q	A	K	V	F	S	H	R	2	
47	A	K	V	F	S	H	R	G	G	N	2	
60	P	C	K	F	Y	R	D	P	T	A	2	
67	P	T	A	F	G	S	G	I	H	K	2	
91	E	V	D	V	F	V	S	M	G	Y	2	
99	G	Y	H	K	K	T	Y	G	G	Y	2	
104	T	Y	G	G	Y	Q	G	R	V	F	2	
110	G	R	V	F	L	K	G	G	S	D	2	
160	V	F	P	Y	F	P	R	L	G	R	2	
164	F	P	R	L	G	R	Y	N	L	N	2	
165	P	R	L	G	R	Y	N	L	N	F	2	
169	R	Y	N	L	N	F	H	E	A	Q	2	
184	Q	D	A	V	I	A	S	F	D	Q	2	
194	L	Y	D	A	W	R	G	G	L	D	2	
199	R	G	G	L	D	W	C	N	A	G	2	
203	D	W	C	N	A	G	W	L	S	D	2	
216	Q	Y	P	I	T	K	P	R	E	P	2	
222	P	R	E	P	C	G	G	Q	N	T	2	
236	R	N	Y	G	F	W	D	K	D	K	2	
243	K	D	K	S	R	Y	D	V	F	C	2	
247	R	Y	D	V	F	C	F	T	S	N	2	
257	F	N	G	R	F	Y	Y	L	I	H	2	
273	D	E	A	V	Q	A	C	L	N	D	2	
296	W	K	I	L	G	Y	D	R	C	D	2	
302	D	R	C	D	A	G	W	L	A	D	2	
325	C	S	P	T	E	A	A	V	R	F	2	
337	F	P	D	K	K	H	K	L	Y	G	2	
16	D	H	L	S	D	N	Y	T	L	D	1	
61	C	K	F	Y	R	D	P	T	A	F	1	
69	A	F	G	S	G	I	H	K	I	R	1	
100	Y	H	K	K	T	Y	G	G	Y	Q	1	
109	Q	G	R	V	F	L	K	G	G	S	1	
167	L	G	R	Y	N	L	N	F	H	E	1	
191	F	D	Q	L	Y	D	A	W	R	G	1	

TABLE XXXVI 151P3D4 v.1: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
192	D	Q	L	Y	D	A	W	R	G	G	1	
212	D	G	S	V	Q	Y	P	I	T	K	1	
220	T	K	P	R	E	P	C	G	G	Q	1	
225	P	C	G	G	Q	N	T	V	P	G	1	
227	G	G	Q	N	T	V	P	G	V	R	1	
232	V	P	G	V	R	N	Y	G	F	W	1	
237	N	Y	G	F	W	D	K	D	K	S	1	
240	F	W	D	K	D	K	S	R	Y	D	1	
248	Y	D	V	F	C	F	T	S	N	F	1	
272	Y	D	E	A	V	Q	A	C	L	N	1	
295	A	W	K	I	L	G	Y	D	R	C	1	
311	D	G	S	V	R	Y	P	I	S	R	1	
336	G	F	P	D	K	K	H	K	L	Y	1	
342	H	K	L	Y	G	V	Y	C	F	R	1	
183	D	Q	D	A	V	I	A	S	F	D	-1	
224	E	P	C	G	G	Q	N	T	V	P	-1	
242	D	K	D	K	S	R	Y	D	V	F	-1	
252	C	F	T	S	N	F	N	G	R	F	-1	
281	N	D	G	A	Q	I	A	K	V	G	-1	
66	D	P	T	A	F	G	S	G	I	H	-2	
339	D	K	K	H	K	L	Y	G	V	Y	-2	
233	P	G	V	R	N	Y	G	F	W	D	-3	

TABLE XXXVI 151P3D4 v.2: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
37	L	L	V	P	T	K	V	T	G	I	27	
87	V	L	L	G	R	K	A	V	V	V	27	
377	G	A	L	W	K	A	I	E	S	L	23	
12	R	A	L	H	I	V	V	E	S	I	20	
28	K	M	K	Q	D	K	K	V	D	L	20	
381	K	A	I	E	S	L	E	E	G	L	20	
86	K	V	L	L	G	R	K	A	V	V	19	
278	A	A	S	P	A	A	W	L	P	L	19	
5	T	T	K	T	F	P	L	R	A	L	18	
88	L	L	G	R	K	A	V	V	V	S	18	
233	G	F	I	F	K	T	I	A	P	L	18	
269	A	L	S	A	R	A	P	V	P	A	18	
369	D	L	A	G	S	G	Y	C	G	A	18	
7	K	T	F	P	L	R	A	L	H	I	17	
20	S	I	R	D	H	S	G	Q	K	M	17	
34	K	V	D	L	L	V	P	T	K	V	17	
183	T	L	E	E	K	R	K	E	K	A	17	
241	P	L	A	A	T	R	A	T	R	I	17	
361	Y	V	E	N	G	R	P	A	D	L	17	
370	L	A	G	S	G	Y	C	G	A	L	17	
56	H	V	Q	F	V	G	S	Y	K	L	16	
67	Y	S	N	D	G	E	H	W	T	V	16	
164	V	C	L	S	G	A	P	H	E	V	16	
238	T	I	A	P	L	A	A	T	R	A	16	
8	T	F	P	L	R	A	L	H	I	V	15	
29	M	K	Q	D	K	K	V	D	L	L	15	

TABLE XXXVI 151P3D4 v.2: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
36	D	L	L	V	P	T	K	V	T	G	15	
51	A	K	D	F	G	H	V	Q	F	V	15	
103	I	S	G	S	F	C	R	N	K	L	15	
106	S	F	C	R	N	K	L	K	Y	L	15	
109	R	N	K	L	K	Y	L	A	F	L	15	
175	W	K	Y	Q	A	V	T	A	T	L	15	
196	Y	R	K	N	K	Q	L	M	R	L	15	
223	S	P	G	G	G	S	P	R	G	L	15	
226	G	G	S	P	R	G	L	G	F	I	15	
234	F	I	F	K	T	I	A	P	L	A	15	
276	V	P	A	A	S	P	A	A	W	L	15	
385	S	L	E	E	G	L	G	G	K	Q	15	
389	G	L	G	G	K	Q	K	D	K	E	15	
399	R	K	A	E	N	G	P	H	L	L	15	
38	L	V	P	T	K	V	T	G	I	I	14	
64	K	L	A	Y	S	N	D	G	E	H	14	
92	K	A	V	V	V	S	C	E	G	I	14	
155	G	H	A	S	E	A	Y	K	K	V	14	
202	L	M	R	L	Q	K	Q	A	E	K	14	
231	G	L	G	F	I	F	K	T	I	A	14	
270	L	S	A	R	A	P	V	P	A	A	14	
306	S	L	S	P	Y	G	P	R	N	P	14	
9	F	P	L	R	A	L	H	I	V	V	13	
10	P	L	R	A	L	H	I	V	V	E	13	
94	V	V	V	S	C	E	G	I	N	I	13	
114	Y	L	A	F	L	H	K	R	M	N	13	
157	A	S	E	A	Y	K	K	V	C	L	13	
171	H	E	V	G	W	K	Y	Q	A	V	13	
193	E	I	H	Y	R	K	N	K	Q	L	13	
204	R	L	Q	K	Q	A	E	K	N	M	13	
230	R	G	L	G	F	I	F	K	T	I	13	
261	G	S	S	A	H	R	P	P	A	L	13	
263	S	A	H	R	P	P	A	L	S	A	13	
298	P	T	S	S	S	T	Y	D	S	L	13	
320	R	H	S	P	S	G	G	G	G	L	13	
335	H	C	Q	G	Q	K	H	N	V	L	13	
343	V	L	A	R	G	K	P	Q	R	K	13	
373	S	G	Y	C	G	A	L	W	K	A	13	
378	A	L	W	K	A	I	E	S	L	E	13	
2	L	E	H	T	T	K	T	F	P	L	12	
11	L	R	A	L	H	I	V	V	E	S	12	
13	A	L	H	I	V	V	E	S	I	R	12	
15	H	I	V	V	E	S	I	R	D	H	12	
30	K	Q	D	K	K	V	D	L	L	V	12	
165	C	L	S	G	A	P	H	E	V	G	12	
201	Q	L	M	R	L	Q	K	Q	A	E	12	
208	Q	A	E	K	N	M	K	K	K	I	12	
284	W	L	P	L	R	T	P	W	T	R	12	
307	L	S	P	Y	G	P	R	N	P	L	12	
26	G	Q	K	M	K	Q	D	K	K	V	11	
42	K	V	T	G	I	I	T	Q	G	A	11	
59	F	V	G	S	Y	K	L	A	Y	S	11	
78	Q	D	E	K	Q	R	K	D	K	V	11	

TABLE XXXVI 151P3D4 v.2: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
115	L	A	F	L	H	K	R	M	N	T	11	
117	F	L	H	K	R	M	N	T	N	P	11	
182	A	T	L	E	E	K	R	K	E	K	11	
236	F	K	T	I	A	P	L	A	A	T	11	
237	K	T	I	A	P	L	A	A	T	R	11	
239	I	A	P	L	A	A	T	R	A	T	11	
267	P	P	A	L	S	A	R	A	P	V	11	
283	A	W	L	P	L	R	T	P	W	T	11	
328	G	L	K	K	P	A	R	H	C	Q	11	
334	R	H	C	Q	G	Q	K	H	N	V	11	
374	G	Y	C	G	A	L	W	K	A	I	11	
45	G	I	I	T	Q	G	A	K	D	F	10	
48	T	Q	G	A	K	D	F	G	H	V	10	
89	L	G	R	K	A	V	V	V	S	C	10	
95	V	V	S	C	E	G	I	N	I	S	10	
100	G	I	N	I	S	G	S	F	C	R	10	
102	N	I	S	G	S	F	C	R	N	K	10	
111	K	L	K	Y	L	A	F	L	H	K	10	
112	L	K	Y	L	A	F	L	H	K	R	10	
160	A	Y	K	K	V	C	L	S	G	A	10	
167	S	G	A	P	H	E	V	G	W	K	10	
173	V	G	W	K	Y	Q	A	V	T	A	10	
178	Q	A	V	T	A	T	L	E	E	K	10	
212	N	M	K	K	K	I	D	K	Y	T	10	
244	A	T	R	A	T	R	I	G	H	P	10	
249	R	I	G	H	P	G	G	R	T	P	10	
272	A	R	A	P	V	P	A	A	S	P	10	
274	A	P	V	P	A	A	S	P	A	A	10	
344	L	A	R	G	K	P	Q	R	K	P	10	
1	M	L	E	H	T	T	K	T	F	P	9	
33	K	K	V	D	L	L	V	P	T	K	9	
46	I	I	T	Q	G	A	K	D	F	G	9	
47	I	T	Q	G	A	K	D	F	G	H	9	
80	E	K	Q	R	K	D	K	V	L	L	9	
85	D	K	V	L	L	G	R	K	A	V	9	
121	R	M	N	T	N	P	S	R	R	P	9	
137	S	R	I	F	W	R	Q	E	K	A	9	
138	R	I	F	W	R	Q	E	K	A	D	9	
216	K	I	D	K	Y	T	E	S	P	G	9	
264	A	H	R	P	P	A	L	S	A	R	9	
271	S	A	R	A	P	V	P	A	A	S	9	
280	S	P	A	A	W	L	P	L	R	T	9	
281	P	A	A	W	L	P	L	R	T	P	9	
291	W	T	R	P	S	S	C	P	T	S	9	
302	S	T	Y	D	S	L	S	P	Y	G	9	
353	P	K	S	E	N	N	S	W	Y	V	9	
364	N	G	R	P	A	D	L	A	G	S	9	
382	A	I	E	S	L	E	E	G	L	G	9	
4	H	T	T	K	T	F	P	L	R	A	8	
16	I	V	V	E	S	I	R	D	H	S	8	
32	D	K	K	V	D	L	L	V	P	T	8	
97	S	C	E	G	I	N	I	S	G	S	8	
123	N	T	N	P	S	R	R	P	Y	H	8	

TABLE XXXVI 151P3D4 v.2: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
129	R	P	Y	H	F	Q	V	P	S	R	8	
150	S	C	C	P	Q	G	H	A	S	E	8	
174	G	W	K	Y	Q	A	V	T	A	T	8	
185	E	E	K	R	K	E	K	A	E	I	8	
211	K	N	M	K	K	K	I	D	K	Y	8	
240	A	P	L	A	A	T	R	A	T	R	8	
242	L	A	A	T	R	A	T	R	I	G	8	
248	T	R	I	G	H	P	G	G	R	T	8	
251	G	H	P	G	G	R	T	P	R	A	8	
255	G	R	T	P	R	A	G	S	S	A	8	
265	H	R	P	P	A	L	S	A	R	A	8	
273	R	A	P	V	P	A	A	S	P	A	8	
316	L	P	N	P	R	H	S	P	S	G	8	
362	V	E	N	G	R	P	A	D	L	A	8	
380	W	K	A	I	E	S	L	E	E	G	8	
17	V	V	E	S	I	R	D	H	S	G	7	
50	G	A	K	D	F	G	H	V	Q	F	7	
54	F	G	H	V	Q	F	V	G	S	Y	7	
65	L	A	Y	S	N	D	G	E	H	W	7	
66	A	Y	S	N	D	G	E	H	W	T	7	
79	D	E	K	Q	R	K	D	K	V	L	7	
116	A	F	L	H	K	R	M	N	T	N	7	
126	P	S	R	R	P	Y	H	F	Q	V	7	
133	F	Q	V	P	S	R	I	F	W	R	7	
145	K	A	D	G	G	S	C	C	P	Q	7	
158	S	E	A	Y	K	K	V	C	L	S	7	
168	G	A	P	H	E	V	G	W	K	Y	7	
172	E	V	G	W	K	Y	Q	A	V	T	7	
177	Y	Q	A	V	T	A	T	L	E	E	7	
179	A	V	T	A	T	L	E	E	K	R	7	
192	A	E	I	H	Y	R	K	N	K	Q	7	
194	I	H	Y	R	K	N	K	Q	L	M	7	
220	Y	T	E	S	P	G	G	G	S	P	7	
229	P	R	G	L	G	F	I	F	K	T	7	
235	I	F	K	T	I	A	P	L	A	A	7	
247	A	T	R	I	G	H	P	G	G	R	7	
260	A	G	S	S	A	H	R	P	P	A	7	
279	A	S	P	A	A	W	L	P	L	R	7	
282	A	A	W	L	P	L	R	T	P	W	7	
286	P	L	R	T	P	W	T	R	P	S	7	
310	Y	G	P	R	N	P	L	P	N	P	7	
314	N	P	L	P	N	P	R	H	S	P	7	
315	P	L	P	N	P	R	H	S	P	S	7	
322	S	P	S	G	G	G	G	L	K	K	7	
324	S	G	G	G	G	L	K	K	P	A	7	
342	N	V	L	A	R	G	K	P	Q	R	7	
355	S	E	N	N	S	W	Y	V	E	N	7	
359	S	W	Y	V	E	N	G	R	P	A	7	
392	G	K	Q	K	D	K	E	R	K	A	7	
398	E	R	K	A	E	N	G	P	H	L	7	
35	V	D	L	L	V	P	T	K	V	T	6	
40	P	T	K	V	T	G	I	I	T	Q	6	
43	V	T	G	I	I	T	Q	G	A	K	6	

TABLE XXXVI 151P3D4 v.2: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
44	T	G	I	I	T	Q	G	A	K	D	6	
81	K	Q	R	K	D	K	V	L	L	G	6	
82	Q	R	K	D	K	V	L	L	G	R	6	
84	K	D	K	V	L	L	G	R	K	A	6	
93	A	V	V	V	S	C	E	G	I	N	6	
107	F	C	R	N	K	L	K	Y	L	A	6	
113	K	Y	L	A	F	L	H	K	R	M	6	
151	C	C	P	Q	G	H	A	S	E	A	6	
163	K	V	C	L	S	G	A	P	H	E	6	
180	V	T	A	T	L	E	E	K	R	K	6	
199	N	K	Q	L	M	R	L	Q	K	Q	6	
200	K	Q	L	M	R	L	Q	K	Q	A	6	
207	K	Q	A	E	K	N	M	K	K	K	6	
215	K	K	I	D	K	Y	T	E	S	P	6	
243	A	A	T	R	A	T	R	I	G	H	6	
262	S	S	A	H	R	P	P	A	L	S	6	
287	L	R	T	P	W	T	R	P	S	S	6	
288	R	T	P	W	T	R	P	S	S	C	6	
295	S	S	C	P	T	S	S	S	T	Y	6	
308	S	P	Y	G	P	R	N	P	L	P	6	
336	C	Q	G	Q	K	H	N	V	L	A	6	
337	Q	G	Q	K	H	N	V	L	A	R	6	
338	G	Q	K	H	N	V	L	A	R	G	6	
371	A	G	S	G	Y	C	G	A	L	W	6	
384	E	S	L	E	E	G	L	G	G	K	6	
57	V	Q	F	V	G	S	Y	K	L	A	5	
63	Y	K	L	A	Y	S	N	D	G	E	5	
75	T	V	Y	Q	D	E	K	Q	R	K	5	
96	V	S	C	E	G	I	N	I	S	G	5	
105	G	S	F	C	R	N	K	L	K	Y	5	
139	I	F	W	R	Q	E	K	A	D	G	5	
146	A	D	G	G	S	C	C	P	Q	G	5	
148	G	G	S	C	C	P	Q	G	H	A	5	
156	H	A	S	E	A	Y	K	K	V	C	5	
159	E	A	Y	K	K	V	C	L	S	G	5	
166	L	S	G	A	P	H	E	V	G	W	5	
181	T	A	T	L	E	E	K	R	K	E	5	
246	R	A	T	R	I	G	H	P	G	G	5	
256	R	T	P	R	A	G	S	S	A	H	5	
300	S	S	S	T	Y	D	S	L	S	P	5	
325	G	G	G	G	L	K	K	P	A	R	5	
368	A	D	L	A	G	S	G	Y	C	G	5	
14	L	H	I	V	V	E	S	I	R	D	4	
25	S	G	Q	K	M	K	Q	D	K	K	4	
31	Q	D	K	K	V	D	L	L	V	P	4	
39	V	P	T	K	V	T	G	I	I	T	4	
41	T	K	V	T	G	I	I	T	Q	G	4	
52	K	D	F	G	H	V	Q	F	V	G	4	
58	Q	F	V	G	S	Y	K	L	A	Y	4	
68	S	N	D	G	E	H	W	T	V	Y	4	
69	N	D	G	E	H	W	T	V	Y	Q	4	
76	V	Y	Q	D	E	K	Q	R	K	D	4	
83	R	K	D	K	V	L	L	G	R	K	4	

TABLE XXXVI 151P3D4 v.2: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
90	G	R	K	A	V	V	V	S	C	E	4	
91	R	K	A	V	V	V	S	C	E	G	4	
101	I	N	I	S	G	S	F	C	R	N	4	
127	S	R	R	P	Y	H	F	Q	V	P	4	
130	P	Y	H	F	Q	V	P	S	R	I	4	
134	Q	V	P	S	R	I	F	W	R	Q	4	
188	R	K	E	K	A	E	I	H	Y	R	4	
203	M	R	L	Q	K	Q	A	E	K	N	4	
228	S	P	R	G	L	G	F	I	F	K	4	
232	L	G	F	I	F	K	T	I	A	P	4	
250	I	G	H	P	G	G	R	T	P	R	4	
259	R	A	G	S	S	A	H	R	P	P	4	
268	P	A	L	S	A	R	A	P	V	P	4	
275	P	V	P	A	A	S	P	A	A	W	4	
285	L	P	L	R	T	P	W	T	R	P	4	
301	S	S	T	Y	D	S	L	S	P	Y	4	
323	P	S	G	G	G	G	L	K	K	P	4	
340	K	H	N	V	L	A	R	G	K	P	4	
346	R	G	K	P	Q	R	K	P	K	S	4	
360	W	Y	V	E	N	G	R	P	A	D	4	
366	R	P	A	D	L	A	G	S	G	Y	4	
375	Y	C	G	A	L	W	K	A	I	E	4	
376	C	G	A	L	W	K	A	I	E	S	4	
379	L	W	K	A	I	E	S	L	E	E	4	
383	I	E	S	L	E	E	G	L	G	G	4	
394	Q	K	D	K	E	R	K	A	E	N	4	
49	Q	G	A	K	D	F	G	H	V	Q	3	
60	V	G	S	Y	K	L	A	Y	S	N	3	
70	D	G	E	H	W	T	V	Y	Q	D	3	
77	Y	Q	D	E	K	Q	R	K	D	K	3	
108	C	R	N	K	L	K	Y	L	A	F	3	
119	H	K	R	M	N	T	N	P	S	R	3	
131	Y	H	F	Q	V	P	S	R	I	F	3	
141	W	R	Q	E	K	A	D	G	G	S	3	
149	G	S	C	C	P	Q	G	H	A	S	3	
152	C	P	Q	G	H	A	S	E	A	Y	3	
154	Q	G	H	A	S	E	A	Y	K	K	3	
162	K	K	V	C	L	S	G	A	P	H	3	
169	A	P	H	E	V	G	W	K	Y	Q	3	
190	E	K	A	E	I	H	Y	R	K	N	3	
191	K	A	E	I	H	Y	R	K	N	K	3	
219	K	Y	T	E	S	P	G	G	G	S	3	
225	G	G	G	S	P	R	G	L	G	F	3	
245	T	R	A	T	R	I	G	H	P	G	3	
252	H	P	G	G	R	T	P	R	A	G	3	
254	G	G	R	T	P	R	A	G	S	S	3	
277	P	A	A	S	P	A	A	W	L	P	3	
294	P	S	S	C	P	T	S	S	S	T	3	
326	G	G	G	L	K	K	P	A	R	H	3	
327	G	G	L	K	K	P	A	R	H	C	3	
329	L	K	K	P	A	R	H	C	Q	G	3	
331	K	P	A	R	H	C	Q	G	Q	K	3	
332	P	A	R	H	C	Q	G	Q	K	H	3	

TABLE XXXVI 151P3D4 v.2: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
348	K	P	Q	R	K	P	K	S	E	N	3	
351	R	K	P	K	S	E	N	N	S	W	3	
365	G	R	P	A	D	L	A	G	S	G	3	
390	L	G	G	K	Q	K	D	K	E	R	3	
18	V	E	S	I	R	D	H	S	G	Q	2	
22	R	D	H	S	G	Q	K	M	K	Q	2	
53	D	F	G	H	V	Q	F	V	G	S	2	
61	G	S	Y	K	L	A	Y	S	N	D	2	
62	S	Y	K	L	A	Y	S	N	D	G	2	
74	W	T	V	Y	Q	D	E	K	Q	R	2	
98	C	E	G	I	N	I	S	G	S	F	2	
110	N	K	L	K	Y	L	A	F	L	H	2	
118	L	H	K	R	M	N	T	N	P	S	2	
120	K	R	M	N	T	N	P	S	R	R	2	
140	F	W	R	Q	E	K	A	D	G	G	2	
161	Y	K	K	V	C	L	S	G	A	P	2	
187	K	R	K	E	K	A	E	I	H	Y	2	
205	L	Q	K	Q	A	E	K	N	M	K	2	
206	Q	K	Q	A	E	K	N	M	K	K	2	
213	M	K	K	K	I	D	K	Y	T	E	2	
214	K	K	K	I	D	K	Y	T	E	S	2	
217	I	D	K	Y	T	E	S	P	G	G	2	
221	T	E	S	P	G	G	G	S	P	R	2	
257	T	P	R	A	G	S	S	A	H	R	2	
258	P	R	A	G	S	S	A	H	R	P	2	
292	T	R	P	S	S	C	P	T	S	S	2	
293	R	P	S	S	C	P	T	S	S	S	2	
296	S	C	P	T	S	S	S	T	Y	D	2	
303	T	Y	D	S	L	S	P	Y	G	P	2	
304	Y	D	S	L	S	P	Y	G	P	R	2	
305	D	S	L	S	P	Y	G	P	R	N	2	
311	G	P	R	N	P	L	P	N	P	R	2	
330	K	K	P	A	R	H	C	Q	G	Q	2	
347	G	K	P	Q	R	K	P	K	S	E	2	
350	Q	R	K	P	K	S	E	N	N	S	2	
356	E	N	N	S	W	Y	V	E	N	G	2	
357	N	N	S	W	Y	V	E	N	G	R	2	
386	L	E	E	G	L	G	G	K	Q	K	2	
395	K	D	K	E	R	K	A	E	N	G	2	
21	I	R	D	H	S	G	Q	K	M	K	1	
55	G	H	V	Q	F	V	G	S	Y	K	1	
71	G	E	H	W	T	V	Y	Q	D	E	1	
73	H	W	T	V	Y	Q	D	E	K	Q	1	
124	T	N	P	S	R	R	P	Y	H	F	1	
125	N	P	S	R	R	P	Y	H	F	Q	1	
128	R	R	P	Y	H	F	Q	V	P	S	1	
135	V	P	S	R	I	F	W	R	Q	E	1	
142	R	Q	E	K	A	D	G	G	S	C	1	
170	P	H	E	V	G	W	K	Y	Q	A	1	
176	K	Y	Q	A	V	T	A	T	L	E	1	
184	L	E	E	K	R	K	E	K	A	E	1	
189	K	E	K	A	E	I	H	Y	R	K	1	
195	H	Y	R	K	N	K	Q	L	M	R	1	

TABLE XXXVI 151P3D4 v.2: HLA Peptide Scoring Results A*0201 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
197	R	K	N	K	Q	L	M	R	L	Q	1	
198	K	N	K	Q	L	M	R	L	Q	K	1	
218	D	K	Y	T	E	S	P	G	G	G	1	
227	G	S	P	R	G	L	G	F	I	F	1	
266	R	P	P	A	L	S	A	R	A	P	1	
289	T	P	W	T	R	P	S	S	C	P	1	
312	P	R	N	P	L	P	N	P	R	H	1	
318	N	P	R	H	S	P	S	G	G	G	1	
333	A	R	H	C	Q	G	Q	K	H	N	1	
339	Q	K	H	N	V	L	A	R	G	K	1	
345	A	R	G	K	P	Q	R	K	P	K	1	
354	K	S	E	N	N	S	W	Y	V	E	1	
367	P	A	D	L	A	G	S	G	Y	C	1	
372	G	S	G	Y	C	G	A	L	W	K	1	
393	K	Q	K	D	K	E	R	K	A	E	1	
397	K	E	R	K	A	E	N	G	P	H	1	
19	E	S	I	R	D	H	S	G	Q	K	-1	
99	E	G	I	N	I	S	G	S	F	C	-1	
122	M	N	T	N	P	S	R	R	P	Y	-1	
136	P	S	R	I	F	W	R	Q	E	K	-1	
143	Q	E	K	A	D	G	G	S	C	C	-1	
153	P	Q	G	H	A	S	E	A	Y	K	-1	
224	P	G	G	G	S	P	R	G	L	G	-1	
341	H	N	V	L	A	R	G	K	P	Q	-1	
363	E	N	G	R	P	A	D	L	A	G	-1	
387	E	E	G	L	G	G	K	Q	K	D	-1	
210	E	K	N	M	K	K	K	I	D	K	-2	
317	P	N	P	R	H	S	P	S	G	G	-2	
319	P	R	H	S	P	S	G	G	G	G	-2	
3	E	H	T	T	K	T	F	P	L	R	-3	
186	E	K	R	K	E	K	A	E	I	H	-3	
349	P	Q	R	K	P	K	S	E	N	N	-3	

TABLE XXXVII 151P3D4 v.1: HLA Peptide Scoring Results A*0202 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
293	F	A	A	W	K	I	L	G	Y	D	5	
329	E	A	A	V	R	F	V	G	F	P	5	
13	C	W	A	D	H	L	S	D	N	Y	3	
27	D	R	A	I	H	I	Q	A	E	N	3	
32	I	Q	A	E	N	G	P	H	L	L	3	
42	V	E	A	E	Q	A	K	V	F	S	3	
45	E	Q	A	K	V	F	S	H	R	G	3	
67	P	T	A	F	G	S	G	I	H	K	3	
120	S	D	A	S	L	V	I	T	D	L	3	
151	V	V	A	L	D	L	Q	G	V	V	3	
175	H	E	A	Q	Q	A	C	L	D	Q	3	
178	Q	Q	A	C	L	D	Q	D	A	V	3	
184	Q	D	A	V	I	A	S	F	D	Q	3	
187	V	I	A	S	F	D	Q	L	Y	D	3	
195	Y	D	A	W	R	G	G	L	D	W	3	
205	C	N	A	G	W	L	S	D	G	S	3	
273	D	E	A	V	Q	A	C	L	N	D	3	
276	V	Q	A	C	L	N	D	G	A	Q	3	
282	D	G	A	Q	I	A	K	V	G	Q	3	
285	Q	I	A	K	V	G	Q	I	F	A	3	
292	I	F	A	A	W	K	I	L	G	Y	3	
294	A	A	W	K	I	L	G	Y	D	R	3	
304	C	D	A	G	W	L	A	D	G	S	3	
308	W	L	A	D	G	S	V	R	Y	P	3	
328	T	E	A	A	V	R	F	V	G	F	3	
330	A	A	V	R	F	V	G	F	P	D	3	
14	W	A	D	H	L	S	D	N	Y	T	2	
28	R	A	I	H	I	Q	A	E	N	G	2	
33	Q	A	E	N	G	P	H	L	L	V	2	
43	E	A	E	Q	A	K	V	F	S	H	2	
46	Q	A	K	V	F	S	H	R	G	G	2	
68	T	A	F	G	S	G	I	H	K	I	2	
121	D	A	S	L	V	I	T	D	L	T	2	
152	V	A	L	D	L	Q	G	V	V	F	2	
176	E	A	Q	Q	A	C	L	D	Q	D	2	
179	Q	A	C	L	D	Q	D	A	V	I	2	
185	D	A	V	I	A	S	F	D	Q	L	2	
188	I	A	S	F	D	Q	L	Y	D	A	2	
196	D	A	W	R	G	G	L	D	W	C	2	
206	N	A	G	W	L	S	D	G	S	V	2	
274	E	A	V	Q	A	C	L	N	D	G	2	
277	Q	A	C	L	N	D	G	A	Q	I	2	
283	G	A	Q	I	A	K	V	G	Q	I	2	
286	I	A	K	V	G	Q	I	F	A	A	2	
305	D	A	G	W	L	A	D	G	S	V	2	
309	L	A	D	G	S	V	R	Y	P	I	2	
15	A	D	H	L	S	D	N	Y	T	L	1	
29	A	I	H	I	Q	A	E	N	G	P	1	
34	A	E	N	G	P	H	L	L	V	E	1	
44	A	E	Q	A	K	V	F	S	H	R	1	
47	A	K	V	F	S	H	R	G	G	N	1	
69	A	F	G	S	G	I	H	K	I	R	1	
122	A	S	L	V	I	T	D	L	T	L	1	
153	A	L	D	L	Q	G	V	V	F	P	1	
177	A	Q	Q	A	C	L	D	Q	D	A	1	
180	A	C	L	D	Q	D	A	V	I	A	1	
186	A	V	I	A	S	F	D	Q	L	Y	1	
189	A	S	F	D	Q	L	Y	D	A	W	1	
197	A	W	R	G	G	L	D	W	C	N	1	
207	A	G	W	L	S	D	G	S	V	Q	1	
275	A	V	Q	A	C	L	N	D	G	A	1	
278	A	C	L	N	D	G	A	Q	I	A	1	
284	A	Q	I	A	K	V	G	Q	I	F	1	
287	A	K	V	G	Q	I	F	A	A	W	1	
295	A	W	K	I	L	G	Y	D	R	C	1	
306	A	G	W	L	A	D	G	S	V	R	1	
310	A	D	G	S	V	R	Y	P	I	S	1	
331	A	V	R	F	V	G	F	P	D	K	1	

TABLE XXXVII 151P3D4 v.2: HLA Peptide Scoring Results A*0202 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
242	L	A	A	T	R	A	T	R	I	G	5	
277	P	A	A	S	P	A	A	W	L	P	5	
281	P	A	A	W	L	P	L	R	T	P	5	
272	A	R	A	P	V	P	A	A	S	P	4	
11	L	R	A	L	H	I	V	V	E	S	3	
49	Q	G	A	K	D	F	G	H	V	Q	3	
64	K	L	A	Y	S	N	D	G	E	H	3	
91	R	K	A	V	V	V	S	C	E	G	3	
114	Y	L	A	F	L	H	K	R	M	N	3	
144	E	K	A	D	G	G	S	C	C	P	3	
155	G	H	A	S	E	A	Y	K	K	V	3	
158	S	E	A	Y	K	K	V	C	L	S	3	
167	S	G	A	P	H	E	V	G	W	K	3	
177	Y	Q	A	V	T	A	T	L	E	E	3	
180	V	T	A	T	L	E	E	K	R	K	3	
190	E	K	A	E	I	H	Y	R	K	N	3	
207	K	Q	A	E	K	N	M	K	K	K	3	
238	T	I	A	P	L	A	A	T	R	A	3	
241	P	L	A	A	T	R	A	T	R	I	3	
243	A	A	T	R	A	T	R	I	G	H	3	
245	T	R	A	T	R	I	G	H	P	G	3	
258	P	R	A	G	S	S	A	H	R	P	3	
262	S	S	A	H	R	P	P	A	L	S	3	
267	P	P	A	L	S	A	R	A	P	V	3	
270	L	S	A	R	A	P	V	P	A	A	3	
276	V	P	A	A	S	P	A	A	W	L	3	
278	A	A	S	P	A	A	W	L	P	L	3	
280	S	P	A	A	W	L	P	L	R	T	3	
282	A	A	W	L	P	L	R	T	P	W	3	
331	K	P	A	R	H	C	Q	G	Q	K	3	
343	V	L	A	R	G	K	P	Q	R	K	3	
366	R	P	A	D	L	A	G	S	G	Y	3	
369	D	L	A	G	S	G	Y	C	G	A	3	
376	C	G	A	L	W	K	A	I	E	S	3	
380	W	K	A	I	E	S	L	E	E	G	3	
399	R	K	A	E	N	G	P	H	L	L	3	
12	R	A	L	H	I	V	V	E	S	I	2	
50	G	A	K	D	F	G	H	V	Q	F	2	
65	L	A	Y	S	N	D	G	E	H	W	2	
92	K	A	V	V	V	S	C	E	G	I	2	
115	L	A	F	L	H	K	R	M	N	T	2	
145	K	A	D	G	G	S	C	C	P	Q	2	
156	H	A	S	E	A	Y	K	K	V	C	2	
159	E	A	Y	K	K	V	C	L	S	G	2	
168	G	A	P	H	E	V	G	W	K	Y	2	
178	Q	A	V	T	A	T	L	E	E	K	2	
181	T	A	T	L	E	E	K	R	K	E	2	
191	K	A	E	I	H	Y	R	K	N	K	2	
208	Q	A	E	K	N	M	K	K	K	I	2	
239	I	A	P	L	A	A	T	R	A	T	2	
246	R	A	T	R	I	G	H	P	G	G	2	
259	R	A	G	S	S	A	H	R	P	P	2	
263	S	A	H	R	P	P	A	L	S	A	2	

TABLE XXXVII 151P3D4 v.2: HLA Peptide Scoring Results A*0202 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
268	P	A	L	S	A	R	A	P	V	P	2	
271	S	A	R	A	P	V	P	A	A	S	2	
273	R	A	P	V	P	A	A	S	P	A	2	
332	P	A	R	H	C	Q	G	Q	K	H	2	
344	L	A	R	G	K	P	Q	R	K	P	2	
367	P	A	D	L	A	G	S	G	Y	C	2	
370	L	A	G	S	G	Y	C	G	A	L	2	
377	G	A	L	W	K	A	I	E	S	L	2	
381	K	A	I	E	S	L	E	E	G	L	2	
13	A	L	H	I	V	V	E	S	I	R	1	
51	A	K	D	F	G	H	V	Q	F	V	1	
66	A	Y	S	N	D	G	E	H	W	T	1	
93	A	V	V	V	S	C	E	G	I	N	1	
116	A	F	L	H	K	R	M	N	T	N	1	
146	A	D	G	G	S	C	C	P	Q	G	1	
157	A	S	E	A	Y	K	K	V	C	L	1	
160	A	Y	K	K	V	C	L	S	G	A	1	
169	A	P	H	E	V	G	W	K	Y	Q	1	
179	A	V	T	A	T	L	E	E	K	R	1	
182	A	T	L	E	E	K	R	K	E	K	1	
192	A	E	I	H	Y	R	K	N	K	Q	1	
209	A	E	K	N	M	K	K	K	I	D	1	
240	A	P	L	A	A	T	R	A	T	R	1	
244	A	T	R	A	T	R	I	G	H	P	1	
247	A	T	R	I	G	H	P	G	G	R	1	
260	A	G	S	S	A	H	R	P	P	A	1	
264	A	H	R	P	P	A	L	S	A	R	1	
269	A	L	S	A	R	A	P	V	P	A	1	
274	A	P	V	P	A	A	S	P	A	A	1	
279	A	S	P	A	A	W	L	P	L	R	1	
283	A	W	L	P	L	R	T	P	W	T	1	
333	A	R	H	C	Q	G	Q	K	H	N	1	
345	A	R	G	K	P	Q	R	K	P	K	1	
368	A	D	L	A	G	S	G	Y	C	G	1	
371	A	G	S	G	Y	C	G	A	L	W	1	
378	A	L	W	K	A	I	E	S	L	E	1	
382	A	I	E	S	L	E	E	G	L	G	1	

TABLE XXXVIII 151P3D4 v.1: HLA Peptide Scoring Results A*0203 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
286	I	A	K	V	G	Q	I	F	A	A	19	
322	R	R	R	C	S	P	T	E	A	A	19	
287	A	K	V	G	Q	I	F	A	A	W	17	
323	R	R	C	S	P	T	E	A	A	V	17	
6	L	L	V	L	I	S	I	C	W	A	10	
20	D	N	Y	T	L	D	H	D	R	A	10	
25	D	H	D	R	A	I	H	I	Q	A	10	
35	E	N	G	P	H	L	L	V	E	A	10	
38	P	H	L	L	V	E	A	E	Q	A	10	
60	P	C	K	F	Y	R	D	P	T	A	10	
113	F	L	K	G	G	S	D	S	D	A	10	

TABLE XXXVIII 151P3D4 v.1: HLA Peptide Scoring Results A*0203 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
144	G L E D D T V V V A	10	
168	G R Y N L N F H E A	10	
171	N L N F H E A Q Q A	10	
177	A Q Q A C L D Q D A	10	
180	A C L D Q D A V I A	10	
188	I A S F D Q L Y D A	10	
198	W R G G L D W C N A	10	
266	H P T K L T Y D E A	10	
269	K L T Y D E A V Q A	10	
275	A V Q A C L N D G A	10	
278	A C L N D G A Q I A	10	
285	Q I A K V G Q I F A	10	
297	K I L G Y D R C D A	10	
301	Y D R C D A G W L A	10	
321	P R R R C S P T E A	10	
343	K L Y G V Y C F R A	10	
7	L V L I S I C W A D	9	
21	N Y T L D H D R A I	9	
26	H D R A I H I Q A E	9	
36	N G P H L L V E A E	9	
39	H L L V E A E Q A K	9	
61	C K F Y R D P T A F	9	
114	L K G G S D S D A S	9	
145	L E D D T V V V A L	9	
169	R Y N L N F H E A Q	9	
172	L N F H E A Q Q A C	9	
178	Q Q A C L D Q D A V	9	
181	C L D Q D A V I A S	9	
189	A S F D Q L Y D A W	9	
199	R G G L D W C N A G	9	
267	P T K L T Y D E A V	9	
270	L T Y D E A V Q A C	9	
276	V Q A C L N D G A Q	9	
279	C L N D G A Q I A K	9	
298	I L G Y D R C D A G	9	
302	D R C D A G W L A D	9	
344	L Y G V Y C F R A Y	9	
8	V L I S I C W A D H	8	
22	Y T L D H D R A I H	8	
27	D R A I H I Q A E N	8	
37	G P H L L V E A E Q	8	
40	L L V E A E Q A K V	8	
62	K F Y R D P T A F G	8	
115	K G G S D S D A S L	8	
146	E D D T V V V A L D	8	
170	Y N L N F H E A Q Q	8	
173	N F H E A Q Q A C L	8	
179	Q A C L D Q D A V I	8	
182	L D Q D A V I A S F	8	
190	S F D Q L Y D A W R	8	
200	G G L D W C N A G W	8	
268	T K L T Y D E A V Q	8	
271	T Y D E A V Q A C L	8	

TABLE XXXVIII 151P3D4 v.1: HLA Peptide Scoring Results A*0203 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
277	Q A C L N D G A Q I	8	
280	L N D G A Q I A K V	8	
288	K V G Q I F A A W K	8	
299	L G Y D R C D A G W	8	
303	R C D A G W L A D G	8	
324	R C S P T E A A V R	8	
345	Y G V Y C F R A Y N	8	

TABLE XXXVIII 151P3D4 v.2: HLA Peptide Scoring Results A*0203 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
235	I F K T I A P L A A	19	
270	L S A R A P V P A A	19	
274	A P V P A A S P A A	19	
265	H R P P A L S A R A	18	
236	F K T I A P L A A T	17	
271	S A R A P V P A A S	17	
275	P V P A A S P A A W	17	
4	H T T K T F P L R A	10	
42	K V T G I I T Q G A	10	
57	V Q F V G S Y K L A	10	
84	K D K V L L G R K A	10	
107	F C R N K L K Y L A	10	
137	S R I F W R Q E K A	10	
148	G G S C C P Q G H A	10	
151	C C P Q G H A S E A	10	
160	A Y K K V C L S G A	10	
170	P H E V G W K Y Q A	10	
173	V G W K Y Q A V T A	10	
183	T L E E K R K E K A	10	
200	K Q L M R L Q K Q A	10	
231	G L G F I F K T I A	10	
234	F I F K T I A P L A	10	
238	T I A P L A A T R A	10	
251	G H P G G R T P R A	10	
255	G R T P R A G S S A	10	
260	A G S S A H R P P A	10	
263	S A H R P P A L S A	10	
269	A L S A R A P V P A	10	
273	R A P V P A A S P A	10	
324	S G G G G L K K P A	10	
336	C Q G Q K H N V L A	10	
359	S W Y V E N G R P A	10	
362	V E N G R P A D L A	10	
369	D L A G S G Y C G A	10	
373	S G Y C G A L W K A	10	
392	G K Q K D K E R K A	10	
5	T T K T F P L R A L	9	
43	V T G I I T Q G A K	9	
58	Q F V G S Y K L A Y	9	
85	D K V L L G R K A V	9	
108	C R N K L K Y L A F	9	

TABLE XXXVIII 151P3D4 v.2: HLA Peptide Scoring Results A*0203 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
138	R I F W R Q E K A D	9	
149	G S C C P Q G H A S	9	
152	C P Q G H A S E A Y	9	
161	Y K K V C L S G A P	9	
171	H E V G W K Y Q A V	9	
174	G W K Y Q A V T A T	9	
184	L E E K R K E K A E	9	
201	Q L M R L Q K Q A E	9	
232	L G F I F K T I A P	9	
239	I A P L A A T R A T	9	
252	H P G G R T P R A G	9	
256	R T P R A G S S A H	9	
261	G S S A H R P P A L	9	
264	A H R P P A L S A R	9	
266	R P P A L S A R A P	9	
325	G G G G L K K P A R	9	
337	Q G Q K H N V L A R	9	
360	W Y V E N G R P A D	9	
363	E N G R P A D L A G	9	
370	L A G S G Y C G A L	9	
374	G Y C G A L W K A I	9	
393	K Q K D K E R K A E	9	
6	T K T F P L R A L H	8	
44	T G I I T Q G A K D	8	
59	F V G S Y K L A Y S	8	
86	K V L L G R K A V V	8	
109	R N K L K Y L A F L	8	
139	I F W R Q E K A D G	8	
150	S C C P Q G H A S E	8	
153	P Q G H A S E A Y K	8	
162	K K V C L S G A P H	8	
172	E V G W K Y Q A V T	8	
175	W K Y Q A V T A T L	8	
185	E E K R K E K A E I	8	
202	L M R L Q K Q A E K	8	
233	G F I F K T I A P L	8	
237	K T I A P L A A T R	8	
240	A P L A A T R A T R	8	
253	P G G R T P R A G S	8	
257	T P R A G S S A H R	8	
262	S S A H R P P A L S	8	
267	P P A L S A R A P V	8	
272	A R A P V P A A S P	8	
276	V P A A S P A A W L	8	
326	G G G L K K P A R H	8	
338	G Q K H N V L A R G	8	
361	Y V E N G R P A D L	8	
364	N G R P A D L A G S	8	
371	A G S G Y C G A L W	8	
375	Y C G A L W K A I E	8	
394	Q K D K E R K A E N	8	

TABLE XXXIX 151P3D4 v.1: HLA Peptide Scoring Results A3 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
288	K V G Q I F A A W K	30	
263	Y L I H P T K L T Y	26	
331	A V R F V G F P D K	26	
186	A V I A S F D Q L Y	24	
234	G V R N Y G F W D K	24	
39	H L L V E A E Q A K	23	
41	L V E A E Q A K V F	23	
93	D V F V S M G Y H K	23	
269	K L T Y D E A V Q A	23	
260	R F Y Y L I H P T K	22	
279	C L N D G A Q I A K	22	
111	R V F L K G G S D S	21	
166	R L G R Y N L N F H	21	
324	R C S P T E A A V R	21	
8	V L I S I C W A D H	20	
236	R N Y G F W D K D K	20	
334	F V G F P D K K H K	20	
144	G L E D D T V V V A	19	
193	Q L Y D A W R G G L	19	
343	K L Y G V Y C F R A	19	
17	H L S D N Y T L D H	18	
74	I H K I R I K W T K	18	
128	D L T L E D Y G R Y	18	
152	V A L D L Q G V V F	18	
153	A L D L Q G V V F P	18	
306	A G W L A D G S V R	18	
313	S V R Y P I S R P R	18	
48	K V F S H R G G N V	17	
91	E V D V F V S M G Y	17	
151	V V A L D L Q G V V	17	
3	S L L L L V L I S I	16	
4	L L L L V L I S I C	16	
78	R I K W T K L T S D	16	
88	Y L K E V D V F V S	16	
113	F L K G G S D S D A	16	
124	L V I T D L T L E D	16	
129	L T L E D Y G R Y K	16	
149	T V V V A L D L Q G	16	
155	D L Q G V V F P Y F	16	
171	N L N F H E A Q Q A	16	
231	T V P G V R N Y G F	16	
297	K I L G Y D R C D A	16	
53	R G G N V T L P C K	15	
56	N V T L P C K F Y R	15	
76	K I R I K W T K L T	15	
125	V I T D L T L E D Y	15	
201	G L D W C N A G W L	15	
208	G W L S D G S V Q Y	15	
212	D G S V Q Y P I T K	15	
214	S V Q Y P I T K P R	15	
275	A V Q A C L N D G A	15	
284	A Q I A K V G Q I F	15	
7	L V L I S I C W A D	14	

TABLE XXXIX 151P3D4 v.1: HLA Peptide Scoring Results A3 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
11	S	I	C	W	A	D	H	L	S	D	14	
40	L	L	V	E	A	E	Q	A	K	V	14	
67	P	T	A	F	G	S	G	I	H	K	14	
86	S	D	Y	L	K	E	V	D	V	F	14	
106	G	G	Y	Q	G	R	V	F	L	K	14	
140	E	V	I	E	G	L	E	D	D	T	14	
141	V	I	E	G	L	E	D	D	T	V	14	
159	V	V	F	P	Y	F	P	R	L	G	14	
207	A	G	W	L	S	D	G	S	V	Q	14	
221	K	P	R	E	P	C	G	G	Q	N	14	
292	I	F	A	A	W	K	I	L	G	Y	14	
307	G	W	L	A	D	G	S	V	R	Y	14	
320	R	P	R	R	R	C	S	P	T	E	14	
23	T	L	D	H	D	R	A	I	H	I	13	
31	H	I	Q	A	E	N	G	P	H	L	13	
62	K	F	Y	R	D	P	T	A	F	G	13	
83	K	L	T	S	D	Y	L	K	E	V	13	
104	T	Y	G	G	Y	Q	G	R	V	F	13	
123	S	L	V	I	T	D	L	T	L	E	13	
180	A	C	L	D	Q	D	A	V	I	A	13	
298	I	L	G	Y	D	R	C	D	A	G	13	
5	L	L	L	V	L	I	S	I	C	W	12	
6	L	L	V	L	I	S	I	C	W	A	12	
9	L	I	S	I	C	W	A	D	H	L	12	
29	A	I	H	I	Q	A	E	N	G	P	12	
34	A	E	N	G	P	H	L	L	V	E	12	
44	A	E	Q	A	K	V	F	S	H	R	12	
77	I	R	I	K	W	T	K	L	T	S	12	
81	W	T	K	L	T	S	D	Y	L	K	12	
96	V	S	M	G	Y	H	K	K	T	Y	12	
122	A	S	L	V	I	T	D	L	T	L	12	
130	T	L	E	D	Y	G	R	Y	K	C	12	
150	V	V	V	A	L	D	L	Q	G	V	12	
187	V	I	A	S	F	D	Q	L	Y	D	12	
264	L	I	H	P	T	K	L	T	Y	D	12	
277	Q	A	C	L	N	D	G	A	Q	I	12	
291	Q	I	F	A	A	W	K	I	L	G	12	
308	W	L	A	D	G	S	V	R	Y	P	12	
314	V	R	Y	P	I	S	R	P	R	R	12	
317	P	I	S	R	P	R	R	R	C	S	12	
339	D	K	K	H	K	L	Y	G	V	Y	12	
22	Y	T	L	D	H	D	R	A	I	H	11	
50	F	S	H	R	G	G	N	V	T	L	11	
71	G	S	G	I	H	K	I	R	I	K	11	
79	I	K	W	T	K	L	T	S	D	Y	11	
143	E	G	L	E	D	D	T	V	V	V	11	
161	F	P	Y	F	P	R	L	G	R	Y	11	
165	P	R	L	G	R	Y	N	L	N	F	11	
181	C	L	D	Q	D	A	V	I	A	S	11	
209	W	L	S	D	G	S	V	Q	Y	P	11	
227	G	G	Q	N	T	V	P	G	V	R	11	
285	Q	I	A	K	V	G	Q	I	F	A	11	
318	I	S	R	P	R	R	R	C	S	P	11	

TABLE XXXIX 151P3D4 v.1: HLA Peptide Scoring Results A3 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
325	C	S	P	T	E	A	A	V	R	F	11	
328	T	E	A	A	V	R	F	V	G	F	11	
332	V	R	F	V	G	F	P	D	K	K	11	
28	R	A	I	H	I	Q	A	E	N	G	10	
30	I	H	I	Q	A	E	N	G	P	H	10	
58	T	L	P	C	K	F	Y	R	D	P	10	
65	R	D	P	T	A	F	G	S	G	I	10	
94	V	F	V	S	M	G	Y	H	K	K	10	
95	F	V	S	M	G	Y	H	K	K	T	10	
103	K	T	Y	G	G	Y	Q	G	R	V	10	
158	G	V	V	F	P	Y	F	P	R	L	10	
179	Q	A	C	L	D	Q	D	A	V	I	10	
182	L	D	Q	D	A	V	I	A	S	F	10	
239	G	F	W	D	K	D	K	S	R	Y	10	
246	S	R	Y	D	V	F	C	F	T	S	10	
249	D	V	F	C	F	T	S	N	F	N	10	
253	F	T	S	N	F	N	G	R	F	Y	10	
257	F	N	G	R	F	Y	Y	L	I	H	10	
294	A	A	W	K	I	L	G	Y	D	R	10	
315	R	Y	P	I	S	R	P	R	R	R	10	
333	R	F	V	G	F	P	D	K	K	H	10	
340	K	K	H	K	L	Y	G	V	Y	C	10	
2	K	S	L	L	L	L	V	L	I	S	9	
38	P	H	L	L	V	E	A	E	Q	A	9	
73	G	I	H	K	I	R	I	K	W	T	9	
138	K	C	E	V	I	E	G	L	E	D	9	
170	Y	N	L	N	F	H	E	A	Q	Q	9	
190	S	F	D	Q	L	Y	D	A	W	R	9	
268	T	K	L	T	Y	D	E	A	V	Q	9	
278	A	C	L	N	D	G	A	Q	I	A	9	
281	N	D	G	A	Q	I	A	K	V	G	9	
287	A	K	V	G	Q	I	F	A	A	W	9	
303	R	C	D	A	G	W	L	A	D	G	9	
330	A	A	V	R	F	V	G	F	P	D	9	
341	K	H	K	L	Y	G	V	Y	C	F	9	
13	C	W	A	D	H	L	S	D	N	Y	8	
15	A	D	H	L	S	D	N	Y	T	L	8	
90	K	E	V	D	V	F	V	S	M	G	8	
115	K	G	G	S	D	S	D	A	S	L	8	
142	I	E	G	L	E	D	D	T	V	V	8	
154	L	D	L	Q	G	V	V	F	P	Y	8	
160	V	F	P	Y	F	P	R	L	G	R	8	
183	D	Q	D	A	V	I	A	S	F	D	8	
197	A	W	R	G	G	L	D	W	C	N	8	
218	P	I	T	K	P	R	E	P	C	G	8	
223	R	E	P	C	G	G	Q	N	T	V	8	
229	Q	N	T	V	P	G	V	R	N	Y	8	
242	D	K	D	K	S	R	Y	D	V	F	8	
243	K	D	K	S	R	Y	D	V	F	C	8	
299	L	G	Y	D	R	C	D	A	G	W	8	
300	G	Y	D	R	C	D	A	G	W	L	8	
321	P	R	R	R	C	S	P	T	E	A	8	
322	R	R	R	C	S	P	T	E	A	A	8	

TABLE XXXIX 151P3D4 v.1: HLA Peptide Scoring Results A3 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
323	R	R	C	S	P	T	E	A	A	V	8	
12	I	C	W	A	D	H	L	S	D	N	7	
35	E	N	G	P	H	L	L	V	E	A	7	
49	V	F	S	H	R	G	G	N	V	T	7	
51	S	H	R	G	G	N	V	T	L	P	7	
61	C	K	F	Y	R	D	P	T	A	F	7	
63	F	Y	R	D	P	T	A	F	G	S	7	
66	D	P	T	A	F	G	S	G	I	H	7	
69	A	F	G	S	G	I	H	K	I	R	7	
75	H	K	I	R	I	K	W	T	K	L	7	
99	G	Y	H	K	K	T	Y	G	G	Y	7	
101	H	K	K	T	Y	G	G	Y	Q	G	7	
102	K	K	T	Y	G	G	Y	Q	G	R	7	
116	G	G	S	D	S	D	A	S	L	V	7	
117	G	S	D	S	D	A	S	L	V	I	7	
133	D	Y	G	R	Y	K	C	E	V	I	7	
134	Y	G	R	Y	K	C	E	V	I	E	7	
195	Y	D	A	W	R	G	G	L	D	W	7	
215	V	Q	Y	P	I	T	K	P	R	E	7	
219	I	T	K	P	R	E	P	C	G	G	7	
224	E	P	C	G	G	Q	N	T	V	P	7	
228	G	Q	N	T	V	P	G	V	R	N	7	
233	P	G	V	R	N	Y	G	F	W	D	7	
244	D	K	S	R	Y	D	V	F	C	F	7	
247	R	Y	D	V	F	C	F	T	S	N	7	
248	Y	D	V	F	C	F	T	S	N	F	7	
254	T	S	N	F	N	G	R	F	Y	Y	7	
261	F	Y	Y	L	I	H	P	T	K	L	7	
311	D	G	S	V	R	Y	P	I	S	R	7	
319	S	R	P	R	R	R	C	S	P	T	7	
327	P	T	E	A	A	V	R	F	V	G	7	
336	G	F	P	D	K	K	H	K	L	Y	7	
344	L	Y	G	V	Y	C	F	R	A	Y	7	
25	D	H	D	R	A	I	H	I	Q	A	6	
26	H	D	R	A	I	H	I	Q	A	E	6	
33	Q	A	E	N	G	P	H	L	L	V	6	
42	V	E	A	E	Q	A	K	V	F	S	6	
43	E	A	E	Q	A	K	V	F	S	H	6	
55	G	N	V	T	L	P	C	K	F	Y	6	
64	Y	R	D	P	T	A	F	G	S	G	6	
87	D	Y	L	K	E	V	D	V	F	V	6	
89	L	K	E	V	D	V	F	V	S	M	6	
109	Q	G	R	V	F	L	K	G	G	S	6	
110	G	R	V	F	L	K	G	G	S	D	6	
118	S	D	S	D	A	S	L	V	I	T	6	
119	D	S	D	A	S	L	V	I	T	D	6	
127	T	D	L	T	L	E	D	Y	G	R	6	
132	E	D	Y	G	R	Y	K	C	E	V	6	
145	L	E	D	D	T	V	V	V	A	L	6	
147	D	D	T	V	V	V	A	L	D	L	6	
157	Q	G	V	V	F	P	Y	F	P	R	6	
162	P	Y	F	P	R	L	G	R	Y	N	6	
169	R	Y	N	L	N	F	H	E	A	Q	6	

TABLE XXXIX 151P3D4 v.1: HLA Peptide Scoring Results A3 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
194	L	Y	D	A	W	R	G	G	L	D	6	
199	R	G	G	L	D	W	C	N	A	G	6	
200	G	G	L	D	W	C	N	A	G	W	6	
203	D	W	C	N	A	G	W	L	S	D	6	
222	P	R	E	P	C	G	G	Q	N	T	6	
225	P	C	G	G	Q	N	T	V	P	G	6	
238	Y	G	F	W	D	K	D	K	S	R	6	
245	K	S	R	Y	D	V	F	C	F	T	6	
270	L	T	Y	D	E	A	V	Q	A	C	6	
301	Y	D	R	C	D	A	G	W	L	A	6	
304	C	D	A	G	W	L	A	D	G	S	6	
312	G	S	V	R	Y	P	I	S	R	P	6	
342	H	K	L	Y	G	V	Y	C	F	R	6	
1	M	K	S	L	L	L	L	V	L	I	5	
10	I	S	I	C	W	A	D	H	L	S	5	
19	S	D	N	Y	T	L	D	H	D	R	5	
27	D	R	A	I	H	I	Q	A	E	N	5	
32	I	Q	A	E	N	G	P	H	L	L	5	
47	A	K	V	F	S	H	R	G	G	N	5	
52	H	R	G	G	N	V	T	L	P	C	5	
54	G	G	N	V	T	L	P	C	K	F	5	
57	V	T	L	P	C	K	F	Y	R	D	5	
60	P	C	K	F	Y	R	D	P	T	A	5	
72	S	G	I	H	K	I	R	I	K	W	5	
82	T	K	L	T	S	D	Y	L	K	E	5	
84	L	T	S	D	Y	L	K	E	V	D	5	
92	V	D	V	F	V	S	M	G	Y	H	5	
100	Y	H	K	K	T	Y	G	G	Y	Q	5	
105	Y	G	G	Y	Q	G	R	V	F	L	5	
107	G	Y	Q	G	R	V	F	L	K	G	5	
136	R	Y	K	C	E	V	I	E	G	L	5	
168	G	R	Y	N	L	N	F	H	E	A	5	
174	F	H	E	A	Q	Q	A	C	L	D	5	
177	A	Q	Q	A	C	L	D	Q	D	A	5	
189	A	S	F	D	Q	L	Y	D	A	W	5	
204	W	C	N	A	G	W	L	S	D	G	5	
252	C	F	T	S	N	F	N	G	R	F	5	
272	Y	D	E	A	V	Q	A	C	L	N	5	
280	L	N	D	G	A	Q	I	A	K	V	5	
282	D	G	A	Q	I	A	K	V	G	Q	5	
283	G	A	Q	I	A	K	V	G	Q	I	5	
295	A	W	K	I	L	G	Y	D	R	C	5	
302	D	R	C	D	A	G	W	L	A	D	5	
20	D	N	Y	T	L	D	H	D	R	A	4	
37	G	P	H	L	L	V	E	A	E	Q	4	
85	T	S	D	Y	L	K	E	V	D	V	4	
98	M	G	Y	H	K	K	T	Y	G	G	4	
112	V	F	L	K	G	G	S	D	S	D	4	
135	G	R	Y	K	C	E	V	I	E	G	4	
163	Y	F	P	R	L	G	R	Y	N	L	4	
164	F	P	R	L	G	R	Y	N	L	N	4	
173	N	F	H	E	A	Q	Q	A	C	L	4	
175	H	E	A	Q	Q	A	C	L	D	Q	4	

TABLE XXXIX 151P3D4 v.1: HLA Peptide Scoring Results A3 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
178	Q	Q	A	C	L	D	Q	D	A	V	4	
185	D	A	V	I	A	S	F	D	Q	L	4	
191	F	D	Q	L	Y	D	A	W	R	G	4	
196	D	A	W	R	G	G	L	D	W	C	4	
216	Q	Y	P	I	T	K	P	R	E	P	4	
217	Y	P	I	T	K	P	R	E	P	C	4	
220	T	K	P	R	E	P	C	G	G	Q	4	
230	N	T	V	P	G	V	R	N	Y	G	4	
251	F	C	F	T	S	N	F	N	G	R	4	
271	T	Y	D	E	A	V	Q	A	C	L	4	
273	D	E	A	V	Q	A	C	L	N	D	4	
286	I	A	K	V	G	Q	I	F	A	A	4	
289	V	G	Q	I	F	A	A	W	K	I	4	
296	W	K	I	L	G	Y	D	R	C	D	4	
316	Y	P	I	S	R	P	R	R	R	C	4	
345	Y	G	V	Y	C	F	R	A	Y	N	4	
16	D	H	L	S	D	N	Y	T	L	D	3	
46	Q	A	K	V	F	S	H	R	G	G	3	
80	K	W	T	K	L	T	S	D	Y	L	3	
108	Y	Q	G	R	V	F	L	K	G	G	3	
114	L	K	G	G	S	D	S	D	A	S	3	
120	S	D	A	S	L	V	I	T	D	L	3	
126	I	T	D	L	T	L	E	D	Y	G	3	
146	E	D	D	T	V	V	V	A	L	D	3	
167	L	G	R	Y	N	L	N	F	H	E	3	
176	E	A	Q	Q	A	C	L	D	Q	D	3	
184	Q	D	A	V	I	A	S	F	D	Q	3	
202	L	D	W	C	N	A	G	W	L	S	3	
205	C	N	A	G	W	L	S	D	G	S	3	
206	N	A	G	W	L	S	D	G	S	V	3	
241	W	D	K	D	K	S	R	Y	D	V	3	
258	N	G	R	F	Y	Y	L	I	H	P	3	
262	Y	Y	L	I	H	P	T	K	L	T	3	
267	P	T	K	L	T	Y	D	E	A	V	3	
276	V	Q	A	C	L	N	D	G	A	Q	3	
290	G	Q	I	F	A	A	W	K	I	L	3	
305	D	A	G	W	L	A	D	G	S	V	3	
309	L	A	D	G	S	V	R	Y	P	I	3	
310	A	D	G	S	V	R	Y	P	I	S	3	
335	V	G	F	P	D	K	K	H	K	L	3	
337	F	P	D	K	K	H	K	L	Y	G	3	
21	N	Y	T	L	D	H	D	R	A	I	2	
68	T	A	F	G	S	G	I	H	K	I	2	
70	F	G	S	G	I	H	K	I	R	I	2	
97	S	M	G	Y	H	K	K	T	Y	G	2	
137	Y	K	C	E	V	I	E	G	L	E	2	
188	I	A	S	F	D	Q	L	Y	D	A	2	
192	D	Q	L	Y	D	A	W	R	G	G	2	
198	W	R	G	G	L	D	W	C	N	A	2	
210	L	S	D	G	S	V	Q	Y	P	I	2	
255	S	N	F	N	G	R	F	Y	Y	L	2	
256	N	F	N	G	R	F	Y	Y	L	I	2	
265	I	H	P	T	K	L	T	Y	D	E	2	

TABLE XXXIX 151P3D4 v.1: HLA Peptide Scoring Results A3 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
293	F	A	A	W	K	I	L	G	Y	D	2	
326	S	P	T	E	A	A	V	R	F	V	2	
329	E	A	A	V	R	F	V	G	F	P	2	
18	L	S	D	N	Y	T	L	D	H	D	1	
24	L	D	H	D	R	A	I	H	I	Q	1	
36	N	G	P	H	L	L	V	E	A	E	1	
45	E	Q	A	K	V	F	S	H	R	G	1	
59	L	P	C	K	F	Y	R	D	P	T	1	
121	D	A	S	L	V	I	T	D	L	T	1	
139	C	E	V	I	E	G	L	E	D	D	1	
156	L	Q	G	V	V	F	P	Y	F	P	1	
172	L	N	F	H	E	A	Q	Q	A	C	1	
211	S	D	G	S	V	Q	Y	P	I	T	1	
213	G	S	V	Q	Y	P	I	T	K	P	1	
232	V	P	G	V	R	N	Y	G	F	W	1	
338	P	D	K	K	H	K	L	Y	G	V	1	

TABLE XXXIX 151P3D4 v.2: HLA Peptide Scoring Results A3 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
111	K	L	K	Y	L	A	F	L	H	K	27	
87	V	L	L	G	R	K	A	V	V	V	25	
343	V	L	A	R	G	K	P	Q	R	K	25	
75	T	V	Y	Q	D	E	K	Q	R	K	24	
10	P	L	R	A	L	H	I	V	V	E	23	
86	K	V	L	L	G	R	K	A	V	V	23	
237	K	T	I	A	P	L	A	A	T	R	22	
13	A	L	H	I	V	V	E	S	I	R	21	
88	L	L	G	R	K	A	V	V	V	S	21	
198	K	N	K	Q	L	M	R	L	Q	K	21	
331	K	P	A	R	H	C	Q	G	Q	K	21	
342	N	V	L	A	R	G	K	P	Q	R	21	
19	E	S	I	R	D	H	S	G	Q	K	20	
36	D	L	L	V	P	T	K	V	T	G	20	
102	N	I	S	G	S	F	C	R	N	K	20	
269	A	L	S	A	R	A	P	V	P	A	20	
284	W	L	P	L	R	T	P	W	T	R	20	
64	K	L	A	Y	S	N	D	G	E	H	19	
179	A	V	T	A	T	L	E	E	K	R	19	
240	A	P	L	A	A	T	R	A	T	R	19	
249	R	I	G	H	P	G	G	R	T	P	19	
322	S	P	S	G	G	G	G	L	K	K	19	
33	K	K	V	D	L	L	V	P	T	K	18	
45	G	I	I	T	Q	G	A	K	D	F	18	
366	R	P	A	D	L	A	G	S	G	Y	18	
386	L	E	E	G	L	G	G	K	Q	K	18	
154	Q	G	H	A	S	E	A	Y	K	K	17	
163	K	V	C	L	S	G	A	P	H	E	17	
167	S	G	A	P	H	E	V	G	W	K	17	
172	E	V	G	W	K	Y	Q	A	V	T	17	
182	A	T	L	E	E	K	R	K	E	K	17	
202	L	M	R	L	Q	K	Q	A	E	K	17	

TABLE XXXIX 151P3D4 v.2: HLA Peptide Scoring Results A3 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
241	P L A A T R A T R I	17	
264	A H R P P A L S A R	17	
275	P V P A A S P A A W	17	
295	S S C P T S S S T Y	17	
372	G S G Y C G A L W K	17	
20	S I R D H S G Q K M	16	
34	K V D L L V P T K V	16	
55	G H V Q F V G S Y K	16	
165	C L S G A P H E V G	16	
189	K E K A E I H Y R K	16	
201	Q L M R L Q K Q A E	16	
228	S P R G L G F I F K	16	
238	T I A P L A A T R A	16	
339	Q K H N V L A R G K	16	
378	A L W K A I E S L E	16	
385	S L E E G L G G K Q	16	
42	K V T G I I T Q G A	15	
83	R K D K V L L G R K	15	
136	P S R I F W R Q E K	15	
191	K A E I H Y R K N K	15	
206	Q K Q A E K N M K K	15	
207	K Q A E K N M K K K	15	
256	R T P R A G S S A H	15	
272	A R A P V P A A S P	15	
306	S L S P Y G P R N P	15	
361	Y V E N G R P A D L	15	
16	I V V E S I R D H S	14	
37	L L V P T K V T G I	14	
58	Q F V G S Y K L A Y	14	
68	S N D G E H W T V Y	14	
93	A V V V S C E G I N	14	
129	R P Y H F Q V P S R	14	
204	R L Q K Q A E K N M	14	
216	K I D K Y T E S P G	14	
315	P L P N P R H S P S	14	
321	H S P S G G G G L K	14	
345	A R G K P Q R K P K	14	
352	K P K S E N N S W Y	14	
384	E S L E E G L G G K	14	
388	E G L G G K Q K D K	14	
21	I R D H S G Q K M K	13	
43	V T G I I T Q G A K	13	
50	G A K D F G H V Q F	13	
59	F V G S Y K L A Y S	13	
94	V V V S C E G I N I	13	
100	G I N I S G S F C R	13	
138	R I F W R Q E K A D	13	
153	P Q G H A S E A Y K	13	
162	K K V C L S G A P H	13	
221	T E S P G G G S P R	13	
247	A T R I G H P G G R	13	
286	P L R T P W T R P S	13	
369	D L A G S G Y C G A	13	

TABLE XXXIX 151P3D4 v.2: HLA Peptide Scoring Results A3 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
7	K T F P L R A L H I	12	
15	H I V V E S I R D H	12	
17	V V E S I R D H S G	12	
77	Y Q D E K Q R K D K	12	
114	Y L A F L H K R M N	12	
120	K R M N T N P S R R	12	
134	Q V P S R I F W R Q	12	
178	Q A V T A T L E E K	12	
205	L Q K Q A E K N M K	12	
230	R G L G F I F K T I	12	
257	T P R A G S S A H R	12	
263	S A H R P P A L S A	12	
328	G L K K P A R H C Q	12	
382	A I E S L E E G L G	12	
389	G L G G K Q K D K E	12	
1	M L E H T T K T F P	11	
25	S G Q K M K Q D K K	11	
38	L V P T K V T G I I	11	
82	Q R K D K V L L G R	11	
104	S G S F C R N K L K	11	
117	F L H K R M N T N P	11	
127	S R R P Y H F Q V P	11	
143	Q E K A D G G S C C	11	
173	V G W K Y Q A V T A	11	
175	W K Y Q A V T A T L	11	
180	V T A T L E E K R K	11	
183	T L E E K R K E K A	11	
187	K R K E K A E I H Y	11	
193	E I H Y R K N K Q L	11	
195	H Y R K N K Q L M R	11	
231	G L G F I F K T I A	11	
234	F I F K T I A P L A	11	
243	A A T R A T R I G H	11	
250	I G H P G G R T P R	11	
255	G R T P R A G S S A	11	
271	S A R A P V P A A S	11	
320	R H S P S G G G G L	11	
371	A G S G Y C G A L W	11	
391	G G K Q K D K E R K	11	
397	K E R K A E N G P H	11	
24	H S G Q K M K Q D K	10	
31	Q D K K V D L L V P	10	
44	T G I I T Q G A K D	10	
46	I I T Q G A K D F G	10	
49	Q G A K D F G H V Q	10	
56	H V Q F V G S Y K L	10	
72	E H W T V Y Q D E K	10	
95	V V S C E G I N I S	10	
99	E G I N I S G S F C	10	
142	R Q E K A D G G S C	10	
186	E K R K E K A E I H	10	
210	E K N M K K K I D K	10	
225	G G G S P R G L G F	10	

TABLE XXXIX 151P3D4 v.2: HLA Peptide Scoring Results A3 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
227	G	S	P	R	G	L	G	F	I	F	10	
266	R	P	P	A	L	S	A	R	A	P	10	
273	R	A	P	V	P	A	A	S	P	A	10	
276	V	P	A	A	S	P	A	A	W	L	10	
288	R	T	P	W	T	R	P	S	S	C	10	
291	W	T	R	P	S	S	C	P	T	S	10	
301	S	S	T	Y	D	S	L	S	P	Y	10	
332	P	A	R	H	C	Q	G	Q	K	H	10	
337	Q	G	Q	K	H	N	V	L	A	R	10	
368	A	D	L	A	G	S	G	Y	C	G	10	
9	F	P	L	R	A	L	H	I	V	V	9	
52	K	D	F	G	H	V	Q	F	V	G	9	
54	F	G	H	V	Q	F	V	G	S	Y	9	
81	K	Q	R	K	D	K	V	L	L	G	9	
89	L	G	R	K	A	V	V	V	S	C	9	
105	G	S	F	C	R	N	K	L	K	Y	9	
109	R	N	K	L	K	Y	L	A	F	L	9	
110	N	K	L	K	Y	L	A	F	L	H	9	
112	L	K	Y	L	A	F	L	H	K	R	9	
116	A	F	L	H	K	R	M	N	T	N	9	
119	H	K	R	M	N	T	N	P	S	R	9	
126	P	S	R	R	P	Y	H	F	Q	V	9	
150	S	C	C	P	Q	G	H	A	S	E	9	
152	C	P	Q	G	H	A	S	E	A	Y	9	
157	A	S	E	A	Y	K	K	V	C	L	9	
159	E	A	Y	K	K	V	C	L	S	G	9	
168	G	A	P	H	E	V	G	W	K	Y	9	
176	K	Y	Q	A	V	T	A	T	L	E	9	
194	I	H	Y	R	K	N	K	Q	L	M	9	
211	K	N	M	K	K	K	I	D	K	Y	9	
215	K	K	I	D	K	Y	T	E	S	P	9	
244	A	T	R	A	T	R	I	G	H	P	9	
248	T	R	I	G	H	P	G	G	R	T	9	
254	G	G	R	T	P	R	A	G	S	S	9	
268	P	A	L	S	A	R	A	P	V	P	9	
278	A	A	S	P	A	A	W	L	P	L	9	
279	A	S	P	A	A	W	L	P	L	R	9	
283	A	W	L	P	L	R	T	P	W	T	9	
293	R	P	S	S	C	P	T	S	S	S	9	
311	G	P	R	N	P	L	P	N	P	R	9	
326	G	G	G	L	K	K	P	A	R	H	9	
348	K	P	Q	R	K	P	K	S	E	N	9	
364	N	G	R	P	A	D	L	A	G	S	9	
383	I	E	S	L	E	E	G	L	G	G	9	
6	T	K	T	F	P	L	R	A	L	H	8	
12	R	A	L	H	I	V	V	E	S	I	8	
28	K	M	K	Q	D	K	K	V	D	L	8	
47	I	T	Q	G	A	K	D	F	G	H	8	
98	C	E	G	I	N	I	S	G	S	F	8	
108	C	R	N	K	L	K	Y	L	A	F	8	
122	M	N	T	N	P	S	R	R	P	Y	8	
123	N	T	N	P	S	R	R	P	Y	H	8	
128	R	R	P	Y	H	F	Q	V	P	S	8	

TABLE XXXIX 151P3D4 v.2: HLA Peptide Scoring Results A3 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
133	F	Q	V	P	S	R	I	F	W	R	8	
139	I	F	W	R	Q	E	K	A	D	G	8	
146	A	D	G	G	S	C	C	P	Q	G	8	
188	R	K	E	K	A	E	I	H	Y	R	8	
200	K	Q	L	M	R	L	Q	K	Q	A	8	
219	K	Y	T	E	S	P	G	G	G	S	8	
235	I	F	K	T	I	A	P	L	A	A	8	
280	S	P	A	A	W	L	P	L	R	T	8	
314	N	P	L	P	N	P	R	H	S	P	8	
346	R	G	K	P	Q	R	K	P	K	S	8	
354	K	S	E	N	N	S	W	Y	V	E	8	
359	S	W	Y	V	E	N	G	R	P	A	8	
365	G	R	P	A	D	L	A	G	S	G	8	
395	K	D	K	E	R	K	A	E	N	G	8	
35	V	D	L	L	V	P	T	K	V	T	7	
61	G	S	Y	K	L	A	Y	S	N	D	7	
65	L	A	Y	S	N	D	G	E	H	W	7	
74	W	T	V	Y	Q	D	E	K	Q	R	7	
80	E	K	Q	R	K	D	K	V	L	L	7	
84	K	D	K	V	L	L	G	R	K	A	7	
113	K	Y	L	A	F	L	H	K	R	M	7	
160	A	Y	K	K	V	C	L	S	G	A	7	
185	E	E	K	R	K	E	K	A	E	I	7	
246	R	A	T	R	I	G	H	P	G	G	7	
253	P	G	G	R	T	P	R	A	G	S	7	
274	A	P	V	P	A	A	S	P	A	A	7	
308	S	P	Y	G	P	R	N	P	L	P	7	
309	P	Y	G	P	R	N	P	L	P	N	7	
312	P	R	N	P	L	P	N	P	R	H	7	
317	P	N	P	R	H	S	P	S	G	G	7	
325	G	G	G	G	L	K	K	P	A	R	7	
329	L	K	K	P	A	R	H	C	Q	G	7	
363	E	N	G	R	P	A	D	L	A	G	7	
381	K	A	I	E	S	L	E	E	G	L	7	
393	K	Q	K	D	K	E	R	K	A	E	7	
399	R	K	A	E	N	G	P	H	L	L	7	
11	L	R	A	L	H	I	V	V	E	S	6	
27	Q	K	M	K	Q	D	K	K	V	D	6	
30	K	Q	D	K	K	V	D	L	L	V	6	
90	G	R	K	A	V	V	V	S	C	E	6	
97	S	C	E	G	I	N	I	S	G	S	6	
135	V	P	S	R	I	F	W	R	Q	E	6	
140	F	W	R	Q	E	K	A	D	G	G	6	
151	C	C	P	Q	G	H	A	S	E	A	6	
166	L	S	G	A	P	H	E	V	G	W	6	
192	A	E	I	H	Y	R	K	N	K	Q	6	
214	K	K	K	I	D	K	Y	T	E	S	6	
218	D	K	Y	T	E	S	P	G	G	G	6	
220	Y	T	E	S	P	G	G	G	S	P	6	
233	G	F	I	F	K	T	I	A	P	L	6	
258	P	R	A	G	S	S	A	H	R	P	6	
262	S	S	A	H	R	P	P	A	L	S	6	
265	H	R	P	P	A	L	S	A	R	A	6	

TABLE XXXIX 151P3D4 v.2: HLA Peptide Scoring Results A3 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
267	P	P	A	L	S	A	R	A	P	V	6	
282	A	A	W	L	P	L	R	T	P	W	6	
285	L	P	L	R	T	P	W	T	R	P	6	
287	L	R	T	P	W	T	R	P	S	S	6	
300	S	S	S	T	Y	D	S	L	S	P	6	
302	S	T	Y	D	S	L	S	P	Y	G	6	
304	Y	D	S	L	S	P	Y	G	P	R	6	
313	R	N	P	L	P	N	P	R	H	S	6	
335	H	C	Q	G	Q	K	H	N	V	L	6	
350	Q	R	K	P	K	S	E	N	N	S	6	
351	R	K	P	K	S	E	N	N	S	W	6	
355	S	E	N	N	S	W	Y	V	E	N	6	
379	L	W	K	A	I	E	S	L	E	E	6	
398	E	R	K	A	E	N	G	P	H	L	6	
22	R	D	H	S	G	Q	K	M	K	Q	5	
23	D	H	S	G	Q	K	M	K	Q	D	5	
32	D	K	K	V	D	L	L	V	P	T	5	
40	P	T	K	V	T	G	I	I	T	Q	5	
60	V	G	S	Y	K	L	A	Y	S	N	5	
66	A	Y	S	N	D	G	E	H	W	T	5	
67	Y	S	N	D	G	E	H	W	T	V	5	
69	N	D	G	E	H	W	T	V	Y	Q	5	
79	D	E	K	Q	R	K	D	K	V	L	5	
91	R	K	A	V	V	V	S	C	E	G	5	
101	I	N	I	S	G	S	F	C	R	N	5	
124	T	N	P	S	R	R	P	Y	H	F	5	
145	K	A	D	G	G	S	C	C	P	Q	5	
147	D	G	G	S	C	C	P	Q	G	H	5	
156	H	A	S	E	A	Y	K	K	V	C	5	
203	M	R	L	Q	K	Q	A	E	K	N	5	
209	A	E	K	N	M	K	K	K	I	D	5	
213	M	K	K	K	I	D	K	Y	T	E	5	
236	F	K	T	I	A	P	L	A	A	T	5	
270	L	S	A	R	A	P	V	P	A	A	5	
281	P	A	A	W	L	P	L	R	T	P	5	
294	P	S	S	C	P	T	S	S	S	T	5	
305	D	S	L	S	P	Y	G	P	R	N	5	
316	L	P	N	P	R	H	S	P	S	G	5	
327	G	G	L	K	K	P	A	R	H	C	5	
330	K	K	P	A	R	H	C	Q	G	Q	5	
340	K	H	N	V	L	A	R	G	K	P	5	
344	L	A	R	G	K	P	Q	R	K	P	5	
362	V	E	N	G	R	P	A	D	L	A	5	
373	S	G	Y	C	G	A	L	W	K	A	5	
375	Y	C	G	A	L	W	K	A	I	E	5	
376	C	G	A	L	W	K	A	I	E	S	5	
394	Q	K	D	K	E	R	K	A	E	N	5	
3	E	H	T	T	K	T	F	P	L	R	4	
4	H	T	T	K	T	F	P	L	R	A	4	
18	V	E	S	I	R	D	H	S	G	Q	4	
41	T	K	V	T	G	I	I	T	Q	G	4	
53	D	F	G	H	V	Q	F	V	G	S	4	
63	Y	K	L	A	Y	S	N	D	G	E	4	
106	S	F	C	R	N	K	L	K	Y	L	4	
107	F	C	R	N	K	L	K	Y	L	A	4	
118	L	H	K	R	M	N	T	N	P	S	4	
121	R	M	N	T	N	P	S	R	R	P	4	
130	P	Y	H	F	Q	V	P	S	R	I	4	
131	Y	H	F	Q	V	P	S	R	I	F	4	
137	S	R	I	F	W	R	Q	E	K	A	4	
149	G	S	C	C	P	Q	G	H	A	S	4	
169	A	P	H	E	V	G	W	K	Y	Q	4	
177	Y	Q	A	V	T	A	T	L	E	E	4	
197	R	K	N	K	Q	L	M	R	L	Q	4	
223	S	P	G	G	G	S	P	R	G	L	4	
224	P	G	G	G	S	P	R	G	L	G	4	
226	G	G	S	P	R	G	L	G	F	I	4	
239	I	A	P	L	A	A	T	R	A	T	4	
245	T	R	A	T	R	I	G	H	P	G	4	
252	H	P	G	G	R	T	P	R	A	G	4	
259	R	A	G	S	S	A	H	R	P	P	4	
260	A	G	S	S	A	H	R	P	P	A	4	
261	G	S	S	A	H	R	P	P	A	L	4	
277	P	A	A	S	P	A	A	W	L	P	4	
292	T	R	P	S	S	C	P	T	S	S	4	
318	N	P	R	H	S	P	S	G	G	G	4	
319	P	R	H	S	P	S	G	G	G	G	4	
334	R	H	C	Q	G	Q	K	H	N	V	4	
336	C	Q	G	Q	K	H	N	V	L	A	4	
338	G	Q	K	H	N	V	L	A	R	G	4	
341	H	N	V	L	A	R	G	K	P	Q	4	
357	N	N	S	W	Y	V	E	N	G	R	4	
377	G	A	L	W	K	A	I	E	S	L	4	
390	L	G	G	K	Q	K	D	K	E	R	4	
14	L	H	I	V	V	E	S	I	R	D	3	
39	V	P	T	K	V	T	G	I	I	T	3	
48	T	Q	G	A	K	D	F	G	H	V	3	
51	A	K	D	F	G	H	V	Q	F	V	3	
62	S	Y	K	L	A	Y	S	N	D	G	3	
70	D	G	E	H	W	T	V	Y	Q	D	3	
85	D	K	V	L	L	G	R	K	A	V	3	
92	K	A	V	V	V	S	C	E	G	I	3	
96	V	S	C	E	G	I	N	I	S	G	3	
103	I	S	G	S	F	C	R	N	K	L	3	
115	L	A	F	L	H	K	R	M	N	T	3	
125	N	P	S	R	R	P	Y	H	F	Q	3	
161	Y	K	K	V	C	L	S	G	A	P	3	
164	V	C	L	S	G	A	P	H	E	V	3	
170	P	H	E	V	G	W	K	Y	Q	A	3	
171	H	E	V	G	W	K	Y	Q	A	V	3	
174	G	W	K	Y	Q	A	V	T	A	T	3	
196	Y	R	K	N	K	Q	L	M	R	L	3	
217	I	D	K	Y	T	E	S	P	G	G	3	
289	T	P	W	T	R	P	S	S	C	P	3	
290	P	W	T	R	P	S	S	C	P	T	3	
299	T	S	S	S	T	Y	D	S	L	S	3	

TABLE XXXIX 151P3D4 v.2: HLA Peptide Scoring Results A3 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
310	Y	G	P	R	N	P	L	P	N	P	3	
324	S	G	G	G	G	L	K	K	P	A	3	
333	A	R	H	C	Q	G	Q	K	H	N	3	
347	G	K	P	Q	R	K	P	K	S	E	3	
349	P	Q	R	K	P	K	S	E	N	N	3	
360	W	Y	V	E	N	G	R	P	A	D	3	
374	G	Y	C	G	A	L	W	K	A	I	3	
396	D	K	E	R	K	A	E	N	G	P	3	
5	T	T	K	T	F	P	L	R	A	L	2	
78	Q	D	E	K	Q	R	K	D	K	V	2	
141	W	R	Q	E	K	A	D	G	G	S	2	
144	E	K	A	D	G	G	S	C	C	P	2	
158	S	E	A	Y	K	K	V	C	L	S	2	
190	E	K	A	E	I	H	Y	R	K	N	2	
208	Q	A	E	K	N	M	K	K	K	I	2	
222	E	S	P	G	G	G	S	P	R	G	2	
232	L	G	F	I	F	K	T	I	A	P	2	
251	G	H	P	G	G	R	T	P	R	A	2	
296	S	C	P	T	S	S	S	T	Y	D	2	
298	P	T	S	S	S	T	Y	D	S	L	2	
323	P	S	G	G	G	G	L	K	K	P	2	
367	P	A	D	L	A	G	S	G	Y	C	2	
370	L	A	G	S	G	Y	C	G	A	L	2	
380	W	K	A	I	E	S	L	E	E	G	2	
8	T	F	P	L	R	A	L	H	I	V	1	
26	G	Q	K	M	K	Q	D	K	K	V	1	
29	M	K	Q	D	K	K	V	D	L	L	1	
76	V	Y	Q	D	E	K	Q	R	K	D	1	
132	H	F	Q	V	P	S	R	I	F	W	1	
148	G	G	S	C	C	P	Q	G	H	A	1	
155	G	H	A	S	E	A	Y	K	K	V	1	
181	T	A	T	L	E	E	K	R	K	E	1	
184	L	E	E	K	R	K	E	K	A	E	1	
199	N	K	Q	L	M	R	L	Q	K	Q	1	
212	N	M	K	K	K	I	D	K	Y	T	1	
229	P	R	G	L	G	F	I	F	K	T	1	
242	L	A	A	T	R	A	T	R	I	G	1	
303	T	Y	D	S	L	S	P	Y	G	P	1	
307	L	S	P	Y	G	P	R	N	P	L	1	
353	P	K	S	E	N	N	S	W	Y	V	1	
358	N	S	W	Y	V	E	N	G	R	P	1	
387	E	E	G	L	G	G	K	Q	K	D	1	

TABLE XL 151P3D4 v.1: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
155	D	L	Q	G	V	V	F	P	Y	F	31	
91	E	V	D	V	F	V	S	M	G	Y	29	
128	D	L	T	L	E	D	Y	G	R	Y	29	
125	V	I	T	D	L	T	L	E	D	Y	25	
158	G	V	V	F	P	Y	F	P	R	L	24	
231	T	V	P	G	V	R	N	Y	G	F	24	
186	A	V	I	A	S	F	D	Q	L	Y	23	
242	D	K	D	K	S	R	Y	D	V	F	22	
292	I	F	A	A	W	K	I	L	G	Y	22	
339	D	K	K	H	K	L	Y	G	V	Y	21	
31	H	I	Q	A	E	N	G	P	H	L	20	
41	L	V	E	A	E	Q	A	K	V	F	20	
140	E	V	I	E	G	L	E	D	D	T	20	
148	D	T	V	V	V	A	L	D	L	Q	20	
244	D	K	S	R	Y	D	V	F	C	F	20	
253	F	T	S	N	F	N	G	R	F	Y	20	
263	Y	L	I	H	P	T	K	L	T	Y	20	
9	L	I	S	I	C	W	A	D	H	L	19	
93	D	V	F	V	S	M	G	Y	H	K	19	
185	D	A	V	I	A	S	F	D	Q	L	19	
239	G	F	W	D	K	D	K	S	R	Y	19	
193	Q	L	Y	D	A	W	R	G	G	L	18	
249	D	V	F	C	F	T	S	N	F	N	18	
252	C	F	T	S	N	F	N	G	R	F	18	
336	G	F	P	D	K	K	H	K	L	Y	18	
57	V	T	L	P	C	K	F	Y	R	D	17	
173	N	F	H	E	A	Q	Q	A	C	L	17	
182	L	D	Q	D	A	V	I	A	S	F	17	
201	G	L	D	W	C	N	A	G	W	L	17	
270	L	T	Y	D	E	A	V	Q	A	C	17	
328	T	E	A	A	V	R	F	V	G	F	17	
78	R	I	K	W	T	K	L	T	S	D	16	
99	G	Y	H	K	K	T	Y	G	G	Y	16	
145	L	E	D	D	T	V	V	V	A	L	16	
150	V	V	V	A	L	D	L	Q	G	V	16	
163	Y	F	P	R	L	G	R	Y	N	L	16	
264	L	I	H	P	T	K	L	T	Y	D	16	
73	G	I	H	K	I	R	I	K	W	T	15	
88	Y	L	K	E	V	D	V	F	V	S	15	
154	L	D	L	Q	G	V	V	F	P	Y	15	
161	F	P	Y	F	P	R	L	G	R	Y	15	
181	C	L	D	Q	D	A	V	I	A	S	15	
229	Q	N	T	V	P	G	V	R	N	Y	15	
331	A	V	R	F	V	G	F	P	D	K	15	
341	K	H	K	L	Y	G	V	Y	C	F	15	
344	L	Y	G	V	Y	C	F	R	A	Y	15	
35	E	N	G	P	H	L	L	V	E	A	14	
48	K	V	F	S	H	R	G	G	N	V	14	
83	K	L	T	S	D	Y	L	K	E	V	14	
86	S	D	Y	L	K	E	V	D	V	F	14	
89	L	K	E	V	D	V	F	V	S	M	14	
120	S	D	A	S	L	V	I	T	D	L	14	
136	R	Y	K	C	E	V	I	E	G	L	14	
144	G	L	E	D	D	T	V	V	V	A	14	
147	D	D	T	V	V	V	A	L	D	L	14	
153	A	L	D	L	Q	G	V	V	F	P	14	
159	V	V	F	P	Y	F	P	R	L	G	14	
209	W	L	S	D	G	S	V	Q	Y	P	14	
219	I	T	K	P	R	E	P	C	G	G	14	

TABLE XL 151P3D4 v.1: HLA Peptide Scoring Results A26 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
234	G	V	R	N	Y	G	F	W	D	K	14	
255	S	N	F	N	G	R	F	Y	Y	L	14	
308	W	L	A	D	G	S	V	R	Y	P	14	
3	S	L	L	L	L	V	L	I	S	I	13	
4	L	L	L	L	V	L	I	S	I	C	13	
13	C	W	A	D	H	L	S	D	N	Y	13	
58	T	L	P	C	K	F	Y	R	D	P	13	
61	C	K	F	Y	R	D	P	T	A	F	13	
103	K	T	Y	G	G	Y	Q	G	R	V	13	
111	R	V	F	L	K	G	G	S	D	S	13	
124	L	V	I	T	D	L	T	L	E	D	13	
165	P	R	L	G	R	Y	N	L	N	F	13	
208	G	W	L	S	D	G	S	V	Q	Y	13	
284	A	Q	I	A	K	V	G	Q	I	F	13	
325	C	S	P	T	E	A	A	V	R	F	13	
335	V	G	F	P	D	K	K	H	K	L	13	
6	L	L	V	L	I	S	I	C	W	A	12	
8	V	L	I	S	I	C	W	A	D	H	12	
22	Y	T	L	D	H	D	R	A	I	H	12	
40	L	L	V	E	A	E	Q	A	K	V	12	
43	E	A	E	Q	A	K	V	F	S	H	12	
67	P	T	A	F	G	S	G	I	H	K	12	
94	V	F	V	S	M	G	Y	H	K	K	12	
96	V	S	M	G	Y	H	K	K	T	Y	12	
104	T	Y	G	G	Y	Q	G	R	V	F	12	
113	F	L	K	G	G	S	D	S	D	A	12	
123	S	L	V	I	T	D	L	T	L	E	12	
129	L	T	L	E	D	Y	G	R	Y	K	12	
141	V	I	E	G	L	E	D	D	T	V	12	
146	E	D	D	T	V	V	V	A	L	D	12	
152	V	A	L	D	L	Q	G	V	V	F	12	
166	R	L	G	R	Y	N	L	N	F	H	12	
176	E	A	Q	Q	A	C	L	D	Q	D	12	
187	V	I	A	S	F	D	Q	L	Y	D	12	
218	P	I	T	K	P	R	E	P	C	G	12	
230	N	T	V	P	G	V	R	N	Y	G	12	
248	Y	D	V	F	C	F	T	S	N	F	12	
256	N	F	N	G	R	F	Y	Y	L	I	12	
267	P	T	K	L	T	Y	D	E	A	V	12	
271	T	Y	D	E	A	V	Q	A	C	L	12	
285	Q	I	A	K	V	G	Q	I	F	A	12	
288	K	V	G	Q	I	F	A	A	W	K	12	
291	Q	I	F	A	A	W	K	I	L	G	12	
297	K	I	L	G	Y	D	R	C	D	A	12	
307	G	W	L	A	D	G	S	V	R	Y	12	
7	L	V	L	I	S	I	C	W	A	D	11	
11	S	I	C	W	A	D	H	L	S	D	11	
16	D	H	L	S	D	N	Y	T	L	D	11	
29	A	I	H	I	Q	A	E	N	G	P	11	
32	I	Q	A	E	N	G	P	H	L	L	11	
54	G	G	N	V	T	L	P	C	K	F	11	
75	H	K	I	R	I	K	W	T	K	L	11	
79	I	K	W	T	K	L	T	S	D	Y	11	

TABLE XL 151P3D4 v.1: HLA Peptide Scoring Results A26 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
81	W	T	K	L	T	S	D	Y	L	K	11	
84	L	T	S	D	Y	L	K	E	V	D	11	
95	F	V	S	M	G	Y	H	K	K	T	11	
115	K	G	G	S	D	S	D	A	S	L	11	
119	D	S	D	A	S	L	V	I	T	D	11	
126	I	T	D	L	T	L	E	D	Y	G	11	
149	T	V	V	V	A	L	D	L	Q	G	11	
151	V	V	A	L	D	L	Q	G	V	V	11	
274	E	A	V	Q	A	C	L	N	D	G	11	
275	A	V	Q	A	C	L	N	D	G	A	11	
329	E	A	A	V	R	F	V	G	F	P	11	
334	F	V	G	F	P	D	K	K	H	K	11	
343	K	L	Y	G	V	Y	C	F	R	A	11	
23	T	L	D	H	D	R	A	I	H	I	10	
39	H	L	L	V	E	A	E	Q	A	K	10	
55	G	N	V	T	L	P	C	K	F	Y	10	
56	N	V	T	L	P	C	K	F	Y	R	10	
76	K	I	R	I	K	W	T	K	L	T	10	
130	T	L	E	D	Y	G	R	Y	K	C	10	
171	N	L	N	F	H	E	A	Q	Q	A	10	
196	D	A	W	R	G	G	L	D	W	C	10	
214	S	V	Q	Y	P	I	T	K	P	R	10	
254	T	S	N	F	N	G	R	F	Y	Y	10	
269	K	L	T	Y	D	E	A	V	Q	A	10	
279	C	L	N	D	G	A	Q	I	A	K	10	
282	D	G	A	Q	I	A	K	V	G	Q	10	
290	G	Q	I	F	A	A	W	K	I	L	10	
313	S	V	R	Y	P	I	S	R	P	R	10	
317	P	I	S	R	P	R	R	R	C	S	10	
327	P	T	E	A	A	V	R	F	V	G	10	
17	H	L	S	D	N	Y	T	L	D	H	9	
27	D	R	A	I	H	I	Q	A	E	N	9	
45	E	Q	A	K	V	F	S	H	R	G	9	
50	F	S	H	R	G	G	N	V	T	L	9	
68	T	A	F	G	S	G	I	H	K	I	9	
80	K	W	T	K	L	T	S	D	Y	L	9	
105	Y	G	G	Y	Q	G	R	V	F	L	9	
132	E	D	Y	G	R	Y	K	C	E	V	9	
143	E	G	L	E	D	D	T	V	V	V	9	
190	S	F	D	Q	L	Y	D	A	W	R	9	
261	F	Y	Y	L	I	H	P	T	K	L	9	
280	L	N	D	G	A	Q	I	A	K	V	9	
298	I	L	G	Y	D	R	C	D	A	G	9	
300	G	Y	D	R	C	D	A	G	W	L	9	
333	R	F	V	G	F	P	D	K	K	H	9	
5	L	L	L	V	L	I	S	I	C	W	8	
15	A	D	H	L	S	D	N	Y	T	L	8	
25	D	H	D	R	A	I	H	I	Q	A	8	
64	Y	R	D	P	T	A	F	G	S	G	8	
87	D	Y	L	K	E	V	D	V	F	V	8	
112	V	F	L	K	G	G	S	D	S	D	8	
122	A	S	L	V	I	T	D	L	T	L	8	
160	V	F	P	Y	F	P	R	L	G	R	8	

TABLE XL 151P3D4 v.1: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
183	D Q D A V I A S F D	8	
189	A S F D Q L Y D A W	8	
224	E P C G G Q N T V P	8	
273	D E A V Q A C L N D	8	
287	A K V G Q I F A A W	8	
302	D R C D A G W L A D	8	
20	D N Y T L D H D R A	7	
62	K F Y R D P T A F G	7	
69	A F G S G I H K I R	7	
90	K E V D V F V S M G	7	
107	G Y Q G R V F L K G	7	
192	D Q L Y D A W R G G	7	
203	D W C N A G W L S D	7	
226	C G G Q N T V P G V	7	
250	V F C F T S N F N G	7	
251	F C F T S N F N G R	7	
260	R F Y Y L I H P T K	7	
305	D A G W L A D G S V	7	
311	D G S V R Y P I S R	7	
338	P D K K H K L Y G V	7	
18	L S D N Y T L D H D	6	
26	H D R A I H I Q A E	6	
34	A E N G P H L L V E	6	
36	N G P H L L V E A E	6	
44	A E Q A K V F S H R	6	
49	V F S H R G G N V T	6	
51	S H R G G N V T L P	6	
66	D P T A F G S G I H	6	
102	K K T Y G G Y Q G R	6	
118	S D S D A S L V I T	6	
121	D A S L V I T D L T	6	
133	D Y G R Y K C E V I	6	
135	G R Y K C E V I E G	6	
211	S D G S V Q Y P I T	6	
212	D G S V Q Y P I T K	6	
213	G S V Q Y P I T K P	6	
247	R Y D V F C F T S N	6	
259	G R F Y Y L I H P T	6	
266	H P T K L T Y D E A	6	
286	I A K V G Q I F A A	6	
295	A W K I L G Y D R C	6	
303	R C D A G W L A D G	6	
310	A D G S V R Y P I S	6	
312	G S V R Y P I S R P	6	
326	S P T E A A V R F V	6	
1	M K S L L L L V L I	5	
12	I C W A D H L S D N	5	
24	L D H D R A I H I Q	5	
53	R G G N V T L P C K	5	
82	T K L T S D Y L K E	5	
106	G G Y Q G R V F L K	5	
108	Y Q G R V F L K G G	5	
131	L E D Y G R Y K C E	5	

TABLE XL 151P3D4 v.1: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
168	G R Y N L N F H E A	5	
204	W C N A G W L S D G	5	
258	N G R F Y Y L I H P	5	
283	G A Q I A K V G Q I	5	
293	F A A W K I L G Y D	5	
2	K S L L L L V L I S	4	
42	V E A E Q A K V F S	4	
71	G S G I H K I R I K	4	
92	V D V F V S M G Y H	4	
139	C E V I E G L E D D	4	
157	Q G V V F P Y F P R	4	
162	P Y F P R L G R Y N	4	
164	F P R L G R Y N L N	4	
172	L N F H E A Q Q A C	4	
188	I A S F D Q L Y D A	4	
205	C N A G W L S D G S	4	
215	V Q Y P I T K P R E	4	
222	P R E P C G G Q N T	4	
232	V P G V R N Y G F W	4	
245	K S R Y D V F C F T	4	
257	F N G R F Y Y L I H	4	
304	C D A G W L A D G S	4	
314	V R Y P I S R P R R	4	
316	Y P I S R P R R R C	4	
342	H K L Y G V Y C F R	4	
28	R A I H I Q A E N G	3	
30	I H I Q A E N G P H	3	
65	R D P T A F G S G I	3	
70	F G S G I H K I R I	3	
72	S G I H K I R I K W	3	
77	I R I K W T K L T S	3	
114	L K G G S D S D A S	3	
198	W R G G L D W C N A	3	
200	G G L D W C N A G W	3	
210	L S D G S V Q Y P I	3	
221	K P R E P C G G Q N	3	
225	P C G G Q N T V P G	3	
238	Y G F W D K D K S R	3	
243	K D K S R Y D V F C	3	
299	L G Y D R C D A G W	3	
309	L A D G S V R Y P I	3	
318	I S R P R R R C S P	3	
323	R R C S P T E A A V	3	
324	R C S P T E A A V R	3	
332	V R F V G F P D K K	3	
10	I S I C W A D H L S	2	
37	G P H L L V E A E Q	2	
46	Q A K V F S H R G G	2	
52	H R G G N V T L P C	2	
60	P C K F Y R D P T A	2	
63	F Y R D P T A F G S	2	
85	T S D Y L K E V D V	2	
100	Y H K K T Y G G Y Q	2	

TABLE XL 151P3D4 v.1: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
101	H K K T Y G G Y Q G	2	
116	G G S D S D A S L V	2	
117	G S D S D A S L V I	2	
137	Y K C E V I E G L E	2	
170	Y N L N F H E A Q Q	2	
175	H E A Q Q A C L D Q	2	
178	Q Q A C L D Q D A V	2	
180	A C L D Q D A V I A	2	
197	A W R G G L D W C N	2	
216	Q Y P I T K P R E P	2	
217	Y P I T K P R E P C	2	
220	T K P R E P C G G Q	2	
228	G Q N T V P G V R N	2	
236	R N Y G F W D K D K	2	
240	F W D K D K S R Y D	2	
241	W D K D K S R Y D V	2	
276	V Q A C L N D G A Q	2	
277	Q A C L N D G A Q I	2	
296	W K I L G Y D R C D	2	
315	R Y P I S R P R R R	2	
319	S R P R R R C S P T	2	
337	F P D K K H K L Y G	2	
340	K K H K L Y G V Y C	2	
14	W A D H L S D N Y T	1	
21	N Y T L D H D R A I	1	
38	P H L L V E A E Q A	1	
47	A K V F S H R G G N	1	
59	L P C K F Y R D P T	1	
74	I H K I R I K W T K	1	
98	M G Y H K K T Y G G	1	
109	Q G R V F L K G G S	1	
110	G R V F L K G G S D	1	
127	T D L T L E D Y G R	1	
134	Y G R Y K C E V I E	1	
138	K C E V I E G L E D	1	
167	L G R Y N L N F H E	1	
169	R Y N L N F H E A Q	1	
177	A Q Q A C L D Q D A	1	
179	Q A C L D Q D A V I	1	
184	Q D A V I A S F D Q	1	
191	F D Q L Y D A W R G	1	
194	L Y D A W R G G L D	1	
195	Y D A W R G G L D W	1	
199	R G G L D W C N A G	1	
206	N A G W L S D G S V	1	
207	A G W L S D G S V Q	1	
223	R E P C G G Q N T V	1	
235	V R N Y G F W D K D	1	
237	N Y G F W D K D K S	1	
246	S R Y D V F C F T S	1	
265	I H P T K L T Y D E	1	
268	T K L T Y D E A V Q	1	
278	A C L N D G A Q I A	1	

TABLE XL 151P3D4 v.1: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
289	V G Q I F A A W K I	1	
294	A A W K I L G Y D R	1	
306	A G W L A D G S V R	1	
320	R P R R R C S P T E	1	
321	P R R R C S P T E A	1	
322	R R R C S P T E A A	1	
345	Y G V Y C F R A Y N	1	

TABLE XL 151P3D4 v.2: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
193	E I H Y R K N K Q L	25	
5	T T K T F P L R A L	24	
298	P T S S S T Y D S L	24	
45	G I I T Q G A K D F	22	
369	D L A G S G Y C G A	22	
20	S I R D H S G Q K M	21	
233	G F I F K T I A P L	21	
56	H V Q F V G S Y K L	19	
58	Q F V G S Y K L A Y	19	
361	Y V E N G R P A D L	19	
53	D F G H V Q F V G S	18	
106	S F C R N K L K Y L	18	
204	R L Q K Q A E K N M	18	
134	Q V P S R I F W R Q	17	
172	E V G W K Y Q A V T	17	
398	E R K A E N G P H L	17	
59	F V G S Y K L A Y S	16	
79	D E K Q R K D K V L	16	
108	C R N K L K Y L A F	16	
211	K N M K K K I D K Y	16	
7	K T F P L R A L H I	15	
36	D L L V P T K V T G	15	
37	L L V P T K V T G I	15	
40	P T K V T G I I T Q	15	
54	F G H V Q F V G S Y	15	
80	E K Q R K D K V L L	15	
196	Y R K N K Q L M R L	15	
244	A T R A T R I G H P	15	
301	S S T Y D S L S P Y	15	
15	H I V V E S I R D H	14	
42	K V T G I I T Q G A	14	
50	G A K D F G H V Q F	14	
95	V V S C E G I N I S	14	
109	R N K L K Y L A F L	14	
111	K L K Y L A F L H K	14	
187	K R K E K A E I H Y	14	
190	E K A E I H Y R K N	14	
234	F I F K T I A P L A	14	
238	T I A P L A A T R A	14	
366	R P A D L A G S G Y	14	
10	P L R A L H I V V E	13	

TABLE XL 151P3D4 v.2: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
16	I	V	V	E	S	I	R	D	H	S	13	
23	D	H	S	G	Q	K	M	K	Q	D	13	
29	M	K	Q	D	K	K	V	D	L	L	13	
47	I	T	Q	G	A	K	D	F	G	H	13	
68	S	N	D	G	E	H	W	T	V	Y	13	
75	T	V	Y	Q	D	E	K	Q	R	K	13	
88	L	L	G	R	K	A	V	V	V	S	13	
102	N	I	S	G	S	F	C	R	N	K	13	
105	G	S	F	C	R	N	K	L	K	Y	13	
123	N	T	N	P	S	R	R	P	Y	H	13	
124	T	N	P	S	R	R	P	Y	H	F	13	
131	Y	H	F	Q	V	P	S	R	I	F	13	
138	R	I	F	W	R	Q	E	K	A	D	13	
152	C	P	Q	G	H	A	S	E	A	Y	13	
182	A	T	L	E	E	K	R	K	E	K	13	
216	K	I	D	K	Y	T	E	S	P	G	13	
237	K	T	I	A	P	L	A	A	T	R	13	
256	R	T	P	R	A	G	S	S	A	H	13	
275	P	V	P	A	A	S	P	A	A	W	13	
288	R	T	P	W	T	R	P	S	S	C	13	
291	W	T	R	P	S	S	C	P	T	S	13	
295	S	S	C	P	T	S	S	S	T	Y	13	
352	K	P	K	S	E	N	N	S	W	Y	13	
377	G	A	L	W	K	A	I	E	S	L	13	
381	K	A	I	E	S	L	E	E	G	L	13	
384	E	S	L	E	E	G	L	G	G	K	13	
4	H	T	T	K	T	F	P	L	R	A	12	
17	V	V	E	S	I	R	D	H	S	G	12	
32	D	K	K	V	D	L	L	V	P	T	12	
34	K	V	D	L	L	V	P	T	K	V	12	
94	V	V	V	S	C	E	G	I	N	I	12	
163	K	V	C	L	S	G	A	P	H	E	12	
168	G	A	P	H	E	V	G	W	K	Y	12	
180	V	T	A	T	L	E	E	K	R	K	12	
220	Y	T	E	S	P	G	G	G	S	P	12	
225	G	G	G	S	P	R	G	L	G	F	12	
302	S	T	Y	D	S	L	S	P	Y	G	12	
342	N	V	L	A	R	G	K	P	Q	R	12	
356	E	N	N	S	W	Y	V	E	N	G	12	
3	E	H	T	T	K	T	F	P	L	R	11	
8	T	F	P	L	R	A	L	H	I	V	11	
28	K	M	K	Q	D	K	K	V	D	L	11	
38	L	V	P	T	K	V	T	G	I	I	11	
43	V	T	G	I	I	T	Q	G	A	K	11	
46	I	I	T	Q	G	A	K	D	F	G	11	
70	D	G	E	H	W	T	V	Y	Q	D	11	
74	W	T	V	Y	Q	D	E	K	Q	R	11	
86	K	V	L	L	G	R	K	A	V	V	11	
87	V	L	L	G	R	K	A	V	V	V	11	
98	C	E	G	I	N	I	S	G	S	F	11	
179	A	V	T	A	T	L	E	E	K	R	11	
183	T	L	E	E	K	R	K	E	K	A	11	
222	E	S	P	G	G	G	S	P	R	G	11	

TABLE XL 151P3D4 v.2: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
223	S	P	G	G	G	S	P	R	G	L	11	
227	G	S	P	R	G	L	G	F	I	F	11	
247	A	T	R	I	G	H	P	G	G	R	11	
306	S	L	S	P	Y	G	P	R	N	P	11	
320	R	H	S	P	S	G	G	G	G	L	11	
343	V	L	A	R	G	K	P	Q	R	K	11	
382	A	I	E	S	L	E	E	G	L	G	11	
385	S	L	E	E	G	L	G	G	K	Q	11	
389	G	L	G	G	K	Q	K	D	K	E	11	
399	R	K	A	E	N	G	P	H	L	L	11	
64	K	L	A	Y	S	N	D	G	E	H	10	
93	A	V	V	V	S	C	E	G	I	N	10	
100	G	I	N	I	S	G	S	F	C	R	10	
103	I	S	G	S	F	C	R	N	K	L	10	
114	Y	L	A	F	L	H	K	R	M	N	10	
116	A	F	L	H	K	R	M	N	T	N	10	
117	F	L	H	K	R	M	N	T	N	P	10	
122	M	N	T	N	P	S	R	R	P	Y	10	
165	C	L	S	G	A	P	H	E	V	G	10	
175	W	K	Y	Q	A	V	T	A	T	L	10	
201	Q	L	M	R	L	Q	K	Q	A	E	10	
241	P	L	A	A	T	R	A	T	R	I	10	
249	R	I	G	H	P	G	G	R	T	P	10	
261	G	S	S	A	H	R	P	P	A	L	10	
276	V	P	A	A	S	P	A	A	W	L	10	
278	A	A	S	P	A	A	W	L	P	L	10	
315	P	L	P	N	P	R	H	S	P	S	10	
328	G	L	K	K	P	A	R	H	C	Q	10	
335	H	C	Q	G	Q	K	H	N	V	L	10	
370	L	A	G	S	G	Y	C	G	A	L	10	
378	A	L	W	K	A	I	E	S	L	E	10	
13	A	L	H	I	V	V	E	S	I	R	9	
19	E	S	I	R	D	H	S	G	Q	K	9	
99	E	G	I	N	I	S	G	S	F	C	9	
113	K	Y	L	A	F	L	H	K	R	M	9	
147	D	G	G	S	C	C	P	Q	G	H	9	
157	A	S	E	A	Y	K	K	V	C	L	9	
185	E	E	K	R	K	E	K	A	E	I	9	
194	I	H	Y	R	K	N	K	Q	L	M	9	
269	A	L	S	A	R	A	P	V	P	A	9	
284	W	L	P	L	R	T	P	W	T	R	9	
305	D	S	L	S	P	Y	G	P	R	N	9	
307	L	S	P	Y	G	P	R	N	P	L	9	
1	M	L	E	H	T	T	K	T	F	P	8	
2	L	E	H	T	T	K	T	F	P	L	8	
97	S	C	E	G	I	N	I	S	G	S	8	
101	I	N	I	S	G	S	F	C	R	N	8	
144	E	K	A	D	G	G	S	C	C	P	8	
159	E	A	Y	K	K	V	C	L	S	G	8	
160	A	Y	K	K	V	C	L	S	G	A	8	
171	H	E	V	G	W	K	Y	Q	A	V	8	
207	K	Q	A	E	K	N	M	K	K	K	8	
231	G	L	G	F	I	F	K	T	I	A	8	

TABLE XL 151P3D4 v.2: HLA Peptide Scoring Results A26 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
235	I F K T I A P L A A	8	
264	A H R P P A L S A R	8	
286	P L R T P W T R P S	8	
364	N G R P A D L A G S	8	
387	E E G L G G K Q K D	8	
388	E G L G G K Q K D K	8	
11	L R A L H I V V E S	7	
61	G S Y K L A Y S N D	7	
72	E H W T V Y Q D E K	7	
82	Q R K D K V L L G R	7	
83	R K D K V L L G R K	7	
85	D K V L L G R K A V	7	
89	L G R K A V V V S C	7	
127	S R R P Y H F Q V P	7	
139	I F W R Q E K A D G	7	
155	G H A S E A Y K K V	7	
167	S G A P H E V G W K	7	
186	E K R K E K A E I H	7	
218	D K Y T E S P G G G	7	
270	L S A R A P V P A A	7	
310	Y G P R N P L P N P	7	
323	P S G G G G L K K P	7	
338	G Q K H N V L A R G	7	
363	E N G R P A D L A G	7	
396	D K E R K A E N G P	7	
31	Q D K K V D L L V P	6	
33	K K V D L L V P T K	6	
51	A K D F G H V Q F V	6	
57	V Q F V G S Y K L A	6	
90	G R K A V V V S C E	6	
129	R P Y H F Q V P S R	6	
132	H F Q V P S R I F W	6	
133	F Q V P S R I F W R	6	
174	G W K Y Q A V T A T	6	
199	N K Q L M R L Q K Q	6	
210	E K N M K K K I D K	6	
214	K K K I D K Y T E S	6	
226	G G S P R G L G F I	6	
228	S P R G L G F I F K	6	
230	R G L G F I F K T I	6	
236	F K T I A P L A A T	6	
279	A S P A A W L P L R	6	
337	Q G Q K H N V L A R	6	
355	S E N N S W Y V E N	6	
380	W K A I E S L E E G	6	
12	R A L H I V V E S I	5	
41	T K V T G I I T Q G	5	
48	T Q G A K D F G H V	5	
71	G E H W T V Y Q D E	5	
81	K Q R K D K V L L G	5	
112	L K Y L A F L H K R	5	
158	S E A Y K K V C L S	5	
178	Q A V T A T L E E K	5	

TABLE XL 151P3D4 v.2: HLA Peptide Scoring Results A26 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
188	R K E K A E I H Y R	5	
197	R K N K Q L M R L Q	5	
229	P R G L G F I F K T	5	
248	T R I G H P G G R T	5	
251	G H P G G R T P R A	5	
265	H R P P A L S A R A	5	
272	A R A P V P A A S P	5	
281	P A A W L P L R T P	5	
346	R G K P Q R K P K S	5	
373	S G Y C G A L W K A	5	
44	T G I I T Q G A K D	4	
52	K D F G H V Q F V G	4	
115	L A F L H K R M N T	4	
125	N P S R R P Y H F Q	4	
146	A D G G S C C P Q G	4	
150	S C C P Q G H A S E	4	
151	C C P Q G H A S E A	4	
215	K K I D K Y T E S P	4	
255	G R T P R A G S S A	4	
258	P R A G S S A H R P	4	
274	A P V P A A S P A A	4	
287	L R T P W T R P S S	4	
304	Y D S L S P Y G P R	4	
312	P R N P L P N P R H	4	
316	L P N P R H S P S G	4	
325	G G G G L K K P A R	4	
329	L K K P A R H C Q G	4	
350	Q R K P K S E N N S	4	
360	W Y V E N G R P A D	4	
394	Q K D K E R K A E N	4	
395	K D K E R K A E N G	4	
14	L H I V V E S I R D	3	
22	R D H S G Q K M K Q	3	
69	N D G E H W T V Y Q	3	
77	Y Q D E K Q R K D K	3	
96	V S C E G I N I S G	3	
137	S R I F W R Q E K A	3	
141	W R Q E K A D G G S	3	
145	K A D G G S C C P Q	3	
192	A E I H Y R K N K Q	3	
198	K N K Q L M R L Q K	3	
205	L Q K Q A E K N M K	3	
217	I D K Y T E S P G G	3	
219	K Y T E S P G G G S	3	
221	T E S P G G G S P R	3	
232	L G F I F K T I A P	3	
252	H P G G R T P R A G	3	
283	A W L P L R T P W T	3	
292	T R P S S C P T S S	3	
293	R P S S C P T S S S	3	
303	T Y D S L S P Y G P	3	
308	S P Y G P R N P L P	3	
314	N P L P N P R H S P	3	

TABLE XL 151P3D4 v.2: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
317	P N P R H S P S G G	3	
322	S P S G G G G L K K	3	
330	K K P A R H C Q G Q	3	
344	L A R G K P Q R K P	3	
347	G K P Q R K P K S E	3	
351	R K P K S E N N S W	3	
371	A G S G Y C G A L W	3	
374	G Y C G A L W K A I	3	
386	L E E G L G G K Q K	3	
391	G G K Q K D K E R K	3	
393	K Q K D K E R K A E	3	
18	V E S I R D H S G Q	2	
21	I R D H S G Q K M K	2	
24	H S G Q K M K Q D K	2	
25	S G Q K M K Q D K K	2	
26	G Q K M K Q D K K V	2	
30	K Q D K K V D L L V	2	
49	Q G A K D F G H V Q	2	
55	G H V Q F V G S Y K	2	
65	L A Y S N D G E H W	2	
76	V Y Q D E K Q R K D	2	
78	Q D E K Q R K D K V	2	
84	K D K V L L G R K A	2	
91	R K A V V V S C E G	2	
119	H K R M N T N P S R	2	
120	K R M N T N P S R R	2	
128	R R P Y H F Q V P S	2	
130	P Y H F Q V P S R I	2	
136	P S R I F W R Q E K	2	
140	F W R Q E K A D G G	2	
142	R Q E K A D G G S C	2	
143	Q E K A D G G S C C	2	
156	H A S E A Y K K V C	2	
161	Y K K V C L S G A P	2	
164	V C L S G A P H E V	2	
166	L S G A P H E V G W	2	
169	A P H E V G W K Y Q	2	
173	V G W K Y Q A V T A	2	
177	Y Q A V T A T L E E	2	
184	L E E K R K E K A E	2	
189	K E K A E I H Y R K	2	
195	H Y R K N K Q L M R	2	
202	L M R L Q K Q A E K	2	
203	M R L Q K Q A E K N	2	
206	Q K Q A E K N M K K	2	
208	Q A E K N M K K K I	2	
212	N M K K K I D K Y T	2	
213	M K K K I D K Y T E	2	
224	P G G G S P R G L G	2	
239	I A P L A A T R A T	2	
246	R A T R I G H P G G	2	
250	I G H P G G R T P R	2	
253	P G G R T P R A G S	2	

TABLE XL 151P3D4 v.2: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
257	T P R A G S S A H R	2	
260	A G S S A H R P P A	2	
262	S S A H R P P A L S	2	
266	R P P A L S A R A P	2	
267	P P A L S A R A P V	2	
268	P A L S A R A P V P	2	
271	S A R A P V P A A S	2	
273	R A P V P A A S P A	2	
277	P A A S P A A W L P	2	
280	S P A A W L P L R T	2	
294	P S S C P T S S S T	2	
299	T S S S T Y D S L S	2	
309	P Y G P R N P L P N	2	
313	R N P L P N P R H S	2	
319	P R H S P S G G G G	2	
321	H S P S G G G G L K	2	
324	S G G G G L K K P A	2	
326	G G G L K K P A R H	2	
327	G G L K K P A R H C	2	
331	K P A R H C Q G Q K	2	
332	P A R H C Q G Q K H	2	
334	R H C Q G Q K H N V	2	
336	C Q G Q K H N V L A	2	
348	K P Q R K P K S E N	2	
349	P Q R K P K S E N N	2	
353	P K S E N N S W Y V	2	
362	V E N G R P A D L A	2	
365	G R P A D L A G S G	2	
376	C G A L W K A I E S	2	
379	L W K A I E S L E E	2	
390	L G G K Q K D K E R	2	
392	G K Q K D K E R K A	2	
6	T K T F P L R A L H	1	
27	Q K M K Q D K K V D	1	
39	V P T K V T G I I T	1	
60	V G S Y K L A Y S N	1	
62	S Y K L A Y S N D G	1	
63	Y K L A Y S N D G E	1	
67	Y S N D G E H W T V	1	
73	H W T V Y Q D E K Q	1	
92	K A V V V S C E G I	1	
110	N K L K Y L A F L H	1	
118	L H K R M N T N P S	1	
121	R M N T N P S R R P	1	
126	P S R R P Y H F Q V	1	
135	V P S R I F W R Q E	1	
148	G G S C C P Q G H A	1	
149	G S C C P Q G H A S	1	
153	P Q G H A S E A Y K	1	
154	Q G H A S E A Y K K	1	
162	K K V C L S G A P H	1	
170	P H E V G W K Y Q A	1	
181	T A T L E E K R K E	1	

TABLE XL 151P3D4 v.2: HLA Peptide Scoring Results A26 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
191	K A E I H Y R K N K	1	
200	K Q L M R L Q K Q A	1	
209	A E K N M K K K I D	1	
240	A P L A A T R A T R	1	
242	L A A T R A T R I G	1	
243	A A T R A T R I G H	1	
245	T R A T R I G H P G	1	
254	G G R T P R A G S S	1	
259	R A G S S A H R P P	1	
263	S A H R P P A L S A	1	
285	L P L R T P W T R P	1	
289	T P W T R P S S C P	1	
296	S C P T S S S T Y D	1	
297	C P T S S S T Y D S	1	
300	S S S T Y D S L S P	1	
318	N P R H S P S G G G	1	
333	A R H C Q G Q K H N	1	
339	Q K H N V L A R G K	1	
340	K H N V L A R G K P	1	
345	A R G K P Q R K P K	1	
357	N N S W Y V E N G R	1	
358	N S W Y V E N G R P	1	
367	P A D L A G S G Y C	1	
375	Y C G A L W K A I E	1	
383	I E S L E E G L G G	1	
397	K E R K A E N G P H	1	

TABLE XLI 151P3D4 v.1: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
59	L P C K F Y R D P T	19	
326	S P T E A A V R F V	18	
266	H P T K L T Y D E A	17	
105	Y G G Y Q G R V F L	15	
145	L E D D T V V V A L	15	
224	E P C G G Q N T V P	15	
122	A S L V I T D L T L	14	
320	R P R R R C S P T E	14	
337	F P D K K H K L Y G	14	
115	K G G S D S D A S L	13	
221	K P R E P C G G Q N	13	
9	L I S I C W A D H L	12	
15	A D H L S D N Y T L	12	
31	H I Q A E N G P H L	12	
32	I Q A E N G P H L L	12	
50	F S H R G G N V T L	12	
80	K W T K L T S D Y L	12	
120	S D A S L V I T D L	12	
147	D D T V V V A L D L	12	
158	G V V F P Y F P R L	12	
164	F P R L G R Y N L N	12	
217	Y P I T K P R E P C	12	

TABLE XLI 151P3D4 v.1: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI

Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
232	V P G V R N Y G F W	12	
271	T Y D E A V Q A C L	12	
35	E N G P H L L V E A	11	
37	G P H L L V E A E Q	11	
66	D P T A F G S G I H	11	
75	H K I R I K W T K L	11	
136	R Y K C E V I E G L	11	
143	E G L E D D T V V V	11	
163	Y F P R L G R Y N L	11	
173	N F H E A Q Q A C L	11	
185	D A V I A S F D Q L	11	
193	Q L Y D A W R G G L	11	
201	G L D W C N A G W L	11	
245	K S R Y D V F C F T	11	
255	S N F N G R F Y Y L	11	
261	F Y Y L I H P T K L	11	
300	G Y D R C D A G W L	11	
309	L A D G S V R Y P I	11	
316	Y P I S R P R R R C	11	
322	R R R C S P T E A A	11	
328	T E A A V R F V G F	11	
335	V G F P D K K H K L	11	
1	M K S L L L L V L I	10	
70	F G S G I H K I R I	10	
76	K I R I K W T K L T	10	
87	D Y L K E V D V F V	10	
104	T Y G G Y Q G R V F	10	
117	G S D S D A S L V I	10	
118	S D S D A S L V I T	10	
142	I E G L E D D T V V	10	
144	G L E D D T V V V A	10	
155	D L Q G V V F P Y F	10	
161	F P Y F P R L G R Y	10	
165	P R L G R Y N L N F	10	
180	A C L D Q D A V I A	10	
210	L S D G S V Q Y P I	10	
280	L N D G A Q I A K V	10	
290	G Q I F A A W K I L	10	
297	K I L G Y D R C D A	10	
49	V F S H R G G N V T	9	
85	T S D Y L K E V D V	9	
89	L K E V D V F V S M	9	
103	K T Y G G Y Q G R V	9	
121	D A S L V I T D L T	9	
132	E D Y G R Y K C E V	9	
152	V A L D L Q G V V F	9	
177	A Q Q A C L D Q D A	9	
188	I A S F D Q L Y D A	9	
198	W R G G L D W C N A	9	
226	C G G Q N T V P G V	9	
242	D K D K S R Y D V F	9	
244	D K S R Y D V F C F	9	
269	K L T Y D E A V Q A	9	

TABLE XLI 151P3D4 v.1: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
275	A	V	Q	A	C	L	N	D	G	A	9	
284	A	Q	I	A	K	V	G	Q	I	F	9	
285	Q	I	A	K	V	G	Q	I	F	A	9	
321	P	R	R	R	C	S	P	T	E	A	9	
323	R	R	C	S	P	T	E	A	A	V	9	
343	K	L	Y	G	V	Y	C	F	R	A	9	
33	Q	A	E	N	G	P	H	L	L	V	8	
41	L	V	E	A	E	Q	A	K	V	F	8	
61	C	K	F	Y	R	D	P	T	A	F	8	
68	T	A	F	G	S	G	I	H	K	I	8	
86	S	D	Y	L	K	E	V	D	V	F	8	
95	F	V	S	M	G	Y	H	K	K	T	8	
113	F	L	K	G	G	S	D	S	D	A	8	
116	G	G	S	D	S	D	A	S	L	V	8	
133	D	Y	G	R	Y	K	C	E	V	I	8	
141	V	I	E	G	L	E	D	D	T	V	8	
151	V	V	A	L	D	L	Q	G	V	V	8	
178	Q	Q	A	C	L	D	Q	D	A	V	8	
179	Q	A	C	L	D	Q	D	A	V	I	8	
211	S	D	G	S	V	Q	Y	P	I	T	8	
231	T	V	P	G	V	R	N	Y	G	F	8	
256	N	F	N	G	R	F	Y	Y	L	I	8	
278	A	C	L	N	D	G	A	Q	I	A	8	
286	I	A	K	V	G	Q	I	F	A	A	8	
301	Y	D	R	C	D	A	G	W	L	A	8	
325	C	S	P	T	E	A	A	V	R	F	8	
341	K	H	K	L	Y	G	V	Y	C	F	8	
14	W	A	D	H	L	S	D	N	Y	T	7	
21	N	Y	T	L	D	H	D	R	A	I	7	
23	T	L	D	H	D	R	A	I	H	I	7	
25	D	H	D	R	A	I	H	I	Q	A	7	
34	A	E	N	G	P	H	L	L	V	E	7	
40	L	L	V	E	A	E	Q	A	K	V	7	
48	K	V	F	S	H	R	G	G	N	V	7	
52	H	R	G	G	N	V	T	L	P	C	7	
60	P	C	K	F	Y	R	D	P	T	A	7	
65	R	D	P	T	A	F	G	S	G	I	7	
73	G	I	H	K	I	R	I	K	W	T	7	
83	K	L	T	S	D	Y	L	K	E	V	7	
140	E	V	I	E	G	L	E	D	D	T	7	
150	V	V	V	A	L	D	L	Q	G	V	7	
153	A	L	D	L	Q	G	V	V	F	P	7	
168	G	R	Y	N	L	N	F	H	E	A	7	
182	L	D	Q	D	A	V	I	A	S	F	7	
206	N	A	G	W	L	S	D	G	S	V	7	
222	P	R	E	P	C	G	G	Q	N	T	7	
223	R	E	P	C	G	G	Q	N	T	V	7	
225	P	C	G	G	Q	N	T	V	P	G	7	
241	W	D	K	D	K	S	R	Y	D	V	7	
248	Y	D	V	F	C	F	T	S	N	F	7	
259	G	R	F	Y	Y	L	I	H	P	T	7	
262	Y	Y	L	I	H	P	T	K	L	T	7	
267	P	T	K	L	T	Y	D	E	A	V	7	

TABLE XLI 151P3D4 v.1: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
277	Q	A	C	L	N	D	G	A	Q	I	7	
283	G	A	Q	I	A	K	V	G	Q	I	7	
287	A	K	V	G	Q	I	F	A	A	W	7	
305	D	A	G	W	L	A	D	G	S	V	7	
319	S	R	P	R	R	R	C	S	P	T	7	
338	P	D	K	K	H	K	L	Y	G	V	7	
3	S	L	L	L	L	V	L	I	S	I	6	
6	L	L	V	L	I	S	I	C	W	A	6	
20	D	N	Y	T	L	D	H	D	R	A	6	
38	P	H	L	L	V	E	A	E	Q	A	6	
51	S	H	R	G	G	N	V	T	L	P	6	
54	G	G	N	V	T	L	P	C	K	F	6	
171	N	L	N	F	H	E	A	Q	Q	A	6	
197	A	W	R	G	G	L	D	W	C	N	6	
252	C	F	T	S	N	F	N	G	R	F	6	
289	V	G	Q	I	F	A	A	W	K	I	6	
324	R	C	S	P	T	E	A	A	V	R	6	
331	A	V	R	F	V	G	F	P	D	K	6	
17	H	L	S	D	N	Y	T	L	D	H	5	
107	G	Y	Q	G	R	V	F	L	K	G	5	
292	I	F	A	A	W	K	I	L	G	Y	5	
318	I	S	R	P	R	R	R	C	S	P	5	
2	K	S	L	L	L	L	V	L	I	S	4	
26	H	D	R	A	I	H	I	Q	A	E	4	
42	V	E	A	E	Q	A	K	V	F	S	4	
44	A	E	Q	A	K	V	F	S	H	R	4	
62	K	F	Y	R	D	P	T	A	F	G	4	
77	I	R	I	K	W	T	K	L	T	S	4	
114	L	K	G	G	S	D	S	D	A	S	4	
134	Y	G	R	Y	K	C	E	V	I	E	4	
146	E	D	D	T	V	V	V	A	L	D	4	
243	K	D	K	S	R	Y	D	V	F	C	4	
247	R	Y	D	V	F	C	F	T	S	N	4	
303	R	C	D	A	G	W	L	A	D	G	4	
310	A	D	G	S	V	R	Y	P	I	S	4	
329	E	A	A	V	R	F	V	G	F	P	4	
340	K	K	H	K	L	Y	G	V	Y	C	4	
45	E	Q	A	K	V	F	S	H	R	G	3	
47	A	K	V	F	S	H	R	G	G	N	3	
53	R	G	G	N	V	T	L	P	C	K	3	
64	Y	R	D	P	T	A	F	G	S	G	3	
69	A	F	G	S	G	I	H	K	I	R	3	
84	L	T	S	D	Y	L	K	E	V	D	3	
96	V	S	M	G	Y	H	K	K	T	Y	3	
119	D	S	D	A	S	L	V	I	T	D	3	
124	L	V	I	T	D	L	T	L	E	D	3	
138	K	C	E	V	I	E	G	L	E	D	3	
160	V	F	P	Y	F	P	R	L	G	R	3	
166	R	L	G	R	Y	N	L	N	F	H	3	
175	H	E	A	Q	Q	A	C	L	D	Q	3	
181	C	L	D	Q	D	A	V	I	A	S	3	
183	D	Q	D	A	V	I	A	S	F	D	3	
186	A	V	I	A	S	F	D	Q	L	Y	3	

TABLE XLI 151P3D4 v.1: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
187	V I A S F D Q L Y D	3	
189	A S F D Q L Y D A W	3	
195	Y D A W R G G L D W	3	
199	R G G L D W C N A G	3	
205	C N A G W L S D G S	3	
207	A G W L S D G S V Q	3	
209	W L S D G S V Q Y P	3	
234	G V R N Y G F W D K	3	
236	R N Y G F W D K D K	3	
253	F T S N F N G R F Y	3	
257	F N G R F Y Y L I H	3	
273	D E A V Q A C L N D	3	
281	N D G A Q I A K V G	3	
282	D G A Q I A K V G Q	3	
288	K V G Q I F A A W K	3	
294	A A W K I L G Y D R	3	
298	I L G Y D R C D A G	3	
302	D R C D A G W L A D	3	
304	C D A G W L A D G S	3	
306	A G W L A D G S V R	3	
307	G W L A D G S V R Y	3	
313	S V R Y P I S R P R	3	
314	V R Y P I S R P R R	3	
317	P I S R P R R R C S	3	
327	P T E A A V R F V G	3	
330	A A V R F V G F P D	3	
333	R F V G F P D K K H	3	
344	L Y G V Y C F R A Y	3	
11	S I C W A D H L S D	2	
12	I C W A D H L S D N	2	
22	Y T L D H D R A I H	2	
27	D R A I H I Q A E N	2	
29	A I H I Q A E N G P	2	
30	I H I Q A E N G P H	2	
36	N G P H L L V E A E	2	
43	E A E Q A K V F S H	2	
57	V T L P C K F Y R D	2	
63	F Y R D P T A F G S	2	
78	R I K W T K L T S D	2	
79	I K W T K L T S D Y	2	
82	T K L T S D Y L K E	2	
88	Y L K E V D V F V S	2	
90	K E V D V F V S M G	2	
91	E V D V F V S M G Y	2	
97	S M G Y H K K T Y G	2	
109	Q G R V F L K G G S	2	
126	I T D L T L E D Y G	2	
135	G R Y K C E V I E G	2	
149	T V V V A L D L Q G	2	
154	L D L Q G V V F P Y	2	
156	L Q G V V F P Y F P	2	
167	L G R Y N L N F H E	2	
169	R Y N L N F H E A Q	2	

TABLE XLI 151P3D4 v.1: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
190	S F D Q L Y D A W R	2	
194	L Y D A W R G G L D	2	
203	D W C N A G W L S D	2	
208	G W L S D G S V Q Y	2	
212	D G S V Q Y P I T K	2	
214	S V Q Y P I T K P R	2	
215	V Q Y P I T K P R E	2	
218	P I T K P R E P C G	2	
219	I T K P R E P C G G	2	
228	G Q N T V P G V R N	2	
230	N T V P G V R N Y G	2	
240	F W D K D K S R Y D	2	
258	N G R F Y Y L I H P	2	
260	R F Y Y L I H P T K	2	
263	Y L I H P T K L T Y	2	
264	L I H P T K L T Y D	2	
265	I H P T K L T Y D E	2	
268	T K L T Y D E A V Q	2	
270	L T Y D E A V Q A C	2	
276	V Q A C L N D G A Q	2	
295	A W K I L G Y D R C	2	
308	W L A D G S V R Y P	2	
311	D G S V R Y P I S R	2	
345	Y G V Y C F R A Y N	2	
7	L V L I S I C W A D	1	
8	V L I S I C W A D H	1	
10	I S I C W A D H L S	1	
13	C W A D H L S D N Y	1	
16	D H L S D N Y T L D	1	
18	L S D N Y T L D H D	1	
28	R A I H I Q A E N G	1	
39	H L L V E A E Q A K	1	
55	G N V T L P C K F Y	1	
67	P T A F G S G I H K	1	
71	G S G I H K I R I K	1	
72	S G I H K I R I K W	1	
74	I H K I R I K W T K	1	
98	M G Y H K K T Y G G	1	
99	G Y H K K T Y G G Y	1	
100	Y H K K T Y G G Y Q	1	
102	K K T Y G G Y Q G R	1	
106	G G Y Q G R V F L K	1	
108	Y Q G R V F L K G G	1	
111	R V F L K G G S D S	1	
112	V F L K G G S D S D	1	
123	S L V I T D L T L E	1	
130	T L E D Y G R Y K C	1	
131	L E D Y G R Y K C E	1	
157	Q G V V F P Y F P R	1	
159	V V F P Y F P R L G	1	
162	P Y F P R L G R Y N	1	
170	Y N L N F H E A Q Q	1	
172	L N F H E A Q Q A C	1	

TABLE XLI 151P3D4 v.1: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
174	F	H	E	A	Q	Q	A	C	L	D	1	
176	E	A	Q	Q	A	C	L	D	Q	D	1	
184	Q	D	A	V	I	A	S	F	D	Q	1	
200	G	G	L	D	W	C	N	A	G	W	1	
204	W	C	N	A	G	W	L	S	D	G	1	
213	G	S	V	Q	Y	P	I	T	K	P	1	
227	G	G	Q	N	T	V	P	G	V	R	1	
229	Q	N	T	V	P	G	V	R	N	Y	1	
237	N	Y	G	F	W	D	K	D	K	S	1	
249	D	V	F	C	F	T	S	N	F	N	1	
251	F	C	F	T	S	N	F	N	G	R	1	
254	T	S	N	F	N	G	R	F	Y	Y	1	
272	Y	D	E	A	V	Q	A	C	L	N	1	
274	E	A	V	Q	A	C	L	N	D	G	1	
279	C	L	N	D	G	A	Q	I	A	K	1	
291	Q	I	F	A	A	W	K	I	L	G	1	
293	F	A	A	W	K	I	L	G	Y	D	1	
299	L	G	Y	D	R	C	D	A	G	W	1	
315	R	Y	P	I	S	R	P	R	R	R	1	
334	F	V	G	F	P	D	K	K	H	K	1	
339	D	K	K	H	K	L	Y	G	V	Y	1	
342	H	K	L	Y	G	V	Y	C	F	R	1	

TABLE XLI 151P3D4 v.2: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
223	S	P	G	G	G	S	P	R	G	L	23	
276	V	P	A	A	S	P	A	A	W	L	23	
274	A	P	V	P	A	A	S	P	A	A	21	
267	P	P	A	L	S	A	R	A	P	V	20	
280	S	P	A	A	W	L	P	L	R	T	20	
278	A	A	S	P	A	A	W	L	P	L	18	
9	F	P	L	R	A	L	H	I	V	V	17	
39	V	P	T	K	V	T	G	I	I	T	17	
228	S	P	R	G	L	G	F	I	F	K	16	
322	S	P	S	G	G	G	G	L	K	K	16	
157	A	S	E	A	Y	K	K	V	C	L	15	
240	A	P	L	A	A	T	R	A	T	R	15	
261	G	S	S	A	H	R	P	P	A	L	15	
252	H	P	G	G	R	T	P	R	A	G	14	
257	T	P	R	A	G	S	S	A	H	R	14	
269	A	L	S	A	R	A	P	V	P	A	14	
293	R	P	S	S	C	P	T	S	S	S	14	
320	R	H	S	P	S	G	G	G	G	L	14	
28	K	M	K	Q	D	K	K	V	D	L	13	
80	E	K	Q	R	K	D	K	V	L	L	13	
103	I	S	G	S	F	C	R	N	K	L	13	
109	R	N	K	L	K	Y	L	A	F	L	13	
125	N	P	S	R	R	P	Y	H	F	Q	13	
129	R	P	Y	H	F	Q	V	P	S	R	13	
152	C	P	Q	G	H	A	S	E	A	Y	13	
260	A	G	S	S	A	H	R	P	P	A	13	

TABLE XLI 151P3D4 v.2: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
266	R	P	P	A	L	S	A	R	A	P	13	
308	S	P	Y	G	P	R	N	P	L	P	13	
311	G	P	R	N	P	L	P	N	P	R	13	
335	H	C	Q	G	Q	K	H	N	V	L	13	
398	E	R	K	A	E	N	G	P	H	L	13	
2	L	E	H	T	T	K	T	F	P	L	12	
135	V	P	S	R	I	F	W	R	Q	E	12	
169	A	P	H	E	V	G	W	K	Y	Q	12	
175	W	K	Y	Q	A	V	T	A	T	L	12	
233	G	F	I	F	K	T	I	A	P	L	12	
298	P	T	S	S	S	T	Y	D	S	L	12	
307	L	S	P	Y	G	P	R	N	P	L	12	
314	N	P	L	P	N	P	R	H	S	P	12	
316	L	P	N	P	R	H	S	P	S	G	12	
318	N	P	R	H	S	P	S	G	G	G	12	
331	K	P	A	R	H	C	Q	G	Q	K	12	
366	R	P	A	D	L	A	G	S	G	Y	12	
370	L	A	G	S	G	Y	C	G	A	L	12	
399	R	K	A	E	N	G	P	H	L	L	12	
5	T	T	K	T	F	P	L	R	A	L	11	
29	M	K	Q	D	K	K	V	D	L	L	11	
30	K	Q	D	K	K	V	D	L	L	V	11	
51	A	K	D	F	G	H	V	Q	F	V	11	
79	D	E	K	Q	R	K	D	K	V	L	11	
87	V	L	L	G	R	K	A	V	V	V	11	
193	E	I	H	Y	R	K	N	K	Q	L	11	
283	A	W	L	P	L	R	T	P	W	T	11	
285	L	P	L	R	T	P	W	T	R	P	11	
297	C	P	T	S	S	S	T	Y	D	S	11	
348	K	P	Q	R	K	P	K	S	E	N	11	
352	K	P	K	S	E	N	N	S	W	Y	11	
361	Y	V	E	N	G	R	P	A	D	L	11	
381	K	A	I	E	S	L	E	E	G	L	11	
7	K	T	F	P	L	R	A	L	H	I	10	
42	K	V	T	G	I	I	T	Q	G	A	10	
56	H	V	Q	F	V	G	S	Y	K	L	10	
66	A	Y	S	N	D	G	E	H	W	T	10	
106	S	F	C	R	N	K	L	K	Y	L	10	
108	C	R	N	K	L	K	Y	L	A	F	10	
172	E	V	G	W	K	Y	Q	A	V	T	10	
196	Y	R	K	N	K	Q	L	M	R	L	10	
226	G	G	S	P	R	G	L	G	F	I	10	
230	R	G	L	G	F	I	F	K	T	I	10	
235	I	F	K	T	I	A	P	L	A	A	10	
251	G	H	P	G	G	R	T	P	R	A	10	
270	L	S	A	R	A	P	V	P	A	A	10	
289	T	P	W	T	R	P	S	S	C	P	10	
324	S	G	G	G	G	L	K	K	P	A	10	
377	G	A	L	W	K	A	I	E	S	L	10	
4	H	T	T	K	T	F	P	L	R	A	9	
32	D	K	K	V	D	L	L	V	P	T	9	
34	K	V	D	L	L	V	P	T	K	V	9	
37	L	L	V	P	T	K	V	T	G	I	9	

TABLE XLI 151P3D4 v.2: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
48	T Q G A K D F G H V	9	
86	K V L L G R K A V V	9	
160	A Y K K V C L S G A	9	
171	H E V G W K Y Q A V	9	
173	V G W K Y Q A V T A	9	
174	G W K Y Q A V T A T	9	
225	G G G S P R G L G F	9	
238	T I A P L A A T R A	9	
239	I A P L A A T R A T	9	
241	P L A A T R A T R I	9	
336	C Q G Q K H N V L A	9	
369	D L A G S G Y C G A	9	
374	G Y C G A L W K A I	9	
12	R A L H I V V E S I	8	
20	S I R D H S G Q K M	8	
35	V D L L V P T K V T	8	
50	G A K D F G H V Q F	8	
85	D K V L L G R K A V	8	
107	F C R N K L K Y L A	8	
113	K Y L A F L H K R M	8	
126	P S R R P Y H F Q V	8	
148	G G S C C P Q G H A	8	
185	E E K R K E K A E I	8	
204	R L Q K Q A E K N M	8	
231	G L G F I F K T I A	8	
234	F I F K T I A P L A	8	
236	F K T I A P L A A T	8	
248	T R I G H P G G R T	8	
263	S A H R P P A L S A	8	
265	H R P P A L S A R A	8	
273	R A P V P A A S P A	8	
294	P S S C P T S S S T	8	
353	P K S E N N S W Y V	8	
362	V E N G R P A D L A	8	
38	L V P T K V T G I I	7	
78	Q D E K Q R K D K V	7	
81	K Q R K D K V L L G	7	
84	K D K V L L G R K A	7	
92	K A V V V S C E G I	7	
98	C E G I N I S G S F	7	
115	L A F L H K R M N T	7	
155	G H A S E A Y K K V	7	
194	I H Y R K N K Q L M	7	
200	K Q L M R L Q K Q A	7	
208	Q A E K N M K K K I	7	
212	N M K K K I D K Y T	7	
229	P R G L G F I F K T	7	
255	G R T P R A G S S A	7	
290	P W T R P S S C P T	7	
334	R H C Q G Q K H N V	7	
359	S W Y V E N G R P A	7	
371	A G S G Y C G A L W	7	
392	G K Q K D K E R K A	7	

TABLE XLI 151P3D4 v.2: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
8	T F P L R A L H I V	6	
10	P L R A L H I V V E	6	
26	G Q K M K Q D K K V	6	
45	G I I T Q G A K D F	6	
57	V Q F V G S Y K L A	6	
67	Y S N D G E H W T V	6	
89	L G R K A V V V S C	6	
94	V V V S C E G I N I	6	
124	T N P S R R P Y H F	6	
130	P Y H F Q V P S R I	6	
131	Y H F Q V P S R I F	6	
137	S R I F W R Q E K A	6	
146	A D G G S C C P Q G	6	
151	C C P Q G H A S E A	6	
164	V C L S G A P H E V	6	
170	P H E V G W K Y Q A	6	
183	T L E E K R K E K A	6	
227	G S P R G L G F I F	6	
264	A H R P P A L S A R	6	
345	A R G K P Q R K P K	6	
373	S G Y C G A L W K A	6	
58	Q F V G S Y K L A Y	5	
68	S N D G E H W T V Y	5	
88	L L G R K A V V V S	5	
127	S R R P Y H F Q V P	5	
145	K A D G G S C C P Q	5	
165	C L S G A P H E V G	5	
195	H Y R K N K Q L M R	5	
244	A T R A T R I G H P	5	
250	I G H P G G R T P R	5	
271	S A R A P V P A A S	5	
272	A R A P V P A A S P	5	
282	A A W L P L R T P W	5	
309	P Y G P R N P L P N	5	
325	G G G G L K K P A R	5	
337	Q G Q K H N V L A R	5	
363	E N G R P A D L A G	5	
383	I E S L E E G L G G	5	
397	K E R K A E N G P H	5	
11	L R A L H I V V E S	4	
23	D H S G Q K M K Q D	4	
31	Q D K K V D L L V P	4	
52	K D F G H V Q F V G	4	
53	D F G H V Q F V G S	4	
69	N D G E H W T V Y Q	4	
102	N I S G S F C R N K	4	
111	K L K Y L A F L H K	4	
128	R R P Y H F Q V P S	4	
159	E A Y K K V C L S G	4	
166	L S G A P H E V G W	4	
177	Y Q A V T A T L E E	4	
186	E K R K E K A E I H	4	
198	K N K Q L M R L Q K	4	

TABLE XLI 151P3D4 v.2: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
216	K	I	D	K	Y	T	E	S	P	G	4	
221	T	E	S	P	G	G	G	S	P	R	4	
222	E	S	P	G	G	G	S	P	R	G	4	
224	P	G	G	G	S	P	R	G	L	G	4	
247	A	T	R	I	G	H	P	G	G	R	4	
279	A	S	P	A	A	W	L	P	L	R	4	
286	P	L	R	T	P	W	T	R	P	S	4	
291	W	T	R	P	S	S	C	P	T	S	4	
300	S	S	S	T	Y	D	S	L	S	P	4	
344	L	A	R	G	K	P	Q	R	K	P	4	
364	N	G	R	P	A	D	L	A	G	S	4	
3	E	H	T	T	K	T	F	P	L	R	3	
27	Q	K	M	K	Q	D	K	K	V	D	3	
33	K	K	V	D	L	L	V	P	T	K	3	
47	I	T	Q	G	A	K	D	F	G	H	3	
49	Q	G	A	K	D	F	G	H	V	Q	3	
83	R	K	D	K	V	L	L	G	R	K	3	
119	H	K	R	M	N	T	N	P	S	R	3	
123	N	T	N	P	S	R	R	P	Y	H	3	
136	P	S	R	I	F	W	R	Q	E	K	3	
156	H	A	S	E	A	Y	K	K	V	C	3	
162	K	K	V	C	L	S	G	A	P	H	3	
167	S	G	A	P	H	E	V	G	W	K	3	
176	K	Y	Q	A	V	T	A	T	L	E	3	
179	A	V	T	A	T	L	E	E	K	R	3	
182	A	T	L	E	E	K	R	K	E	K	3	
202	L	M	R	L	Q	K	Q	A	E	K	3	
211	K	N	M	K	K	K	I	D	K	Y	3	
237	K	T	I	A	P	L	A	A	T	R	3	
243	A	A	T	R	A	T	R	I	G	H	3	
253	P	G	G	R	T	P	R	A	G	S	3	
258	P	R	A	G	S	S	A	H	R	P	3	
259	R	A	G	S	S	A	H	R	P	P	3	
275	P	V	P	A	A	S	P	A	A	W	3	
287	L	R	T	P	W	T	R	P	S	S	3	
304	Y	D	S	L	S	P	Y	G	P	R	3	
306	S	L	S	P	Y	G	P	R	N	P	3	
323	P	S	G	G	G	G	L	K	K	P	3	
346	R	G	K	P	Q	R	K	P	K	S	3	
349	P	Q	R	K	P	K	S	E	N	N	3	
360	W	Y	V	E	N	G	R	P	A	D	3	
368	A	D	L	A	G	S	G	Y	C	G	3	
372	G	S	G	Y	C	G	A	L	W	K	3	
375	Y	C	G	A	L	W	K	A	I	E	3	
378	A	L	W	K	A	I	E	S	L	E	3	
379	L	W	K	A	I	E	S	L	E	E	3	
388	E	G	L	G	G	K	Q	K	D	K	3	
389	G	L	G	G	K	Q	K	D	K	E	3	
393	K	Q	K	D	K	E	R	K	A	E	3	
394	Q	K	D	K	E	R	K	A	E	N	3	
1	M	L	E	H	T	T	K	T	F	P	2	
6	T	K	T	F	P	L	R	A	L	H	2	
13	A	L	H	I	V	V	E	S	I	R	2	

TABLE XLI 151P3D4 v.2: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
16	I	V	V	E	S	I	R	D	H	S	2	
18	V	E	S	I	R	D	H	S	G	Q	2	
21	I	R	D	H	S	G	Q	K	M	K	2	
36	D	L	L	V	P	T	K	V	T	G	2	
43	V	T	G	I	I	T	Q	G	A	K	2	
46	I	I	T	Q	G	A	K	D	F	G	2	
59	F	V	G	S	Y	K	L	A	Y	S	2	
60	V	G	S	Y	K	L	A	Y	S	N	2	
64	K	L	A	Y	S	N	D	G	E	H	2	
77	Y	Q	D	E	K	Q	R	K	D	K	2	
82	Q	R	K	D	K	V	L	L	G	R	2	
90	G	R	K	A	V	V	V	S	C	E	2	
91	R	K	A	V	V	V	S	C	E	G	2	
93	A	V	V	V	S	C	E	G	I	N	2	
95	V	V	S	C	E	G	I	N	I	S	2	
97	S	C	E	G	I	N	I	S	G	S	2	
99	E	G	I	N	I	S	G	S	F	C	2	
101	I	N	I	S	G	S	F	C	R	N	2	
104	S	G	S	F	C	R	N	K	L	K	2	
105	G	S	F	C	R	N	K	L	K	Y	2	
116	A	F	L	H	K	R	M	N	T	N	2	
117	F	L	H	K	R	M	N	T	N	P	2	
118	L	H	K	R	M	N	T	N	P	S	2	
120	K	R	M	N	T	N	P	S	R	R	2	
122	M	N	T	N	P	S	R	R	P	Y	2	
132	H	F	Q	V	P	S	R	I	F	W	2	
138	R	I	F	W	R	Q	E	K	A	D	2	
139	I	F	W	R	Q	E	K	A	D	G	2	
140	F	W	R	Q	E	K	A	D	G	G	2	
142	R	Q	E	K	A	D	G	G	S	C	2	
144	E	K	A	D	G	G	S	C	C	P	2	
150	S	C	C	P	Q	G	H	A	S	E	2	
153	P	Q	G	H	A	S	E	A	Y	K	2	
158	S	E	A	Y	K	K	V	C	L	S	2	
163	K	V	C	L	S	G	A	P	H	E	2	
184	L	E	E	K	R	K	E	K	A	E	2	
188	R	K	E	K	A	E	I	H	Y	R	2	
189	K	E	K	A	E	I	H	Y	R	K	2	
190	E	K	A	E	I	H	Y	R	K	N	2	
191	K	A	E	I	H	Y	R	K	N	K	2	
192	A	E	I	H	Y	R	K	N	K	Q	2	
197	R	K	N	K	Q	L	M	R	L	Q	2	
201	Q	L	M	R	L	Q	K	Q	A	E	2	
207	K	Q	A	E	K	N	M	K	K	K	2	
209	A	E	K	N	M	K	K	K	I	D	2	
214	K	K	K	I	D	K	Y	T	E	S	2	
215	K	K	I	D	K	Y	T	E	S	P	2	
217	I	D	K	Y	T	E	S	P	G	G	2	
232	L	G	F	I	F	K	T	I	A	P	2	
242	L	A	A	T	R	A	T	R	I	G	2	
245	T	R	A	T	R	I	G	H	P	G	2	
246	R	A	T	R	I	G	H	P	G	G	2	
249	R	I	G	H	P	G	G	R	T	P	2	

TABLE XLI 151P3D4 v.2: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
254	G	G	R	T	P	R	A	G	S	S	2	
256	R	T	P	R	A	G	S	S	A	H	2	
262	S	S	A	H	R	P	P	A	L	S	2	
268	P	A	L	S	A	R	A	P	V	P	2	
299	T	S	S	S	T	Y	D	S	L	S	2	
312	P	R	N	P	L	P	N	P	R	H	2	
326	G	G	G	L	K	K	P	A	R	H	2	
328	G	L	K	K	P	A	R	H	C	Q	2	
330	K	K	P	A	R	H	C	Q	G	Q	2	
332	P	A	R	H	C	Q	G	Q	K	H	2	
333	A	R	H	C	Q	G	Q	K	H	N	2	
340	K	H	N	V	L	A	R	G	K	P	2	
342	N	V	L	A	R	G	K	P	Q	R	2	
351	R	K	P	K	S	E	N	N	S	W	2	
354	K	S	E	N	N	S	W	Y	V	E	2	
355	S	E	N	N	S	W	Y	V	E	N	2	
356	E	N	N	S	W	Y	V	E	N	G	2	
357	N	N	S	W	Y	V	E	N	G	R	2	
382	A	I	E	S	L	E	E	G	L	G	2	
386	L	E	E	G	L	G	G	K	Q	K	2	
387	E	E	G	L	G	G	K	Q	K	D	2	
390	L	G	G	K	Q	K	D	K	E	R	2	
19	E	S	I	R	D	H	S	G	Q	K	1	
22	R	D	H	S	G	Q	K	M	K	Q	1	
24	H	S	G	Q	K	M	K	Q	D	K	1	
25	S	G	Q	K	M	K	Q	D	K	K	1	
41	T	K	V	T	G	I	I	T	Q	G	1	
44	T	G	I	I	T	Q	G	A	K	D	1	
54	F	G	H	V	Q	F	V	G	S	Y	1	
61	G	S	Y	K	L	A	Y	S	N	D	1	
63	Y	K	L	A	Y	S	N	D	G	E	1	
70	D	G	E	H	W	T	V	Y	Q	D	1	
72	E	H	W	T	V	Y	Q	D	E	K	1	
110	N	K	L	K	Y	L	A	F	L	H	1	
114	Y	L	A	F	L	H	K	R	M	N	1	
121	R	M	N	T	N	P	S	R	R	P	1	
133	F	Q	V	P	S	R	I	F	W	R	1	
134	Q	V	P	S	R	I	F	W	R	Q	1	
143	Q	E	K	A	D	G	G	S	C	C	1	
147	D	G	G	S	C	C	P	Q	G	H	1	
149	G	S	C	C	P	Q	G	H	A	S	1	
154	Q	G	H	A	S	E	A	Y	K	K	1	
161	Y	K	K	V	C	L	S	G	A	P	1	
180	V	T	A	T	L	E	E	K	R	K	1	
187	K	R	K	E	K	A	E	I	H	Y	1	
206	Q	K	Q	A	E	K	N	M	K	K	1	
210	E	K	N	M	K	K	K	I	D	K	1	
213	M	K	K	K	I	D	K	Y	T	E	1	
219	K	Y	T	E	S	P	G	G	G	S	1	
277	P	A	A	S	P	A	A	W	L	P	1	
281	P	A	A	W	L	P	L	R	T	P	1	
288	R	T	P	W	T	R	P	S	S	C	1	
292	T	R	P	S	S	C	P	T	S	S	1	

TABLE XLI 151P3D4 v.2: HLA Peptide Scoring Results B*0702 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
295	S	S	C	P	T	S	S	S	T	Y	1	
296	S	C	P	T	S	S	S	T	Y	D	1	
301	S	S	T	Y	D	S	L	S	P	Y	1	
302	S	T	Y	D	S	L	S	P	Y	G	1	
303	T	Y	D	S	L	S	P	Y	G	P	1	
305	D	S	L	S	P	Y	G	P	R	N	1	
310	Y	G	P	R	N	P	L	P	N	P	1	
313	R	N	P	L	P	N	P	R	H	S	1	
315	P	L	P	N	P	R	H	S	P	S	1	
327	G	G	L	K	K	P	A	R	H	C	1	
329	L	K	K	P	A	R	H	C	Q	G	1	
338	G	Q	K	H	N	V	L	A	R	G	1	
341	H	N	V	L	A	R	G	K	P	Q	1	
343	V	L	A	R	G	K	P	Q	R	K	1	
350	Q	R	K	P	K	S	E	N	N	S	1	
365	G	R	P	A	D	L	A	G	S	G	1	
367	P	A	D	L	A	G	S	G	Y	C	1	
376	C	G	A	L	W	K	A	I	E	S	1	
380	W	K	A	I	E	S	L	E	E	G	1	
384	E	S	L	E	E	G	L	G	G	K	1	
395	K	D	K	E	R	K	A	E	N	G	1	

TABLE XLII 151P3D4: HLA Peptide Scoring Results B*08 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
	NO DATA		

TABLE XLIII 151P3D4: HLA Peptide Scoring Results B*1510 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
	NO DATA		

TABLE XLIV 151P3D4: HLA Peptide Scoring Results B*2705 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
	NO DATA		

TABLE XLV 151P3D4: HLA Peptide Scoring Results B*2709 10-mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0	score	SEQ. ID NO.
	NO DATA		

TABLE XLVI 151P3D4 v.1: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
145	L	E	D	D	T	V	V	V	A	L	26	
328	T	E	A	A	V	R	F	V	G	F	22	
189	A	S	F	D	Q	L	Y	D	A	W	18	

TABLE XLVI 151P3D4 v.1: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
34	A	E	N	G	P	H	L	L	V	E	17	
72	S	G	I	H	K	I	R	I	K	W	17	
186	A	V	I	A	S	F	D	Q	L	Y	17	
287	A	K	V	G	Q	I	F	A	A	W	17	
335	V	G	F	P	D	K	K	H	K	L	17	
68	T	A	F	G	S	G	I	H	K	I	16	
122	A	S	L	V	I	T	D	L	T	L	16	
284	A	Q	I	A	K	V	G	Q	I	F	16	
15	A	D	H	L	S	D	N	Y	T	L	15	
61	C	K	F	Y	R	D	P	T	A	F	15	
75	H	K	I	R	I	K	W	T	K	L	15	
96	V	S	M	G	Y	H	K	K	T	Y	15	
255	S	N	F	N	G	R	F	Y	Y	L	15	
263	Y	L	I	H	P	T	K	L	T	Y	15	
290	G	Q	I	F	A	A	W	K	I	L	15	
336	G	F	P	D	K	K	H	K	L	Y	15	
41	L	V	E	A	E	Q	A	K	V	F	14	
44	A	E	Q	A	K	V	F	S	H	R	14	
86	S	D	Y	L	K	E	V	D	V	F	14	
120	S	D	A	S	L	V	I	T	D	L	14	
152	V	A	L	D	L	Q	G	V	V	F	14	
182	L	D	Q	D	A	V	I	A	S	F	14	
292	I	F	A	A	W	K	I	L	G	Y	14	
325	C	S	P	T	E	A	A	V	R	F	14	
344	L	Y	G	V	Y	C	F	R	A	Y	14	
1	M	K	S	L	L	L	L	V	L	I	13	
3	S	L	L	L	L	V	L	I	S	I	13	
21	N	Y	T	L	D	H	D	R	A	I	13	
32	I	Q	A	E	N	G	P	H	L	L	13	
50	F	S	H	R	G	G	N	V	T	L	13	
55	G	N	V	T	L	P	C	K	F	Y	13	
90	K	E	V	D	V	F	V	S	M	G	13	
91	E	V	D	V	F	V	S	M	G	Y	13	
104	T	Y	G	G	Y	Q	G	R	V	F	13	
131	L	E	D	Y	G	R	Y	K	C	E	13	
136	R	Y	K	C	E	V	I	E	G	L	13	
163	Y	F	P	R	L	G	R	Y	N	L	13	
165	P	R	L	G	R	Y	N	L	N	F	13	
208	G	W	L	S	D	G	S	V	Q	Y	13	
223	R	E	P	C	G	G	Q	N	T	V	13	
244	D	K	S	R	Y	D	V	F	C	F	13	
253	F	T	S	N	F	N	G	R	F	Y	13	
261	F	Y	Y	L	I	H	P	T	K	L	13	
300	G	Y	D	R	C	D	A	G	W	L	13	
341	K	H	K	L	Y	G	V	Y	C	F	13	
5	L	L	L	V	L	I	S	I	C	W	12	
9	L	I	S	I	C	W	A	D	H	L	12	
54	G	G	N	V	T	L	P	C	K	F	12	
79	I	K	W	T	K	L	T	S	D	Y	12	
105	Y	G	G	Y	Q	G	R	V	F	L	12	
125	V	I	T	D	L	T	L	E	D	Y	12	
142	I	E	G	L	E	D	D	T	V	V	12	
147	D	D	T	V	V	V	A	L	D	L	12	

TABLE XLVI 151P3D4 v.1: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
154	L	D	L	Q	G	V	V	F	P	Y	12	
155	D	L	Q	G	V	V	F	P	Y	F	12	
185	D	A	V	I	A	S	F	D	Q	L	12	
193	Q	L	Y	D	A	W	R	G	G	L	12	
200	G	G	L	D	W	C	N	A	G	W	12	
201	G	L	D	W	C	N	A	G	W	L	12	
229	Q	N	T	V	P	G	V	R	N	Y	12	
231	T	V	P	G	V	R	N	Y	G	F	12	
242	D	K	D	K	S	R	Y	D	V	F	12	
307	G	W	L	A	D	G	S	V	R	Y	12	
13	C	W	A	D	H	L	S	D	N	Y	11	
23	T	L	D	H	D	R	A	I	H	I	11	
42	V	E	A	E	Q	A	K	V	F	S	11	
70	F	G	S	G	I	H	K	I	R	I	11	
80	K	W	T	K	L	T	S	D	Y	L	11	
115	K	G	G	S	D	S	D	A	S	L	11	
117	G	S	D	S	D	A	S	L	V	I	11	
128	D	L	T	L	E	D	Y	G	R	Y	11	
139	C	E	V	I	E	G	L	E	D	D	11	
158	G	V	V	F	P	Y	F	P	R	L	11	
161	F	P	Y	F	P	R	L	G	R	Y	11	
173	N	F	H	E	A	Q	Q	A	C	L	11	
175	H	E	A	Q	Q	A	C	L	D	Q	11	
195	Y	D	A	W	R	G	G	L	D	W	11	
239	G	F	W	D	K	D	K	S	R	Y	11	
248	Y	D	V	F	C	F	T	S	N	F	11	
254	T	S	N	F	N	G	R	F	Y	Y	11	
256	N	F	N	G	R	F	Y	Y	L	I	11	
271	T	Y	D	E	A	V	Q	A	C	L	11	
273	D	E	A	V	Q	A	C	L	N	D	11	
299	L	G	Y	D	R	C	D	A	G	W	11	
309	L	A	D	G	S	V	R	Y	P	I	11	
339	D	K	K	H	K	L	Y	G	V	Y	11	
31	H	I	Q	A	E	N	G	P	H	L	10	
65	R	D	P	T	A	F	G	S	G	I	10	
99	G	Y	H	K	K	T	Y	G	G	Y	10	
133	D	Y	G	R	Y	K	C	E	V	I	10	
179	Q	A	C	L	D	Q	D	A	V	I	10	
210	L	S	D	G	S	V	Q	Y	P	I	10	
232	V	P	G	V	R	N	Y	G	F	W	10	
252	C	F	T	S	N	F	N	G	R	F	10	
277	Q	A	C	L	N	D	G	A	Q	I	10	
283	G	A	Q	I	A	K	V	G	Q	I	10	
289	V	G	Q	I	F	A	A	W	K	I	10	
159	V	V	F	P	Y	F	P	R	L	G	8	
35	E	N	G	P	H	L	L	V	E	A	7	
153	A	L	D	L	Q	G	V	V	F	P	7	
180	A	C	L	D	Q	D	A	V	I	A	7	
124	L	V	I	T	D	L	T	L	E	D	6	
143	E	G	L	E	D	D	T	V	V	V	6	
146	E	D	D	T	V	V	V	A	L	D	6	
162	P	Y	F	P	R	L	G	R	Y	N	6	
230	N	T	V	P	G	V	R	N	Y	G	6	

TABLE XLVI 151P3D4 v.1: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
259	G	R	F	Y	Y	L	I	H	P	T	6	
278	A	C	L	N	D	G	A	Q	I	A	6	
280	L	N	D	G	A	Q	I	A	K	V	6	
324	R	C	S	P	T	E	A	A	V	R	6	
2	K	S	L	L	L	L	V	L	I	S	5	
4	L	L	L	L	V	L	I	S	I	C	5	
10	I	S	I	C	W	A	D	H	L	S	5	
24	L	D	H	D	R	A	I	H	I	Q	5	
26	H	D	R	A	I	H	I	Q	A	E	5	
36	N	G	P	H	L	L	V	E	A	E	5	
57	V	T	L	P	C	K	F	Y	R	D	5	
64	Y	R	D	P	T	A	F	G	S	G	5	
69	A	F	G	S	G	I	H	K	I	R	5	
73	G	I	H	K	I	R	I	K	W	T	5	
76	K	I	R	I	K	W	T	K	L	T	5	
77	I	R	I	K	W	T	K	L	T	S	5	
118	S	D	S	D	A	S	L	V	I	T	5	
140	E	V	I	E	G	L	E	D	D	T	5	
181	C	L	D	Q	D	A	V	I	A	S	5	
207	A	G	W	L	S	D	G	S	V	Q	5	
217	Y	P	I	T	K	P	R	E	P	C	5	
251	F	C	F	T	S	N	F	N	G	R	5	
262	Y	Y	L	I	H	P	T	K	L	T	5	
281	N	D	G	A	Q	I	A	K	V	G	5	
286	I	A	K	V	G	Q	I	F	A	A	5	
296	W	K	I	L	G	Y	D	R	C	D	5	
306	A	G	W	L	A	D	G	S	V	R	5	
316	Y	P	I	S	R	P	R	R	R	C	5	
6	L	L	V	L	I	S	I	C	W	A	4	
17	H	L	S	D	N	Y	T	L	D	H	4	
25	D	H	D	R	A	I	H	I	Q	A	4	
28	R	A	I	H	I	Q	A	E	N	G	4	
29	A	I	H	I	Q	A	E	N	G	P	4	
38	P	H	L	L	V	E	A	E	Q	A	4	
47	A	K	V	F	S	H	R	G	G	N	4	
51	S	H	R	G	G	N	V	T	L	P	4	
71	G	S	G	I	H	K	I	R	I	K	4	
82	T	K	L	T	S	D	Y	L	K	E	4	
83	K	L	T	S	D	Y	L	K	E	V	4	
95	F	V	S	M	G	Y	H	K	K	T	4	
107	G	Y	Q	G	R	V	F	L	K	G	4	
108	Y	Q	G	R	V	F	L	K	G	G	4	
116	G	G	S	D	S	D	A	S	L	V	4	
119	D	S	D	A	S	L	V	I	T	D	4	
121	D	A	S	L	V	I	T	D	L	T	4	
144	G	L	E	D	D	T	V	V	V	A	4	
172	L	N	F	H	E	A	Q	Q	A	C	4	
176	E	A	Q	Q	A	C	L	D	Q	D	4	
197	A	W	R	G	G	L	D	W	C	N	4	
199	R	G	G	L	D	W	C	N	A	G	4	
212	D	G	S	V	Q	Y	P	I	T	K	4	
213	G	S	V	Q	Y	P	I	T	K	P	4	
214	S	V	Q	Y	P	I	T	K	P	R	4	

TABLE XLVI 151P3D4 v.1: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
219	I	T	K	P	R	E	P	C	G	G	4	
224	E	P	C	G	G	Q	N	T	V	P	4	
238	Y	G	F	W	D	K	D	K	S	R	4	
264	L	I	H	P	T	K	L	T	Y	D	4	
269	K	L	T	Y	D	E	A	V	Q	A	4	
270	L	T	Y	D	E	A	V	Q	A	C	4	
274	E	A	V	Q	A	C	L	N	D	G	4	
279	C	L	N	D	G	A	Q	I	A	K	4	
291	Q	I	F	A	A	W	K	I	L	G	4	
297	K	I	L	G	Y	D	R	C	D	A	4	
302	D	R	C	D	A	G	W	L	A	D	4	
312	G	S	V	R	Y	P	I	S	R	P	4	
314	V	R	Y	P	I	S	R	P	R	R	4	
317	P	I	S	R	P	R	R	R	C	S	4	
318	I	S	R	P	R	R	R	C	S	P	4	
330	A	A	V	R	F	V	G	F	P	D	4	
331	A	V	R	F	V	G	F	P	D	K	4	
332	V	R	F	V	G	F	P	D	K	K	4	
333	R	F	V	G	F	P	D	K	K	H	4	
7	L	V	L	I	S	I	C	W	A	D	3	
8	V	L	I	S	I	C	W	A	D	H	3	
18	L	S	D	N	Y	T	L	D	H	D	3	
22	Y	T	L	D	H	D	R	A	I	H	3	
30	I	H	I	Q	A	E	N	G	P	H	3	
33	Q	A	E	N	G	P	H	L	L	V	3	
39	H	L	L	V	E	A	E	Q	A	K	3	
43	E	A	E	Q	A	K	V	F	S	H	3	
45	E	Q	A	K	V	F	S	H	R	G	3	
48	K	V	F	S	H	R	G	G	N	V	3	
49	V	F	S	H	R	G	G	N	V	T	3	
52	H	R	G	G	N	V	T	L	P	C	3	
62	K	F	Y	R	D	P	T	A	F	G	3	
84	L	T	S	D	Y	L	K	E	V	D	3	
111	R	V	F	L	K	G	G	S	D	S	3	
114	L	K	G	G	S	D	S	D	A	S	3	
123	S	L	V	I	T	D	L	T	L	E	3	
130	T	L	E	D	Y	G	R	Y	K	C	3	
132	E	D	Y	G	R	Y	K	C	E	V	3	
160	V	F	P	Y	F	P	R	L	G	R	3	
164	F	P	R	L	G	R	Y	N	L	N	3	
166	R	L	G	R	Y	N	L	N	F	H	3	
168	G	R	Y	N	L	N	F	H	E	A	3	
169	R	Y	N	L	N	F	H	E	A	Q	3	
170	Y	N	L	N	F	H	E	A	Q	Q	3	
171	N	L	N	F	H	E	A	Q	Q	A	3	
177	A	Q	Q	A	C	L	D	Q	D	A	3	
209	W	L	S	D	G	S	V	Q	Y	P	3	
215	V	Q	Y	P	I	T	K	P	R	E	3	
216	Q	Y	P	I	T	K	P	R	E	P	3	
222	P	R	E	P	C	G	G	Q	N	T	3	
225	P	C	G	G	Q	N	T	V	P	G	3	
227	G	G	Q	N	T	V	P	G	V	R	3	
236	R	N	Y	G	F	W	D	K	D	K	3	

TABLE XLVI 151P3D4 v.1: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
246	S	R	Y	D	V	F	C	F	T	S	3	
249	D	V	F	C	F	T	S	N	F	N	3	
258	N	G	R	F	Y	Y	L	I	H	P	3	
265	I	H	P	T	K	L	T	Y	D	E	3	
267	P	T	K	L	T	Y	D	E	A	V	3	
268	T	K	L	T	Y	D	E	A	V	Q	3	
275	A	V	Q	A	C	L	N	D	G	A	3	
294	A	A	W	K	I	L	G	Y	D	R	3	
295	A	W	K	I	L	G	Y	D	R	C	3	
308	W	L	A	D	G	S	V	R	Y	P	3	
310	A	D	G	S	V	R	Y	P	I	S	3	
311	D	G	S	V	R	Y	P	I	S	R	3	
315	R	Y	P	I	S	R	P	R	R	R	3	
319	S	R	P	R	R	R	C	S	P	T	3	
322	R	R	R	C	S	P	T	E	A	A	3	
326	S	P	T	E	A	A	V	R	F	V	3	
329	E	A	A	V	R	F	V	G	F	P	3	
11	S	I	C	W	A	D	H	L	S	D	2	
14	W	A	D	H	L	S	D	N	Y	T	2	
16	D	H	L	S	D	N	Y	T	L	D	2	
19	S	D	N	Y	T	L	D	H	D	R	2	
53	R	G	G	N	V	T	L	P	C	K	2	
56	N	V	T	L	P	C	K	F	Y	R	2	
58	T	L	P	C	K	F	Y	R	D	P	2	
63	F	Y	R	D	P	T	A	F	G	S	2	
81	W	T	K	L	T	S	D	Y	L	K	2	
85	T	S	D	Y	L	K	E	V	D	V	2	
87	D	Y	L	K	E	V	D	V	F	V	2	
88	Y	L	K	E	V	D	V	F	V	S	2	
89	L	K	E	V	D	V	F	V	S	M	2	
93	D	V	F	V	S	M	G	Y	H	K	2	
94	V	F	V	S	M	G	Y	H	K	K	2	
101	H	K	K	T	Y	G	G	Y	Q	G	2	
103	K	T	Y	G	G	Y	Q	G	R	V	2	
106	G	G	Y	Q	G	R	V	F	L	K	2	
126	I	T	D	L	T	L	E	D	Y	G	2	
127	T	D	L	T	L	E	D	Y	G	R	2	
129	L	T	L	E	D	Y	G	R	Y	K	2	
135	G	R	Y	K	C	E	V	I	E	G	2	
138	K	C	E	V	I	E	G	L	E	D	2	
141	V	I	E	G	L	E	D	D	T	V	2	
148	D	T	V	V	V	A	L	D	L	Q	2	
149	T	V	V	V	A	L	D	L	Q	G	2	
151	V	V	A	L	D	L	Q	G	V	V	2	
174	F	H	E	A	Q	Q	A	C	L	D	2	
178	Q	Q	A	C	L	D	Q	D	A	V	2	
183	D	Q	D	A	V	I	A	S	F	D	2	
188	I	A	S	F	D	Q	L	Y	D	A	2	
190	S	F	D	Q	L	Y	D	A	W	R	2	
191	F	D	Q	L	Y	D	A	W	R	G	2	
192	D	Q	L	Y	D	A	W	R	G	G	2	
194	L	Y	D	A	W	R	G	G	L	D	2	
196	D	A	W	R	G	G	L	D	W	C	2	

TABLE XLVI 151P3D4 v.1: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
203	D	W	C	N	A	G	W	L	S	D	2	
220	T	K	P	R	E	P	C	G	G	Q	2	
221	K	P	R	E	P	C	G	G	Q	N	2	
228	G	Q	N	T	V	P	G	V	R	N	2	
234	G	V	R	N	Y	G	F	W	D	K	2	
237	N	Y	G	F	W	D	K	D	K	S	2	
240	F	W	D	K	D	K	S	R	Y	D	2	
241	W	D	K	D	K	S	R	Y	D	V	2	
243	K	D	K	S	R	Y	D	V	F	C	2	
245	K	S	R	Y	D	V	F	C	F	T	2	
247	R	Y	D	V	F	C	F	T	S	N	2	
257	F	N	G	R	F	Y	Y	L	I	H	2	
272	Y	D	E	A	V	Q	A	C	L	N	2	
276	V	Q	A	C	L	N	D	G	A	Q	2	
288	K	V	G	Q	I	F	A	A	W	K	2	
298	I	L	G	Y	D	R	C	D	A	G	2	
303	R	C	D	A	G	W	L	A	D	G	2	
304	C	D	A	G	W	L	A	D	G	S	2	
313	S	V	R	Y	P	I	S	R	P	R	2	
320	R	P	R	R	R	C	S	P	T	E	2	
321	P	R	R	R	C	S	P	T	E	A	2	
323	R	R	C	S	P	T	E	A	A	V	2	
327	P	T	E	A	A	V	R	F	V	G	2	
334	F	V	G	F	P	D	K	K	H	K	2	
337	F	P	D	K	K	H	K	L	Y	G	2	
340	K	K	H	K	L	Y	G	V	Y	C	2	
343	K	L	Y	G	V	Y	C	F	R	A	2	
12	I	C	W	A	D	H	L	S	D	N	1	
20	D	N	Y	T	L	D	H	D	R	A	1	
37	G	P	H	L	L	V	E	A	E	Q	1	
40	L	L	V	E	A	E	Q	A	K	V	1	
46	Q	A	K	V	F	S	H	R	G	G	1	
59	L	P	C	K	F	Y	R	D	P	T	1	
60	P	C	K	F	Y	R	D	P	T	A	1	
67	P	T	A	F	G	S	G	I	H	K	1	
74	I	H	K	I	R	I	K	W	T	K	1	
78	R	I	K	W	T	K	L	T	S	D	1	
97	S	M	G	Y	H	K	K	T	Y	G	1	
98	M	G	Y	H	K	K	T	Y	G	G	1	
102	K	K	T	Y	G	G	Y	Q	G	R	1	
112	V	F	L	K	G	G	S	D	S	D	1	
113	F	L	K	G	G	S	D	S	D	A	1	
134	Y	G	R	Y	K	C	E	V	I	E	1	
137	Y	K	C	E	V	I	E	G	L	E	1	
150	V	V	V	A	L	D	L	Q	G	V	1	
156	L	Q	G	V	V	F	P	Y	F	P	1	
187	V	I	A	S	F	D	Q	L	Y	D	1	
198	W	R	G	G	L	D	W	C	N	A	1	
202	L	D	W	C	N	A	G	W	L	S	1	
204	W	C	N	A	G	W	L	S	D	G	1	
205	C	N	A	G	W	L	S	D	G	S	1	
206	N	A	G	W	L	S	D	G	S	V	1	
211	S	D	G	S	V	Q	Y	P	I	T	1	

TABLE XLVI 151P3D4 v.1: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
226	C	G	G	Q	N	T	V	P	G	V	1	
233	P	G	V	R	N	Y	G	F	W	D	1	
235	V	R	N	Y	G	F	W	D	K	D	1	
260	R	F	Y	Y	L	I	H	P	T	K	1	
282	D	G	A	Q	I	A	K	V	G	Q	1	
285	Q	I	A	K	V	G	Q	I	F	A	1	
293	F	A	A	W	K	I	L	G	Y	D	1	
301	Y	D	R	C	D	A	G	W	L	A	1	
338	P	D	K	K	H	K	L	Y	G	V	1	
342	H	K	L	Y	G	V	Y	C	F	R	1	
345	Y	G	V	Y	C	F	R	A	Y	N	1	

TABLE XLVI 151P3D4 v.2: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
79	D	E	K	Q	R	K	D	K	V	L	23	
2	L	E	H	T	T	K	T	F	P	L	22	
185	E	E	K	R	K	E	K	A	E	I	21	
98	C	E	G	I	N	I	S	G	S	F	20	
192	A	E	I	H	Y	R	K	N	K	Q	18	
278	A	A	S	P	A	A	W	L	P	L	18	
45	G	I	I	T	Q	G	A	K	D	F	17	
7	K	T	F	P	L	R	A	L	H	I	16	
209	A	E	K	N	M	K	K	K	I	D	16	
211	K	N	M	K	K	K	I	D	K	Y	16	
233	G	F	I	F	K	T	I	A	P	L	16	
371	A	G	S	G	Y	C	G	A	L	W	16	
5	T	T	K	T	F	P	L	R	A	L	15	
80	E	K	Q	R	K	D	K	V	L	L	15	
106	S	F	C	R	N	K	L	K	Y	L	15	
193	E	I	H	Y	R	K	N	K	Q	L	15	
282	A	A	W	L	P	L	R	T	P	W	15	
295	S	S	C	P	T	S	S	S	T	Y	15	
58	Q	F	V	G	S	Y	K	L	A	Y	14	
68	S	N	D	G	E	H	W	T	V	Y	14	
105	G	S	F	C	R	N	K	L	K	Y	14	
157	A	S	E	A	Y	K	K	V	C	L	14	
184	L	E	E	K	R	K	E	K	A	E	14	
221	T	E	S	P	G	G	G	S	P	R	14	
223	S	P	G	G	G	S	P	R	G	L	14	
230	R	G	L	G	F	I	F	K	T	I	14	
261	G	S	S	A	H	R	P	P	A	L	14	
275	P	V	P	A	A	S	P	A	A	W	14	
320	R	H	S	P	S	G	G	G	G	L	14	
377	G	A	L	W	K	A	I	E	S	L	14	
381	K	A	I	E	S	L	E	E	G	L	14	
386	L	E	E	G	L	G	G	K	Q	K	14	
387	E	E	G	L	G	G	K	Q	K	D	14	
29	M	K	Q	D	K	K	V	D	L	L	13	
50	G	A	K	D	F	G	H	V	Q	F	13	
103	I	S	G	S	F	C	R	N	K	L	13	
108	C	R	N	K	L	K	Y	L	A	F	13	
122	M	N	T	N	P	S	R	R	P	Y	13	
131	Y	H	F	Q	V	P	S	R	I	F	13	
152	C	P	Q	G	H	A	S	E	A	Y	13	
158	S	E	A	Y	K	K	V	C	L	S	13	
171	H	E	V	G	W	K	Y	Q	A	V	13	
226	G	G	S	P	R	G	L	G	F	I	13	
307	L	S	P	Y	G	P	R	N	P	L	13	
335	H	C	Q	G	Q	K	H	N	V	L	13	
355	S	E	N	N	S	W	Y	V	E	N	13	
362	V	E	N	G	R	P	A	D	L	A	13	
374	G	Y	C	G	A	L	W	K	A	I	13	
383	I	E	S	L	E	E	G	L	G	G	13	
399	R	K	A	E	N	G	P	H	L	L	13	
28	K	M	K	Q	D	K	K	V	D	L	12	
37	L	L	V	P	T	K	V	T	G	I	12	
109	R	N	K	L	K	Y	L	A	F	L	12	
124	T	N	P	S	R	R	P	Y	H	F	12	
132	H	F	Q	V	P	S	R	I	F	W	12	
168	G	A	P	H	E	V	G	W	K	Y	12	
175	W	K	Y	Q	A	V	T	A	T	L	12	
187	K	R	K	E	K	A	E	I	H	Y	12	
196	Y	R	K	N	K	Q	L	M	R	L	12	
227	G	S	P	R	G	L	G	F	I	F	12	
301	S	S	T	Y	D	S	L	S	P	Y	12	
351	R	K	P	K	S	E	N	N	S	W	12	
361	Y	V	E	N	G	R	P	A	D	L	12	
370	L	A	G	S	G	Y	C	G	A	L	12	
398	E	R	K	A	E	N	G	P	H	L	12	
18	V	E	S	I	R	D	H	S	G	Q	11	
38	L	V	P	T	K	V	T	G	I	I	11	
54	F	G	H	V	Q	F	V	G	S	Y	11	
56	H	V	Q	F	V	G	S	Y	K	L	11	
166	L	S	G	A	P	H	E	V	G	W	11	
189	K	E	K	A	E	I	H	Y	R	K	11	
208	Q	A	E	K	N	M	K	K	K	I	11	
225	G	G	G	S	P	R	G	L	G	F	11	
276	V	P	A	A	S	P	A	A	W	L	11	
298	P	T	S	S	S	T	Y	D	S	L	11	
352	K	P	K	S	E	N	N	S	W	Y	11	
366	R	P	A	D	L	A	G	S	G	Y	11	
397	K	E	R	K	A	E	N	G	P	H	11	
12	R	A	L	H	I	V	V	E	S	I	10	
65	L	A	Y	S	N	D	G	E	H	W	10	
71	G	E	H	W	T	V	Y	Q	D	E	10	
143	Q	E	K	A	D	G	G	S	C	C	10	
92	K	A	V	V	V	S	C	E	G	I	9	
94	V	V	V	S	C	E	G	I	N	I	9	
130	P	Y	H	F	Q	V	P	S	R	I	9	
241	P	L	A	A	T	R	A	T	R	I	9	
264	A	H	R	P	P	A	L	S	A	R	9	
274	A	P	V	P	A	A	S	P	A	A	8	
283	A	W	L	P	L	R	T	P	W	T	8	
19	E	S	I	R	D	H	S	G	Q	K	7	

TABLE XLVI 151P3D4 v.2: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
182	A	T	L	E	E	K	R	K	E	K	7	
272	A	R	A	P	V	P	A	A	S	P	7	
306	S	L	S	P	Y	G	P	R	N	P	7	
314	N	P	L	P	N	P	R	H	S	P	7	
393	K	Q	K	D	K	E	R	K	A	E	7	
35	V	D	L	L	V	P	T	K	V	T	6	
66	A	Y	S	N	D	G	E	H	W	T	6	
85	D	K	V	L	L	G	R	K	A	V	6	
99	E	G	I	N	I	S	G	S	F	C	6	
116	A	F	L	H	K	R	M	N	T	N	6	
127	S	R	R	P	Y	H	F	Q	V	P	6	
133	F	Q	V	P	S	R	I	F	W	R	6	
138	R	I	F	W	R	Q	E	K	A	D	6	
215	K	K	I	D	K	Y	T	E	S	P	6	
232	L	G	F	I	F	K	T	I	A	P	6	
237	K	T	I	A	P	L	A	A	T	R	6	
239	I	A	P	L	A	A	T	R	A	T	6	
240	A	P	L	A	A	T	R	A	T	R	6	
243	A	A	T	R	A	T	R	I	G	H	6	
244	A	T	R	A	T	R	I	G	H	P	6	
269	A	L	S	A	R	A	P	V	P	A	6	
279	A	S	P	A	A	W	L	P	L	R	6	
345	A	R	G	K	P	Q	R	K	P	K	6	
363	E	N	G	R	P	A	D	L	A	G	6	
388	E	G	L	G	G	K	Q	K	D	K	6	
3	E	H	T	T	K	T	F	P	L	R	5	
10	P	L	R	A	L	H	I	V	V	E	5	
23	D	H	S	G	Q	K	M	K	Q	D	5	
34	K	V	D	L	L	V	P	T	K	V	5	
40	P	T	K	V	T	G	I	I	T	Q	5	
41	T	K	V	T	G	I	I	T	Q	G	5	
51	A	K	D	F	G	H	V	Q	F	V	5	
52	K	D	F	G	H	V	Q	F	V	G	5	
57	V	Q	F	V	G	S	Y	K	L	A	5	
87	V	L	L	G	R	K	A	V	V	V	5	
95	V	V	S	C	E	G	I	N	I	S	5	
97	S	C	E	G	I	N	I	S	G	S	5	
104	S	G	S	F	C	R	N	K	L	K	5	
123	N	T	N	P	S	R	R	P	Y	H	5	
137	S	R	I	F	W	R	Q	E	K	A	5	
146	A	D	G	G	S	C	C	P	Q	G	5	
167	S	G	A	P	H	E	V	G	W	K	5	
169	A	P	H	E	V	G	W	K	Y	Q	5	
200	K	Q	L	M	R	L	Q	K	Q	A	5	
229	P	R	G	L	G	F	I	F	K	T	5	
235	I	F	K	T	I	A	P	L	A	A	5	
252	H	P	G	G	R	T	P	R	A	G	5	
260	A	G	S	S	A	H	R	P	P	A	5	
266	R	P	P	A	L	S	A	R	A	P	5	
309	P	Y	G	P	R	N	P	L	P	N	5	
322	S	P	S	G	G	G	G	L	K	K	5	
323	P	S	G	G	G	G	L	K	K	P	5	
333	A	R	H	C	Q	G	Q	K	H	N	5	

TABLE XLVI 151P3D4 v.2: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
364	N	G	R	P	A	D	L	A	G	S	5	
8	T	F	P	L	R	A	L	H	I	V	4	
9	F	P	L	R	A	L	H	I	V	V	4	
14	L	H	I	V	V	E	S	I	R	D	4	
15	H	I	V	V	E	S	I	R	D	H	4	
27	Q	K	M	K	Q	D	K	K	V	D	4	
30	K	Q	D	K	K	V	D	L	L	V	4	
33	K	K	V	D	L	L	V	P	T	K	4	
44	T	G	I	I	T	Q	G	A	K	D	4	
77	Y	Q	D	E	K	Q	R	K	D	K	4	
81	K	Q	R	K	D	K	V	L	L	G	4	
86	K	V	L	L	G	R	K	A	V	V	4	
88	L	L	G	R	K	A	V	V	V	S	4	
101	I	N	I	S	G	S	F	C	R	N	4	
102	N	I	S	G	S	F	C	R	N	K	4	
110	N	K	L	K	Y	L	A	F	L	H	4	
112	L	K	Y	L	A	F	L	H	K	R	4	
113	K	Y	L	A	F	L	H	K	R	M	4	
115	L	A	F	L	H	K	R	M	N	T	4	
120	K	R	M	N	T	N	P	S	R	R	4	
125	N	P	S	R	R	P	Y	H	F	Q	4	
135	V	P	S	R	I	F	W	R	Q	E	4	
150	S	C	C	P	Q	G	H	A	S	E	4	
156	H	A	S	E	A	Y	K	K	V	C	4	
160	A	Y	K	K	V	C	L	S	G	A	4	
179	A	V	T	A	T	L	E	E	K	R	4	
188	R	K	E	K	A	E	I	H	Y	R	4	
190	E	K	A	E	I	H	Y	R	K	N	4	
191	K	A	E	I	H	Y	R	K	N	K	4	
198	K	N	K	Q	L	M	R	L	Q	K	4	
199	N	K	Q	L	M	R	L	Q	K	Q	4	
201	Q	L	M	R	L	Q	K	Q	A	E	4	
207	K	Q	A	E	K	N	M	K	K	K	4	
222	E	S	P	G	G	G	S	P	R	G	4	
228	S	P	R	G	L	G	F	I	F	K	4	
234	F	I	F	K	T	I	A	P	L	A	4	
238	T	I	A	P	L	A	A	T	R	A	4	
247	A	T	R	I	G	H	P	G	G	R	4	
248	T	R	I	G	H	P	G	G	R	T	4	
250	I	G	H	P	G	G	R	T	P	R	4	
256	R	T	P	R	A	G	S	S	A	H	4	
263	S	A	H	R	P	P	A	L	S	A	4	
265	H	R	P	P	A	L	S	A	R	A	4	
270	L	S	A	R	A	P	V	P	A	A	4	
271	S	A	R	A	P	V	P	A	A	S	4	
284	W	L	P	L	R	T	P	W	T	R	4	
287	L	R	T	P	W	T	R	P	S	S	4	
291	W	T	R	P	S	S	C	P	T	S	4	
300	S	S	S	T	Y	D	S	L	S	P	4	
313	R	N	P	L	P	N	P	R	H	S	4	
324	S	G	G	G	G	L	K	K	P	A	4	
329	L	K	K	P	A	R	H	C	Q	G	4	
337	Q	G	Q	K	H	N	V	L	A	R	4	

TABLE XLVI 151P3D4 v.2: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
346	R	G	K	P	Q	R	K	P	K	S	4	
347	G	K	P	Q	R	K	P	K	S	E	4	
350	Q	R	K	P	K	S	E	N	N	S	4	
368	A	D	L	A	G	S	G	Y	C	G	4	
378	A	L	W	K	A	I	E	S	L	E	4	
382	A	I	E	S	L	E	E	G	L	G	4	
384	E	S	L	E	E	G	L	G	G	K	4	
11	L	R	A	L	H	I	V	V	E	S	3	
13	A	L	H	I	V	V	E	S	I	R	3	
20	S	I	R	D	H	S	G	Q	K	M	3	
21	I	R	D	H	S	G	Q	K	M	K	3	
26	G	Q	K	M	K	Q	D	K	K	V	3	
31	Q	D	K	K	V	D	L	L	V	P	3	
36	D	L	L	V	P	T	K	V	T	G	3	
42	K	V	T	G	I	I	T	Q	G	A	3	
62	S	Y	K	L	A	Y	S	N	D	G	3	
69	N	D	G	E	H	W	T	V	Y	Q	3	
72	E	H	W	T	V	Y	Q	D	E	K	3	
74	W	T	V	Y	Q	D	E	K	Q	R	3	
76	V	Y	Q	D	E	K	Q	R	K	D	3	
82	Q	R	K	D	K	V	L	L	G	R	3	
84	K	D	K	V	L	L	G	R	K	A	3	
93	A	V	V	V	S	C	E	G	I	N	3	
111	K	L	K	Y	L	A	F	L	H	K	3	
118	L	H	K	R	M	N	T	N	P	S	3	
144	E	K	A	D	G	G	S	C	C	P	3	
145	K	A	D	G	G	S	C	C	P	Q	3	
149	G	S	C	C	P	Q	G	H	A	S	3	
155	G	H	A	S	E	A	Y	K	K	V	3	
159	E	A	Y	K	K	V	C	L	S	G	3	
163	K	V	C	L	S	G	A	P	H	E	3	
164	V	C	L	S	G	A	P	H	E	V	3	
165	C	L	S	G	A	P	H	E	V	G	3	
172	E	V	G	W	K	Y	Q	A	V	T	3	
173	V	G	W	K	Y	Q	A	V	T	A	3	
174	G	W	K	Y	Q	A	V	T	A	T	3	
176	K	Y	Q	A	V	T	A	T	L	E	3	
180	V	T	A	T	L	E	E	K	R	K	3	
181	T	A	T	L	E	E	K	R	K	E	3	
186	E	K	R	K	E	K	A	E	I	H	3	
203	M	R	L	Q	K	Q	A	E	K	N	3	
210	E	K	N	M	K	K	K	I	D	K	3	
212	N	M	K	K	K	I	D	K	Y	T	3	
224	P	G	G	G	S	P	R	G	L	G	3	
236	F	K	T	I	A	P	L	A	A	T	3	
242	L	A	A	T	R	A	T	R	I	G	3	
251	G	H	P	G	G	R	T	P	R	A	3	
255	G	R	T	P	R	A	G	S	S	A	3	
258	P	R	A	G	S	S	A	H	R	P	3	
262	S	S	A	H	R	P	P	A	L	S	3	
268	P	A	L	S	A	R	A	P	V	P	3	
280	S	P	A	A	W	L	P	L	R	T	3	
281	P	A	A	W	L	P	L	R	T	P	3	

TABLE XLVI 151P3D4 v.2: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI

Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
286	P	L	R	T	P	W	T	R	P	S	3	
296	S	C	P	T	S	S	S	T	Y	D	3	
308	S	P	Y	G	P	R	N	P	L	P	3	
310	Y	G	P	R	N	P	L	P	N	P	3	
311	G	P	R	N	P	L	P	N	P	R	3	
312	P	R	N	P	L	P	N	P	R	H	3	
316	L	P	N	P	R	H	S	P	S	G	3	
317	P	N	P	R	H	S	P	S	G	G	3	
325	G	G	G	G	L	K	K	P	A	R	3	
327	G	G	L	K	K	P	A	R	H	C	3	
331	K	P	A	R	H	C	Q	G	Q	K	3	
339	Q	K	H	N	V	L	A	R	G	K	3	
340	K	H	N	V	L	A	R	G	K	P	3	
341	H	N	V	L	A	R	G	K	P	Q	3	
342	N	V	L	A	R	G	K	P	Q	R	3	
344	L	A	R	G	K	P	Q	R	K	P	3	
354	K	S	E	N	N	S	W	Y	V	E	3	
356	E	N	N	S	W	Y	V	E	N	G	3	
357	N	N	S	W	Y	V	E	N	G	R	3	
360	W	Y	V	E	N	G	R	P	A	D	3	
373	S	G	Y	C	G	A	L	W	K	A	3	
376	C	G	A	L	W	K	A	I	E	S	3	
4	H	T	T	K	T	F	P	L	R	A	2	
6	T	K	T	F	P	L	R	A	L	H	2	
25	S	G	Q	K	M	K	Q	D	K	K	2	
32	D	K	K	V	D	L	L	V	P	T	2	
43	V	T	G	I	I	T	Q	G	A	K	2	
49	Q	G	A	K	D	F	G	H	V	Q	2	
53	D	F	G	H	V	Q	F	V	G	S	2	
60	V	G	S	Y	K	L	A	Y	S	N	2	
67	Y	S	N	D	G	E	H	W	T	V	2	
70	D	G	E	H	W	T	V	Y	Q	D	2	
83	R	K	D	K	V	L	L	G	R	K	2	
89	L	G	R	K	A	V	V	V	S	C	2	
107	F	C	R	N	K	L	K	Y	L	A	2	
121	R	M	N	T	N	P	S	R	R	P	2	
126	P	S	R	R	P	Y	H	F	Q	V	2	
128	R	R	P	Y	H	F	Q	V	P	S	2	
134	Q	V	P	S	R	I	F	W	R	Q	2	
151	C	C	P	Q	G	H	A	S	E	A	2	
154	Q	G	H	A	S	E	A	Y	K	K	2	
161	Y	K	K	V	C	L	S	G	A	P	2	
177	Y	Q	A	V	T	A	T	L	E	E	2	
178	Q	A	V	T	A	T	L	E	E	K	2	
194	I	H	Y	R	K	N	K	Q	L	M	2	
197	R	K	N	K	Q	L	M	R	L	Q	2	
204	R	L	Q	K	Q	A	E	K	N	M	2	
216	K	I	D	K	Y	T	E	S	P	G	2	
218	D	K	Y	T	E	S	P	G	G	G	2	
245	T	R	A	T	R	I	G	H	P	G	2	
249	R	I	G	H	P	G	G	R	T	P	2	
253	P	G	G	R	T	P	R	A	G	S	2	
254	G	G	R	T	P	R	A	G	S	S	2	

TABLE XLVI 151P3D4 v.2: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
267	P	P	A	L	S	A	R	A	P	V	2	
273	R	A	P	V	P	A	A	S	P	A	2	
277	P	A	A	S	P	A	A	W	L	P	2	
285	L	P	L	R	T	P	W	T	R	P	2	
288	R	T	P	W	T	R	P	S	S	C	2	
292	T	R	P	S	S	C	P	T	S	S	2	
293	R	P	S	S	C	P	T	S	S	S	2	
299	T	S	S	S	T	Y	D	S	L	S	2	
302	S	T	Y	D	S	L	S	P	Y	G	2	
303	T	Y	D	S	L	S	P	Y	G	P	2	
304	Y	D	S	L	S	P	Y	G	P	R	2	
315	P	L	P	N	P	R	H	S	P	S	2	
321	H	S	P	S	G	G	G	G	L	K	2	
326	G	G	G	L	K	K	P	A	R	H	2	
328	G	L	K	K	P	A	R	H	C	Q	2	
330	K	K	P	A	R	H	C	Q	G	Q	2	
336	C	Q	G	Q	K	H	N	V	L	A	2	
343	V	L	A	R	G	K	P	Q	R	K	2	
348	K	P	Q	R	K	P	K	S	E	N	2	
359	S	W	Y	V	E	N	G	R	P	A	2	
365	G	R	P	A	D	L	A	G	S	G	2	
367	P	A	D	L	A	G	S	G	Y	C	2	
372	G	S	G	Y	C	G	A	L	W	K	2	
385	S	L	E	E	G	L	G	G	K	Q	2	
389	G	L	G	G	K	Q	K	D	K	E	2	
390	L	G	G	K	Q	K	D	K	E	R	2	
392	G	K	Q	K	D	K	E	R	K	A	2	
395	K	D	K	E	R	K	A	E	N	G	2	
396	D	K	E	R	K	A	E	N	G	P	2	
16	I	V	V	E	S	I	R	D	H	S	1	
17	V	V	E	S	I	R	D	H	S	G	1	
22	R	D	H	S	G	Q	K	M	K	Q	1	
39	V	P	T	K	V	T	G	I	I	T	1	
47	I	T	Q	G	A	K	D	F	G	H	1	
48	T	Q	G	A	K	D	F	G	H	V	1	
59	F	V	G	S	Y	K	L	A	Y	S	1	
63	Y	K	L	A	Y	S	N	D	G	E	1	
64	K	L	A	Y	S	N	D	G	E	H	1	
73	H	W	T	V	Y	Q	D	E	K	Q	1	
78	Q	D	E	K	Q	R	K	D	K	V	1	
90	G	R	K	A	V	V	V	S	C	E	1	
96	V	S	C	E	G	I	N	I	S	G	1	
114	Y	L	A	F	L	H	K	R	M	N	1	
129	R	P	Y	H	F	Q	V	P	S	R	1	
136	P	S	R	I	F	W	R	Q	E	K	1	
139	I	F	W	R	Q	E	K	A	D	G	1	
140	F	W	R	Q	E	K	A	D	G	G	1	
147	D	G	G	S	C	C	P	Q	G	H	1	
148	G	G	S	C	C	P	Q	G	H	A	1	
162	K	K	V	C	L	S	G	A	P	H	1	
170	P	H	E	V	G	W	K	Y	Q	A	1	
183	T	L	E	E	K	R	K	E	K	A	1	
195	H	Y	R	K	N	K	Q	L	M	R	1	

TABLE XLVI 151P3D4 v.2: HLA Peptide Scoring Results B*4402 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
202	L	M	R	L	Q	K	Q	A	E	K	1	
205	L	Q	K	Q	A	E	K	N	M	K	1	
206	Q	K	Q	A	E	K	N	M	K	K	1	
213	M	K	K	K	I	D	K	Y	T	E	1	
214	K	K	K	I	D	K	Y	T	E	S	1	
219	K	Y	T	E	S	P	G	G	G	S	1	
246	R	A	T	R	I	G	H	P	G	G	1	
259	R	A	G	S	S	A	H	R	P	P	1	
289	T	P	W	T	R	P	S	S	C	P	1	
290	P	W	T	R	P	S	S	C	P	T	1	
294	P	S	S	C	P	T	S	S	S	T	1	
297	C	P	T	S	S	S	T	Y	D	S	1	
305	D	S	L	S	P	Y	G	P	R	N	1	
318	N	P	R	H	S	P	S	G	G	G	1	
332	P	A	R	H	C	Q	G	Q	K	H	1	
334	R	H	C	Q	G	Q	K	H	N	V	1	
338	G	Q	K	H	N	V	L	A	R	G	1	
353	P	K	S	E	N	N	S	W	Y	V	1	
358	N	S	W	Y	V	E	N	G	R	P	1	
369	D	L	A	G	S	G	Y	C	G	A	1	
379	L	W	K	A	I	E	S	L	E	E	1	
380	W	K	A	I	E	S	L	E	E	G	1	
394	Q	K	D	K	E	R	K	A	E	N	1	

TABLE XLVII 151P3D4: HLA Peptide Scoring Results B*5101 10-mers SYFPEITHI												
Pos	1	2	3	4	5	6	7	8	9	0	score	SEQ. ID NO.
	NO DATA											

TABLE XLVIII 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
78	R I K W T K L T S D Y L K E V	35	
259	G R F Y Y L I H P T K L T Y D	33	
61	C K F Y R D P T A F G S G I H	30	
214	S V Q Y P I T K P R E P C G G	28	
7	L V L I S I C W A D H L S D N	27	
27	D R A I H I Q A E N G P H L L	27	
102	K K T Y G G Y Q G R V F L K G	27	
148	D T V V V A L D L Q G V V F P	27	
161	F P Y F P R L G R Y N L N F H	27	
169	R Y N L N F H E A Q Q A C L D	27	
109	Q G R V F L K G G S D S D A S	26	
267	P T K L T Y D E A V Q A C L N	26	
298	I L G Y D R C D A G W L A D G	26	
1	M K S L L L L V L I S I C W A	25	
39	H L L V E A E Q A K V F S H R	25	
139	C E V I E G L E D D T V V V A	25	
283	G A Q I A K V G Q I F A A W K	25	
4	L L L L V L I S I C W A D H L	24	
21	N Y T L D H D R A I H I Q A E	24	
29	A I H I Q A E N G P H L L V E	24	
36	N G P H L L V E A E Q A K V F	24	
46	Q A K V F S H R G G N V T L P	24	
150	V V V A L D L Q G V V F P Y F	24	
151	V V A L D L Q G V V F P Y F P	24	
199	R G G L D W C N A G W L S D G	24	
229	Q N T V P G V R N Y G F W D K	24	
86	S D Y L K E V D V F V S M G Y	23	
145	L E D D T V V V A L D L Q G V	23	
293	F A A W K I L G Y D R C D A G	23	
3	S L L L L V L I S I C W A D H	22	
153	A L D L Q G V V F P Y F P R L	22	
178	Q Q A C L D Q D A V I A S F D	22	
286	I A K V G Q I F A A W K I L G	22	
19	S D N Y T L D H D R A I H I Q	21	
134	Y G R Y K C E V I E G L E D D	21	
74	I H K I R I K W T K L T S D Y	20	
85	T S D Y L K E V D V F V S M G	20	
154	L D L Q G V V F P Y F P R L G	20	
235	V R N Y G F W D K D K S R Y D	20	
260	R F Y Y L I H P T K L T Y D E	20	
287	A K V G Q I F A A W K I L G Y	20	
313	S V R Y P I S R P R R R C S P	20	
38	P H L L V E A E Q A K V F S H	19	
47	A K V F S H R G G N V T L P C	19	
92	V D V F V S M G Y H K K T Y G	19	
110	G R V F L K G G S D S D A S L	19	
160	V F P Y F P R L G R Y N L N F	19	
238	Y G F W D K D K S R Y D V F C	19	
250	V F C F T S N F N G R F Y Y L	19	
254	T S N F N G R F Y Y L I H P T	19	
264	L I H P T K L T Y D E A V Q A	19	
63	F Y R D P T A F G S G I H K I	18	
81	W T K L T S D Y L K E V D V F	18	

TABLE XLVIII 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
108	Y Q G R V F L K G G S D S D A	18	
131	L E D Y G R Y K C E V I E G L	18	
156	L Q G V V F P Y F P R L G R Y	18	
171	N L N F H E A Q Q A C L D Q D	18	
188	I A S F D Q L Y D A W R G G L	18	
191	F D Q L Y D A W R G G L D W C	18	
192	D Q L Y D A W R G G L D W C N	18	
258	N G R F Y Y L I H P T K L T Y	18	
269	K L T Y D E A V Q A C L N D G	18	
273	D E A V Q A C L N D G A Q I A	18	
299	L G Y D R C D A G W L A D G S	18	
302	D R C D A G W L A D G S V R Y	18	
329	E A A V R F V G F P D K K H K	18	
338	P D K K H K L Y G V Y C F R A	18	
56	N V T L P C K F Y R D P T A F	17	
71	G S G I H K I R I K W T K L T	17	
111	R V F L K G G S D S D A S L V	17	
118	S D S D A S L V I T D L T L E	17	
123	S L V I T D L T L E D Y G R Y	17	
149	T V V V A L D L Q G V V F P Y	17	
206	N A G W L S D G S V Q Y P I T	17	
275	A V Q A C L N D G A Q I A K V	17	
276	V Q A C L N D G A Q I A K V G	17	
305	D A G W L A D G S V R Y P I S	17	
306	A G W L A D G S V R Y P I S R	17	
311	D G S V R Y P I S R P R R R C	17	
315	R Y P I S R P R R R C S P T E	17	
319	S R P R R R C S P T E A A V R	17	
11	S I C W A D H L S D N Y T L D	16	
18	L S D N Y T L D H D R A I H I	16	
52	H R G G N V T L P C K F Y R D	16	
60	P C K F Y R D P T A F G S G I	16	
73	G I H K I R I K W T K L T S D	16	
83	K L T S D Y L K E V D V F V S	16	
89	L K E V D V F V S M G Y H K K	16	
91	E V D V F V S M G Y H K K T Y	16	
114	L K G G S D S D A S L V I T D	16	
142	I E G L E D D T V V V A L D L	16	
166	R L G R Y N L N F H E A Q Q A	16	
176	E A Q Q A C L D Q D A V I A S	16	
179	Q A C L D Q D A V I A S F D Q	16	
196	D A W R G G L D W C N A G W L	16	
200	G G L D W C N A G W L S D G S	16	
203	D W C N A G W L S D G S V Q Y	16	
204	W C N A G W L S D G S V Q Y P	16	
207	A G W L S D G S V Q Y P I T K	16	
246	S R Y D V F C F T S N F N G R	16	
282	D G A Q I A K V G Q I F A A W	16	
292	I F A A W K I L G Y D R C D A	16	
295	A W K I L G Y D R C D A G W L	16	
303	R C D A G W L A D G S V R Y P	16	
320	R P R R R C S P T E A A V R F	16	
323	R R C S P T E A A V R F V G F	16	
326	S P T E A A V R F V G F P D K	16	

TABLE XLVIII 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
2	K S L L L L V L I S I C W A D	15	
30	I H I Q A E N G P H L L V E A	15	
59	L P C K F Y R D P T A F G S G	15	
103	K T Y G G Y Q G R V F L K G G	15	
136	R Y K C E V I E G L E D D T V	15	
157	Q G V V F P Y F P R L G R Y N	15	
212	D G S V Q Y P I T K P R E P C	15	
226	C G G Q N T V P G V R N Y G F	15	
279	C L N D G A Q I A K V G Q I F	15	
6	L L V L I S I C W A D H L S D	14	
15	A D H L S D N Y T L D H D R A	14	
26	H D R A I H I Q A E N G P H L	14	
40	L L V E A E Q A K V F S H R G	14	
43	E A E Q A K V F S H R G G N V	14	
68	T A F G S G I H K I R I K W T	14	
97	S M G Y H K K T Y G G Y Q G R	14	
112	V F L K G G S D S D A S L V I	14	
115	K G G S D S D A S L V I T D L	14	
120	S D A S L V I T D L T L E D Y	14	
122	A S L V I T D L T L E D Y G R	14	
141	V I E G L E D D T V V V A L D	14	
172	L N F H E A Q Q A C L D Q D A	14	
181	C L D Q D A V I A S F D Q L Y	14	
244	D K S R Y D V F C F T S N F N	14	
247	R Y D V F C F T S N F N G R F	14	
270	L T Y D E A V Q A C L N D G A	14	
308	W L A D G S V R Y P I S R P R	14	
119	D S D A S L V I T D L T L E D	13	
121	D A S L V I T D L T L E D Y G	13	
331	A V R F V G F P D K K H K L Y	13	
336	G F P D K K H K L Y G V Y C F	13	
107	G Y Q G R V F L K G G S D S D	12	
158	G V V F P Y F P R L G R Y N L	12	
167	L G R Y N L N F H E A Q Q A C	12	
182	L D Q D A V I A S F D Q L Y D	12	
183	D Q D A V I A S F D Q L Y D A	12	
195	Y D A W R G G L D W C N A G W	12	
210	L S D G S V Q Y P I T K P R E	12	
223	R E P C G G Q N T V P G V R N	12	
290	G Q I F A A W K I L G Y D R C	12	
5	L L L V L I S I C W A D H L S	11	
49	V F S H R G G N V T L P C K F	11	
67	P T A F G S G I H K I R I K W	11	
93	D V F V S M G Y H K K T Y G G	11	
98	M G Y H K K T Y G G Y Q G R V	11	
105	Y G G Y Q G R V F L K G G S D	11	
125	V I T D L T L E D Y G R Y K C	11	
201	G L D W C N A G W L S D G S V	11	
211	S D G S V Q Y P I T K P R E P	11	
216	Q Y P I T K P R E P C G G Q N	11	
232	V P G V R N Y G F W D K D K S	11	
245	K S R Y D V F C F T S N F N G	11	
248	Y D V F C F T S N F N G R F Y	11	
256	N F N G R F Y Y L I H P T K L	11	

TABLE XLVIII 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
281	N D G A Q I A K V G Q I F A A	11	
334	F V G F P D K K H K L Y G V Y	11	
339	D K K H K L Y G V Y C F R A Y	11	
53	R G G N V T L P C K F Y R D P	10	
54	G G N V T L P C K F Y R D P T	10	
58	T L P C K F Y R D P T A F G S	10	
66	D P T A F G S G I H K I R I K	10	
75	H K I R I K W T K L T S D Y L	10	
76	K I R I K W T K L T S D Y L K	10	
84	L T S D Y L K E V D V F V S M	10	
99	G Y H K K T Y G G Y Q G R V F	10	
126	I T D L T L E D Y G R Y K C E	10	
128	D L T L E D Y G R Y K C E V I	10	
140	E V I E G L E D D T V V V A L	10	
217	Y P I T K P R E P C G G Q N T	10	
219	I T K P R E P C G G Q N T V P	10	
224	E P C G G Q N T V P G V R N Y	10	
237	N Y G F W D K D K S R Y D V F	10	
240	F W D K D K S R Y D V F C F T	10	
265	I H P T K L T Y D E A V Q A C	10	
288	K V G Q I F A A W K I L G Y D	10	
316	Y P I S R P R R R C S P T E A	10	
324	R C S P T E A A V R F V G F P	10	
332	V R F V G F P D K K H K L Y G	10	
13	C W A D H L S D N Y T L D H D	9	
35	E N G P H L L V E A E Q A K V	9	
48	K V F S H R G G N V T L P C K	9	
65	R D P T A F G S G I H K I R I	9	
95	F V S M G Y H K K T Y G G Y Q	9	
106	G G Y Q G R V F L K G G S D S	9	
127	T D L T L E D Y G R Y K C E V	9	
147	D D T V V V A L D L Q G V V F	9	
177	A Q Q A C L D Q D A V I A S F	9	
186	A V I A S F D Q L Y D A W R G	9	
189	A S F D Q L Y D A W R G G L D	9	
193	Q L Y D A W R G G L D W C N A	9	
205	C N A G W L S D G S V Q Y P I	9	
220	T K P R E P C G G Q N T V P G	9	
221	K P R E P C G G Q N T V P G V	9	
222	P R E P C G G Q N T V P G V R	9	
231	T V P G V R N Y G F W D K D K	9	
239	G F W D K D K S R Y D V F C F	9	
251	F C F T S N F N G R F Y Y L I	9	
262	Y Y L I H P T K L T Y D E A V	9	
277	Q A C L N D G A Q I A K V G Q	9	
278	A C L N D G A Q I A K V G Q I	9	
284	A Q I A K V G Q I F A A W K I	9	
304	C D A G W L A D G S V R Y P I	9	
310	A D G S V R Y P I S R P R R R	9	
322	R R R C S P T E A A V R F V G	9	
328	T E A A V R F V G F P D K K H	9	
333	R F V G F P D K K H K L Y G V	9	
8	V L I S I C W A D H L S D N Y	8	
9	L I S I C W A D H L S D N Y T	8	

TABLE XLVIII 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
12	I C W A D H L S D N Y T L D H	8	
23	T L D H D R A I H I Q A E N G	8	
24	L D H D R A I H I Q A E N G P	8	
31	H I Q A E N G P H L L V E A E	8	
33	Q A E N G P H L L V E A E Q A	8	
34	A E N G P H L L V E A E Q A K	8	
37	G P H L L V E A E Q A K V F S	8	
64	Y R D P T A F G S G I H K I R	8	
87	D Y L K E V D V F V S M G Y H	8	
90	K E V D V F V S M G Y H K K T	8	
96	V S M G Y H K K T Y G G Y Q G	8	
101	H K K T Y G G Y Q G R V F L K	8	
113	F L K G G S D S D A S L V I T	8	
130	T L E D Y G R Y K C E V I E G	8	
138	K C E V I E G L E D D T V V V	8	
143	E G L E D D T V V V A L D L Q	8	
163	Y F P R L G R Y N L N F H E A	8	
164	F P R L G R Y N L N F H E A Q	8	
175	H E A Q Q A C L D Q D A V I A	8	
180	A C L D Q D A V I A S F D Q L	8	
184	Q D A V I A S F D Q L Y D A W	8	
185	D A V I A S F D Q L Y D A W R	8	
208	G W L S D G S V Q Y P I T K P	8	
242	D K D K S R Y D V F C F T S N	8	
253	F T S N F N G R F Y Y L I H P	8	
261	F Y Y L I H P T K L T Y D E A	8	
274	E A V Q A C L N D G A Q I A K	8	
280	L N D G A Q I A K V G Q I F A	8	
289	V G Q I F A A W K I L G Y D R	8	
296	W K I L G Y D R C D A G W L A	8	
307	G W L A D G S V R Y P I S R P	8	
318	I S R P R R R C S P T E A A V	8	
321	P R R R C S P T E A A V R F V	8	
327	P T E A A V R F V G F P D K K	8	
88	Y L K E V D V F V S M G Y H K	7	
146	E D D T V V V A L D L Q G V V	7	
285	Q I A K V G Q I F A A W K I L	7	
330	A A V R F V G F P D K K H K L	7	
50	F S H R G G N V T L P C K F Y	6	
51	S H R G G N V T L P C K F Y R	6	
77	I R I K W T K L T S D Y L K E	6	
135	G R Y K C E V I E G L E D D T	6	
144	G L E D D T V V V A L D L Q G	6	
173	N F H E A Q Q A C L D Q D A V	6	
187	V I A S F D Q L Y D A W R G G	6	
209	W L S D G S V Q Y P I T K P R	6	
213	G S V Q Y P I T K P R E P C G	6	
225	P C G G Q N T V P G V R N Y G	6	
263	Y L I H P T K L T Y D E A V Q	6	
271	T Y D E A V Q A C L N D G A Q	6	
309	L A D G S V R Y P I S R P R R	6	
312	G S V R Y P I S R P R R R C S	6	
137	Y K C E V I E G L E D D T V V	5	
44	A E Q A K V F S H R G G N V T	4	

TABLE XLVIII 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
45	E Q A K V F S H R G G N V T L	4	
69	A F G S G I H K I R I K W T K	4	
72	S G I H K I R I K W T K L T S	4	
100	Y H K K T Y G G Y Q G R V F L	4	
25	D H D R A I H I Q A E N G P H	3	
133	D Y G R Y K C E V I E G L E D	3	
162	P Y F P R L G R Y N L N F H E	3	
190	S F D Q L Y D A W R G G L D W	3	
227	G G Q N T V P G V R N Y G F W	3	
252	C F T S N F N G R F Y Y L I H	3	
57	V T L P C K F Y R D P T A F G	2	
79	I K W T K L T S D Y L K E V D	2	
132	E D Y G R Y K C E V I E G L E	2	
165	P R L G R Y N L N F H E A Q Q	2	
198	W R G G L D W C N A G W L S D	2	
218	P I T K P R E P C G G Q N T V	2	
233	P G V R N Y G F W D K D K S R	2	
243	K D K S R Y D V F C F T S N F	2	
249	D V F C F T S N F N G R F Y Y	2	
294	A A W K I L G Y D R C D A G W	2	
297	K I L G Y D R C D A G W L A D	2	
335	V G F P D K K H K L Y G V Y C	2	
14	W A D H L S D N Y T L D H D R	1	
17	H L S D N Y T L D H D R A I H	1	
28	R A I H I Q A E N G P H L L V	1	
32	I Q A E N G P H L L V E A E Q	1	
70	F G S G I H K I R I K W T K L	1	
80	K W T K L T S D Y L K E V D V	1	
94	V F V S M G Y H K K T Y G G Y	1	
124	L V I T D L T L E D Y G R Y K	1	
129	L T L E D Y G R Y K C E V I E	1	
155	D L Q G V V F P Y F P R L G R	1	
159	V V F P Y F P R L G R Y N L N	1	
194	L Y D A W R G G L D W C N A G	1	
197	A W R G G L D W C N A G W L S	1	
202	L D W C N A G W L S D G S V Q	1	
228	G Q N T V P G V R N Y G F W D	1	
234	G V R N Y G F W D K D K S R Y	1	
236	R N Y G F W D K D K S R Y D V	1	
241	W D K D K S R Y D V F C F T S	1	
272	Y D E A V Q A C L N D G A Q I	1	
300	G Y D R C D A G W L A D G S V	1	
314	V R Y P I S R P R R R C S P T	1	
337	F P D K K H K L Y G V Y C F R	1	

TABLE XLVIII 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
301	S S T Y D S L S P Y G P R N P	34	
32	D K K V D L L V P T K V T G I	33	
236	F K T I A P L A A T R A T R I	33	
43	V T G I I T Q G A K D F G H V	32	
40	P T K V T G I I T Q G A K D F	31	
54	F G H V Q F V G S Y K L A Y S	31	
128	R R P Y H F Q V P S R I F W R	31	

TABLE XLVIII 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
233	G F I F K T I A P L A A T R A	31	
158	S E A Y K K V C L S G A P H E	29	
217	I D K Y T E S P G G G S P R G	29	
18	V E S I R D H S G Q K M K Q D	27	
82	Q R K D K V L L G R K A V V V	27	
357	N N S W Y V E N G R P A D L A	27	
51	A K D F G H V Q F V G S Y K L	26	
92	K A V V V S C E G I N I S G S	26	
232	L G F I F K T I A P L A A T R	26	
247	A T R I G H P G G R T P R A G	26	
174	G W K Y Q A V T A T L E E K R	25	
202	L M R L Q K Q A E K N M K K K	25	
239	I A P L A A T R A T R I G H P	25	
264	A H R P P A L S A R A P V P A	25	
284	W L P L R T P W T R P S S C P	25	
5	T T K T F P L R A L H I V V E	24	
85	D K V L L G R K A V V V S C E	24	
119	H K R M N T N P S R R P Y H F	24	
229	P R G L G F I F K T I A P L A	24	
281	P A A W L P L R T P W T R P S	24	
304	Y D S L S P Y G P R N P L P N	24	
377	G A L W K A I E S L E E G L G	24	
36	D L L V P T K V T G I I T Q G	22	
138	R I F W R Q E K A D G G S C C	22	
267	P P A L S A R A P V P A A S P	22	
270	L S A R A P V P A A S P A A W	22	
359	S W Y V E N G R P A D L A G S	22	
116	A F L H K R M N T N P S R R P	21	
129	R P Y H F Q V P S R I F W R Q	21	
35	V D L L V P T K V T G I I T Q	20	
83	R K D K V L L G R K A V V V S	20	
6	T K T F P L R A L H I V V E S	19	
98	C E G I N I S G S F C R N K L	19	
104	S G S F C R N K L K Y L A F L	19	
106	S F C R N K L K Y L A F L H K	19	
111	K L K Y L A F L H K R M N T N	19	
115	L A F L H K R M N T N P S R R	19	
231	G L G F I F K T I A P L A A T	19	
318	N P R H S P S G G G G L K K P	19	
367	P A D L A G S G Y C G A L W K	19	
372	G S G Y C G A L W K A I E S L	19	
8	T F P L R A L H I V V E S I R	18	
60	V G S Y K L A Y S N D G E H W	18	
112	L K Y L A F L H K R M N T N P	18	
161	Y K K V C L S G A P H E V G W	18	
171	H E V G W K Y Q A V T A T L E	18	
172	E V G W K Y Q A V T A T L E E	18	
223	S P G G G S P R G L G F I F K	18	
252	H P G G R T P R A G S S A H R	18	
338	G Q K H N V L A R G K P Q R K	18	
364	N G R P A D L A G S G Y C G A	18	
384	E S L E E G L G G K Q K D K E	18	
2	L E H T T K T F P L R A L H I	17	
11	L R A L H I V V E S I R D H S	17	
14	L H I V V E S I R D H S G Q K	17	

TABLE XLVIII 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
26	G Q K M K Q D K K V D L L V P	17	
29	M K Q D K K V D L L V P T K V	17	
37	L L V P T K V T G I I T Q G A	17	
76	V Y Q D E K Q R K D K V L L G	17	
84	K D K V L L G R K A V V V S C	17	
90	G R K A V V V S C E G I N I S	17	
93	A V V V S C E G I N I S G S F	17	
96	V S C E G I N I S G S F C R N	17	
109	R N K L K Y L A F L H K R M N	17	
137	S R I F W R Q E K A D G G S C	17	
160	A Y K K V C L S G A P H E V G	17	
181	T A T L E E K R K E K A E I H	17	
191	K A E I H Y R K N K Q L M R L	17	
200	K Q L M R L Q K Q A E K N M K	17	
218	D K Y T E S P G G G S P R G L	17	
221	T E S P G G G S P R G L G F I	17	
230	R G L G F I F K T I A P L A A	17	
253	P G G R T P R A G S S A H R P	17	
279	A S P A A W L P L R T P W T R	17	
288	R T P W T R P S S C P T S S S	17	
337	Q G Q K H N V L A R G K P Q R	17	
360	W Y V E N G R P A D L A G S G	17	
374	G Y C G A L W K A I E S L E E	17	
380	W K A I E S L E E G L G G K Q	17	
383	I E S L E E G L G G K Q K D K	17	
396	D K E R K A E N G P H L L V E	17	
57	V Q F V G S Y K L A Y S N D G	16	
86	K V L L G R K A V V V S C E G	16	
95	V V S C E G I N I S G S F C R	16	
147	D G G S C C P Q G H A S E A Y	16	
149	G S C C P Q G H A S E A Y K K	16	
199	N K Q L M R L Q K Q A E K N M	16	
225	G G G S P R G L G F I F K T I	16	
256	R T P R A G S S A H R P P A L	16	
261	G S S A H R P P A L S A R A P	16	
266	R P P A L S A R A P V P A A S	16	
269	A L S A R A P V P A A S P A A	16	
271	S A R A P V P A A S P A A W L	16	
274	A P V P A A S P A A W L P L R	16	
275	P V P A A S P A A W L P L R T	16	
307	L S P Y G P R N P L P N P R H	16	
311	G P R N P L P N P R H S P S G	16	
313	R N P L P N P R H S P S G G G	16	
344	L A R G K P Q R K P K S E N N	16	
142	R Q E K A D G G S C C P Q G H	15	
159	E A Y K K V C L S G A P H E V	15	
272	A R A P V P A A S P A A W L P	15	
282	A A W L P L R T P W T R P S S	15	
290	P W T R P S S C P T S S S T Y	15	
295	S S C P T S S S T Y D S L S P	15	
356	E N N S W Y V E N G R P A D L	15	
397	K E R K A E N G P H L L V E A	15	
10	P L R A L H I V V E S I R D H	14	
15	H I V V E S I R D H S G Q K M	14	
33	K K V D L L V P T K V T G I I	14	

TABLE XLVIII 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
97	S C E G I N I S G S F C R N K	14	
122	M N T N P S R R P Y H F Q V P	14	
162	K K V C L S G A P H E V G W K	14	
173	V G W K Y Q A V T A T L E E K	14	
193	E I H Y R K N K Q L M R L Q K	14	
213	M K K K I D K Y T E S P G G G	14	
249	R I G H P G G R T P R A G S S	14	
259	R A G S S A H R P P A L S A R	14	
260	A G S S A H R P P A L S A R A	14	
263	S A H R P P A L S A R A P V P	14	
273	R A P V P A A S P A A W L P L	14	
287	L R T P W T R P S S C P T S S	14	
291	W T R P S S C P T S S S T Y D	14	
298	P T S S S T Y D S L S P Y G P	14	
333	A R H C Q G Q K H N V L A R G	14	
341	H N V L A R G K P Q R K P K S	14	
351	R K P K S E N N S W Y V E N G	14	
12	R A L H I V V E S I R D H S G	13	
212	N M K K K I D K Y T E S P G G	13	
245	T R A T R I G H P G G R T P R	13	
24	H S G Q K M K Q D K K V D L L	12	
42	K V T G I I T Q G A K D F G H	12	
71	G E H W T V Y Q D E K Q R K D	12	
74	W T V Y Q D E K Q R K D K V L	12	
89	L G R K A V V V S C E G I N I	12	
184	L E E K R K E K A E I H Y R K	12	
206	Q K Q A E K N M K K K I D K Y	12	
210	E K N M K K K I D K Y T E S P	12	
342	N V L A R G K P Q R K P K S E	12	
358	N S W Y V E N G R P A D L A G	12	
362	V E N G R P A D L A G S G Y C	12	
381	K A I E S L E E G L G G K Q K	12	
390	L G G K Q K D K E R K A E N G	12	
56	H V Q F V G S Y K L A Y S N D	11	
64	K L A Y S N D G E H W T V Y Q	11	
226	G G S P R G L G F I F K T I A	11	
321	H S P S G G G G L K K P A R H	11	
325	G G G G L K K P A R H C Q G Q	11	
326	G G G L K K P A R H C Q G Q K	11	
330	K K P A R H C Q G Q K H N V L	11	
339	Q K H N V L A R G K P Q R K P	11	
3	E H T T K T F P L R A L H I V	10	
13	A L H I V V E S I R D H S G Q	10	
28	K M K Q D K K V D L L V P T K	10	
47	I T Q G A K D F G H V Q F V G	10	
48	T Q G A K D F G H V Q F V G S	10	
59	F V G S Y K L A Y S N D G E H	10	
65	L A Y S N D G E H W T V Y Q D	10	
77	Y Q D E K Q R K D K V L L G R	10	
105	G S F C R N K L K Y L A F L H	10	
107	F C R N K L K Y L A F L H K R	10	
108	C R N K L K Y L A F L H K R M	10	
114	Y L A F L H K R M N T N P S R	10	
124	T N P S R R P Y H F Q V P S R	10	
125	N P S R R P Y H F Q V P S R I	10	

TABLE XLVIII 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
130	P Y H F Q V P S R I F W R Q E	10	
135	V P S R I F W R Q E K A D G G	10	
139	I F W R Q E K A D G G S C C P	10	
140	F W R Q E K A D G G S C C P Q	10	
141	W R Q E K A D G G S C C P Q G	10	
152	C P Q G H A S E A Y K K V C L	10	
153	P Q G H A S E A Y K K V C L S	10	
177	Y Q A V T A T L E E K R K E K	10	
178	Q A V T A T L E E K R K E K A	10	
183	T L E E K R K E K A E I H Y R	10	
195	H Y R K N K Q L M R L Q K Q A	10	
198	K N K Q L M R L Q K Q A E K N	10	
214	K K K I D K Y T E S P G G G S	10	
215	K K I D K Y T E S P G G G S P	10	
242	L A A T R A T R I G H P G G R	10	
244	A T R A T R I G H P G G R T P	10	
251	G H P G G R T P R A G S S A H	10	
289	T P W T R P S S C P T S S S T	10	
316	L P N P R H S P S G G G G L K	10	
317	P N P R H S P S G G G G L K K	10	
320	R H S P S G G G G L K K P A R	10	
347	G K P Q R K P K S E N N S W Y	10	
376	C G A L W K A I E S L E E G L	10	
379	L W K A I E S L E E G L G G K	10	
394	Q K D K E R K A E N G P H L L	10	
9	F P L R A L H I V V E S I R D	9	
23	D H S G Q K M K Q D K K V D L	9	
25	S G Q K M K Q D K K V D L L V	9	
31	Q D K K V D L L V P T K V T G	9	
41	T K V T G I I T Q G A K D F G	9	
44	T G I I T Q G A K D F G H V Q	9	
49	Q G A K D F G H V Q F V G S Y	9	
53	D F G H V Q F V G S Y K L A Y	9	
55	G H V Q F V G S Y K L A Y S N	9	
73	H W T V Y Q D E K Q R K D K V	9	
91	R K A V V V S C E G I N I S G	9	
100	G I N I S G S F C R N K L K Y	9	
101	I N I S G S F C R N K L K Y L	9	
136	P S R I F W R Q E K A D G G S	9	
166	L S G A P H E V G W K Y Q A V	9	
169	A P H E V G W K Y Q A V T A T	9	
194	I H Y R K N K Q L M R L Q K Q	9	
196	Y R K N K Q L M R L Q K Q A E	9	
201	Q L M R L Q K Q A E K N M K K	9	
211	K N M K K K I D K Y T E S P G	9	
219	K Y T E S P G G G S P R G L G	9	
224	P G G G S P R G L G F I F K T	9	
228	S P R G L G F I F K T I A P L	9	
257	T P R A G S S A H R P P A L S	9	
265	H R P P A L S A R A P V P A A	9	
283	A W L P L R T P W T R P S S C	9	
285	L P L R T P W T R P S S C P T	9	
310	Y G P R N P L P N P R H S P S	9	
319	P R H S P S G G G G L K K P A	9	
322	S P S G G G G L K K P A R H C	9	

TABLE XLVIII 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
340	K H N V L A R G K P Q R K P K	9	
348	K P Q R K P K S E N N S W Y V	9	
370	L A G S G Y C G A L W K A I E	9	
371	A G S G Y C G A L W K A I E S	9	
387	E E G L G G K Q K D K E R K A	9	
388	E G L G G K Q K D K E R K A E	9	
393	K Q K D K E R K A E N G P H L	9	
7	K T F P L R A L H I V V E S I	8	
27	Q K M K Q D K K V D L L V P T	8	
34	K V D L L V P T K V T G I I T	8	
46	I I T Q G A K D F G H V Q F V	8	
58	Q F V G S Y K L A Y S N D G E	8	
62	S Y K L A Y S N D G E H W T V	8	
63	Y K L A Y S N D G E H W T V Y	8	
72	E H W T V Y Q D E K Q R K D K	8	
78	Q D E K Q R K D K V L L G R K	8	
81	K Q R K D K V L L G R K A V V	8	
126	P S R R P Y H F Q V P S R I F	8	
132	H F Q V P S R I F W R Q E K A	8	
145	K A D G G S C C P Q G H A S E	8	
146	A D G G S C C P Q G H A S E A	8	
155	G H A S E A Y K K V C L S G A	8	
156	H A S E A Y K K V C L S G A P	8	
163	K V C L S G A P H E V G W K Y	8	
167	S G A P H E V G W K Y Q A V T	8	
168	G A P H E V G W K Y Q A V T A	8	
170	P H E V G W K Y Q A V T A T L	8	
188	R K E K A E I H Y R K N K Q L	8	
192	A E I H Y R K N K Q L M R L Q	8	
197	R K N K Q L M R L Q K Q A E K	8	
207	K Q A E K N M K K K I D K Y T	8	
216	K I D K Y T E S P G G G S P R	8	
235	I F K T I A P L A A T R A T R	8	
237	K T I A P L A A T R A T R I G	8	
243	A A T R A T R I G H P G G R T	8	
246	R A T R I G H P G G R T P R A	8	
255	G R T P R A G S S A H R P P A	8	
258	P R A G S S A H R P P A L S A	8	
268	P A L S A R A P V P A A S P A	8	
276	V P A A S P A A W L P L R T P	8	
296	S C P T S S S T Y D S L S P Y	8	
297	C P T S S S T Y D S L S P Y G	8	
303	T Y D S L S P Y G P R N P L P	8	
305	D S L S P Y G P R N P L P N P	8	
306	S L S P Y G P R N P L P N P R	8	
308	S P Y G P R N P L P N P R H S	8	
309	P Y G P R N P L P N P R H S P	8	
312	P R N P L P N P R H S P S G G	8	
315	P L P N P R H S P S G G G G L	8	
323	P S G G G G L K K P A R H C Q	8	
331	K P A R H C Q G Q K H N V L A	8	
332	P A R H C Q G Q K H N V L A R	8	
334	R H C Q G Q K H N V L A R G K	8	
363	E N G R P A D L A G S G Y C G	8	
365	G R P A D L A G S G Y C G A L	8	

TABLE XLVIII 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
366	R P A D L A G S G Y C G A L W	8	
368	A D L A G S G Y C G A L W K A	8	
369	D L A G S G Y C G A L W K A I	8	
373	S G Y C G A L W K A I E S L E	8	
375	Y C G A L W K A I E S L E E G	8	
398	E R K A E N G P H L L V E A E	8	
400	K A E N G P H L L V E A E Q A	8	
21	I R D H S G Q K M K Q D K K V	7	
88	L L G R K A V V V S C E G I N	7	
133	F Q V P S R I F W R Q E K A D	7	
148	G G S C C P Q G H A S E A Y K	7	
220	Y T E S P G G G S P R G L G F	7	
240	A P L A A T R A T R I G H P G	7	
250	I G H P G G R T P R A G S S A	7	
254	G G R T P R A G S S A H R P P	7	
294	P S S C P T S S S T Y D S L S	7	
314	N P L P N P R H S P S G G G G	7	
324	S G G G G L K K P A R H C Q G	7	
345	A R G K P Q R K P K S E N N S	7	
17	V V E S I R D H S G Q K M K Q	6	
52	K D F G H V Q F V G S Y K L A	6	
67	Y S N D G E H W T V Y Q D E K	6	
70	D G E H W T V Y Q D E K Q R K	6	
118	L H K R M N T N P S R R P Y H	6	
150	S C C P Q G H A S E A Y K K V	6	
175	W K Y Q A V T A T L E E K R K	6	
278	A A S P A A W L P L R T P W T	6	
286	P L R T P W T R P S S C P T S	6	
292	T R P S S C P T S S S T Y D S	6	
293	R P S S C P T S S S T Y D S L	6	
300	S S S T Y D S L S P Y G P R N	6	
16	I V V E S I R D H S G Q K M K	5	
134	Q V P S R I F W R Q E K A D G	5	
179	A V T A T L E E K R K E K A E	5	
395	K D K E R K A E N G P H L L V	5	
79	D E K Q R K D K V L L G R K A	4	
87	V L L G R K A V V V S C E G I	4	
189	K E K A E I H Y R K N K Q L M	4	
234	F I F K T I A P L A A T R A T	4	
80	E K Q R K D K V L L G R K A V	3	
117	F L H K R M N T N P S R R P Y	3	
182	A T L E E K R K E K A E I H Y	3	
186	E K R K E K A E I H Y R K N K	3	
209	A E K N M K K K I D K Y T E S	3	
241	P L A A T R A T R I G H P G G	3	
343	V L A R G K P Q R K P K S E N	3	
349	P Q R K P K S E N N S W Y V E	3	
378	A L W K A I E S L E E G L G G	3	
382	A I E S L E E G L G G K Q K D	3	
385	S L E E G L G G K Q K D K E R	3	
391	G G K Q K D K E R K A E N G P	3	
4	H T T K T F P L R A L H I V V	2	
19	E S I R D H S G Q K M K Q D K	2	
38	L V P T K V T G I I T Q G A K	2	
39	V P T K V T G I I T Q G A K D	2	

TABLE XLVIII 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
45	G I I T Q G A K D F G H V Q F	2	
61	G S Y K L A Y S N D G E H W T	2	
102	N I S G S F C R N K L K Y L A	2	
110	N K L K Y L A F L H K R M N T	2	
120	K R M N T N P S R R P Y H F Q	2	
157	A S E A Y K K V C L S G A P H	2	
164	V C L S G A P H E V G W K Y Q	2	
203	M R L Q K Q A E K N M K K K I	2	
205	L Q K Q A E K N M K K K I D K	2	
208	Q A E K N M K K K I D K Y T E	2	
227	G S P R G L G F I F K T I A P	2	
248	T R I G H P G G R T P R A G S	2	
262	S S A H R P P A L S A R A P V	2	
280	S P A A W L P L R T P W T R P	2	
328	G L K K P A R H C Q G Q K H N	2	
335	H C Q G Q K H N V L A R G K P	2	
355	S E N N S W Y V E N G R P A D	2	
392	G K Q K D K E R K A E N G P H	2	
1	M L E H T T K T F P L R A L H	1	
20	S I R D H S G Q K M K Q D K K	1	
30	K Q D K K V D L L V P T K V T	1	
66	A Y S N D G E H W T V Y Q D E	1	
75	T V Y Q D E K Q R K D K V L L	1	
103	I S G S F C R N K L K Y L A F	1	
113	K Y L A F L H K R M N T N P S	1	
121	R M N T N P S R R P Y H F Q V	1	
131	Y H F Q V P S R I F W R Q E K	1	
154	Q G H A S E A Y K K V C L S G	1	
165	C L S G A P H E V G W K Y Q A	1	
176	K Y Q A V T A T L E E K R K E	1	
180	V T A T L E E K R K E K A E I	1	
185	E E K R K E K A E I H Y R K N	1	
187	K R K E K A E I H Y R K N K Q	1	
190	E K A E I H Y R K N K Q L M R	1	
204	R L Q K Q A E K N M K K K I D	1	
299	T S S S T Y D S L S P Y G P R	1	
302	S T Y D S L S P Y G P R N P L	1	
327	G G L K K P A R H C Q G Q K H	1	
336	C Q G Q K H N V L A R G K P Q	1	
350	Q R K P K S E N N S W Y V E N	1	
353	P K S E N N S W Y V E N G R P	1	
354	K S E N N S W Y V E N G R P A	1	
386	L E E G L G G K Q K D K E R K	1	
389	G L G G K Q K D K E R K A E N	1	
399	R K A E N G P H L L V E A E Q	1	

TABLE XLIX 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
149	T V V V A L D L Q G V V F P Y	28	
333	R F V G F P D K K H K L Y G V	27	
261	F Y Y L I H P T K L T Y D E A	26	
161	F P Y F P R L G R Y N L N F H	24	
171	N L N F H E A Q Q A C L D Q D	24	
191	F D Q L Y D A W R G G L D W C	24	

TABLE XLIX 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
229	Q N T V P G V R N Y G F W D K	24	
250	V F C F T S N F N G R F Y Y L	24	
122	A S L V I T D L T L E D Y G R	23	
206	N A G W L S D G S V Q Y P I T	23	
267	P T K L T Y D E A V Q A C L N	23	
81	W T K L T S D Y L K E V D V F	22	
237	N Y G F W D K D K S R Y D V F	22	
305	D A G W L A D G S V R Y P I S	22	
38	P H L L V E A E Q A K V F S H	21	
113	F L K G G S D S D A S L V I T	21	
142	I E G L E D D T V V V A L D L	21	
179	Q A C L D Q D A V I A S F D Q	21	
184	Q D A V I A S F D Q L Y D A W	21	
296	W K I L G Y D R C D A G W L A	21	
21	N Y T L D H D R A I H I Q A E	20	
37	G P H L L V E A E Q A K V F S	20	
60	P C K F Y R D P T A F G S G I	20	
126	I T D L T L E D Y G R Y K C E	20	
123	S L V I T D L T L E D Y G R Y	19	
138	K C E V I E G L E D D T V V V	19	
156	L Q G V V F P Y F P R L G R Y	19	
7	L V L I S I C W A D H L S D N	18	
29	A I H I Q A E N G P H L L V E	18	
39	H L L V E A E Q A K V F S H R	18	
54	G G N V T L P C K F Y R D P T	18	
89	L K E V D V F V S M G Y H K K	18	
128	D L T L E D Y G R Y K C E V I	18	
153	A L D L Q G V V F P Y F P R L	18	
163	Y F P R L G R Y N L N F H E A	18	
185	D A V I A S F D Q L Y D A W R	18	
199	R G G L D W C N A G W L S D G	18	
290	G Q I F A A W K I L G Y D R C	18	
295	A W K I L G Y D R C D A G W L	18	
334	F V G F P D K K H K L Y G V Y	18	
27	D R A I H I Q A E N G P H L L	17	
95	F V S M G Y H K K T Y G G Y Q	17	
216	Q Y P I T K P R E P C G G Q N	17	
273	D E A V Q A C L N D G A Q I A	17	
277	Q A C L N D G A Q I A K V G Q	17	
283	G A Q I A K V G Q I F A A W K	17	
289	V G Q I F A A W K I L G Y D R	17	
48	K V F S H R G G N V T L P C K	16	
103	K T Y G G Y Q G R V F L K G G	16	
158	G V V F P Y F P R L G R Y N L	16	
248	Y D V F C F T S N F N G R F Y	16	
269	K L T Y D E A V Q A C L N D G	16	
315	R Y P I S R P R R R C S P T E	16	
332	V R F V G F P D K K H K L Y G	16	
13	C W A D H L S D N Y T L D H D	15	
252	C F T S N F N G R F Y Y L I H	15	
2	K S L L L L V L I S I C W A D	14	
14	W A D H L S D N Y T L D H D R	14	
94	V F V S M G Y H K K T Y G G Y	14	
141	V I E G L E D D T V V V A L D	14	

TABLE XLIX 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
276	V Q A C L N D G A Q I A K V G	14	
1	M K S L L L L V L I S I C W A	13	
4	L L L L V L I S I C W A D H L	13	
5	L L L V L I S I C W A D H L S	13	
6	L L V L I S I C W A D H L S D	13	
19	S D N Y T L D H D R A I H I Q	13	
127	T D L T L E D Y G R Y K C E V	13	
147	D D T V V V A L D L Q G V V F	13	
151	V V A L D L Q G V V F P Y F P	13	
197	A W R G G L D W C N A G W L S	13	
3	S L L L L V L I S I C W A D H	12	
46	Q A K V F S H R G G N V T L P	12	
74	I H K I R I K W T K L T S D Y	12	
76	K I R I K W T K L T S D Y L K	12	
86	S D Y L K E V D V F V S M G Y	12	
92	V D V F V S M G Y H K K T Y G	12	
93	D V F V S M G Y H K K T Y G G	12	
109	Q G R V F L K G G S D S D A S	12	
111	R V F L K G G S D S D A S L V	12	
115	K G G S D S D A S L V I T D L	12	
121	D A S L V I T D L T L E D Y G	12	
148	D T V V V A L D L Q G V V F P	12	
157	Q G V V F P Y F P R L G R Y N	12	
169	R Y N L N F H E A Q Q A C L D	12	
177	A Q Q A C L D Q D A V I A S F	12	
190	S F D Q L Y D A W R G G L D W	12	
207	A G W L S D G S V Q Y P I T K	12	
232	V P G V R N Y G F W D K D K S	12	
262	Y Y L I H P T K L T Y D E A V	12	
299	L G Y D R C D A G W L A D G S	12	
329	E A A V R F V G F P D K K H K	12	
9	L I S I C W A D H L S D N Y T	11	
15	A D H L S D N Y T L D H D R A	11	
30	I H I Q A E N G P H L L V E A	11	
73	G I H K I R I K W T K L T S D	11	
87	D Y L K E V D V F V S M G Y H	11	
110	G R V F L K G G S D S D A S L	11	
120	S D A S L V I T D L T L E D Y	11	
139	C E V I E G L E D D T V V V A	11	
150	V V V A L D L Q G V V F P Y F	11	
164	F P R L G R Y N L N F H E A Q	11	
227	G G Q N T V P G V R N Y G F W	11	
236	R N Y G F W D K D K S R Y D V	11	
238	Y G F W D K D K S R Y D V F C	11	
243	K D K S R Y D V F C F T S N F	11	
247	R Y D V F C F T S N F N G R F	11	
286	I A K V G Q I F A A W K I L G	11	
306	A G W L A D G S V R Y P I S R	11	
311	D G S V R Y P I S R P R R R C	11	
331	A V R F V G F P D K K H K L Y	11	
339	D K K H K L Y G V Y C F R A Y	11	
10	I S I C W A D H L S D N Y T L	10	
11	S I C W A D H L S D N Y T L D	10	
47	A K V F S H R G G N V T L P C	10	

TABLE XLIX 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
52	H R G G N V T L P C K F Y R D	10	
53	R G G N V T L P C K F Y R D P	10	
56	N V T L P C K F Y R D P T A F	10	
71	G S G I H K I R I K W T K L T	10	
84	L T S D Y L K E V D V F V S M	10	
91	E V D V F V S M G Y H K K T Y	10	
143	E G L E D D T V V V A L D L Q	10	
145	L E D D T V V V A L D L Q G V	10	
152	V A L D L Q G V V F P Y F P R	10	
183	D Q D A V I A S F D Q L Y D A	10	
186	A V I A S F D Q L Y D A W R G	10	
212	D G S V Q Y P I T K P R E P C	10	
246	S R Y D V F C F T S N F N G R	10	
259	G R F Y Y L I H P T K L T Y D	10	
282	D G A Q I A K V G Q I F A A W	10	
337	F P D K K H K L Y G V Y C F R	10	
20	D N Y T L D H D R A I H I Q A	9	
59	L P C K F Y R D P T A F G S G	9	
67	P T A F G S G I H K I R I K W	9	
77	I R I K W T K L T S D Y L K E	9	
78	R I K W T K L T S D Y L K E V	9	
118	S D S D A S L V I T D L T L E	9	
134	Y G R Y K C E V I E G L E D D	9	
168	G R Y N L N F H E A Q Q A C L	9	
180	A C L D Q D A V I A S F D Q L	9	
188	I A S F D Q L Y D A W R G G L	9	
198	W R G G L D W C N A G W L S D	9	
228	G Q N T V P G V R N Y G F W D	9	
254	T S N F N G R F Y Y L I H P T	9	
266	H P T K L T Y D E A V Q A C L	9	
288	K V G Q I F A A W K I L G Y D	9	
314	V R Y P I S R P R R R C S P T	9	
321	P R R R C S P T E A A V R F V	9	
323	R R C S P T E A A V R F V G F	9	
326	S P T E A A V R F V G F P D K	9	
28	R A I H I Q A E N G P H L L V	8	
35	E N G P H L L V E A E Q A K V	8	
40	L L V E A E Q A K V F S H R G	8	
70	F G S G I H K I R I K W T K L	8	
75	H K I R I K W T K L T S D Y L	8	
83	K L T S D Y L K E V D V F V S	8	
97	S M G Y H K K T Y G G Y Q G R	8	
102	K K T Y G G Y Q G R V F L K G	8	
107	G Y Q G R V F L K G G S D S D	8	
124	L V I T D L T L E D Y G R Y K	8	
132	E D Y G R Y K C E V I E G L E	8	
135	G R Y K C E V I E G L E D D T	8	
159	V V F P Y F P R L G R Y N L N	8	
165	P R L G R Y N L N F H E A Q Q	8	
170	Y N L N F H E A Q Q A C L D Q	8	
215	V Q Y P I T K P R E P C G G Q	8	
221	K P R E P C G G Q N T V P G V	8	
239	G F W D K D K S R Y D V F C F	8	
240	F W D K D K S R Y D V F C F T	8	

TABLE XLIX 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
242	D K D K S R Y D V F C F T S N	8	
251	F C F T S N F N G R F Y Y L I	8	
253	F T S N F N G R F Y Y L I H P	8	
258	N G R F Y Y L I H P T K L T Y	8	
298	I L G Y D R C D A G W L A D G	8	
312	G S V R Y P I S R P R R R C S	8	
316	Y P I S R P R R R C S P T E A	8	
25	D H D R A I H I Q A E N G P H	7	
45	E Q A K V F S H R G G N V T L	7	
72	S G I H K I R I K W T K L T S	7	
82	T K L T S D Y L K E V D V F V	7	
176	E A Q Q A C L D Q D A V I A S	7	
213	G S V Q Y P I T K P R E P C G	7	
235	V R N Y G F W D K D K S R Y D	7	
280	L N D G A Q I A K V G Q I F A	7	
335	V G F P D K K H K L Y G V Y C	7	
57	V T L P C K F Y R D P T A F G	6	
68	T A F G S G I H K I R I K W T	6	
101	H K K T Y G G Y Q G R V F L K	6	
130	T L E D Y G R Y K C E V I E G	6	
208	G W L S D G S V Q Y P I T K P	6	
222	P R E P C G G Q N T V P G V R	6	
307	G W L A D G S V R Y P I S R P	6	
325	C S P T E A A V R F V G F P D	6	
36	N G P H L L V E A E Q A K V F	4	
55	G N V T L P C K F Y R D P T A	4	
79	I K W T K L T S D Y L K E V D	4	
80	K W T K L T S D Y L K E V D V	4	
162	P Y F P R L G R Y N L N F H E	4	
220	T K P R E P C G G Q N T V P G	4	
260	R F Y Y L I H P T K L T Y D E	4	
24	L D H D R A I H I Q A E N G P	3	
31	H I Q A E N G P H L L V E A E	3	
33	Q A E N G P H L L V E A E Q A	3	
85	T S D Y L K E V D V F V S M G	3	
100	Y H K K T Y G G Y Q G R V F L	3	
125	V I T D L T L E D Y G R Y K C	3	
178	Q Q A C L D Q D A V I A S F D	3	
211	S D G S V Q Y P I T K P R E P	3	
217	Y P I T K P R E P C G G Q N T	3	
241	W D K D K S R Y D V F C F T S	3	
265	I H P T K L T Y D E A V Q A C	3	
285	Q I A K V G Q I F A A W K I L	3	
300	G Y D R C D A G W L A D G S V	3	
320	R P R R R C S P T E A A V R F	3	
322	R R R C S P T E A A V R F V G	3	
8	V L I S I C W A D H L S D N Y	2	
12	I C W A D H L S D N Y T L D H	2	
26	H D R A I H I Q A E N G P H L	2	
34	A E N G P H L L V E A E Q A K	2	
44	A E Q A K V F S H R G G N V T	2	
49	V F S H R G G N V T L P C K F	2	
64	Y R D P T A F G S G I H K I R	2	
66	D P T A F G S G I H K I R I K	2	

TABLE XLIX 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
90	K E V D V F V S M G Y H K K T	2	
99	G Y H K K T Y G G Y Q G R V F	2	
105	Y G G Y Q G R V F L K G G S D	2	
108	Y Q G R V F L K G G S D S D A	2	
116	G G S D S D A S L V I T D L T	2	
119	D S D A S L V I T D L T L E D	2	
136	R Y K C E V I E G L E D D T V	2	
137	Y K C E V I E G L E D D T V V	2	
144	G L E D D T V V V A L D L Q G	2	
146	E D D T V V V A L D L Q G V V	2	
155	D L Q G V V F P Y F P R L G R	2	
160	V F P Y F P R L G R Y N L N F	2	
167	L G R Y N L N F H E A Q Q A C	2	
175	H E A Q Q A C L D Q D A V I A	2	
187	V I A S F D Q L Y D A W R G G	2	
193	Q L Y D A W R G G L D W C N A	2	
195	Y D A W R G G L D W C N A G W	2	
201	G L D W C N A G W L S D G S V	2	
219	I T K P R E P C G G Q N T V P	2	
226	C G G Q N T V P G V R N Y G F	2	
268	T K L T Y D E A V Q A C L N D	2	
271	T Y D E A V Q A C L N D G A Q	2	
272	Y D E A V Q A C L N D G A Q I	2	
275	A V Q A C L N D G A Q I A K V	2	
278	A C L N D G A Q I A K V G Q I	2	
284	A Q I A K V G Q I F A A W K I	2	
293	F A A W K I L G Y D R C D A G	2	
294	A A W K I L G Y D R C D A G W	2	
310	A D G S V R Y P I S R P R R R	2	
319	S R P R R R C S P T E A A V R	2	
324	R C S P T E A A V R F V G F P	2	
336	G F P D K K H K L Y G V Y C F	2	
340	K K H K L Y G V Y C F R A Y N	2	
17	H L S D N Y T L D H D R A I H	1	
32	I Q A E N G P H L L V E A E Q	1	
41	L V E A E Q A K V F S H R G G	1	
50	F S H R G G N V T L P C K F Y	1	
58	T L P C K F Y R D P T A F G S	1	
61	C K F Y R D P T A F G S G I H	1	
62	K F Y R D P T A F G S G I H K	1	
65	R D P T A F G S G I H K I R I	1	
69	A F G S G I H K I R I K W T K	1	
88	Y L K E V D V F V S M G Y H K	1	
96	V S M G Y H K K T Y G G Y Q G	1	
98	M G Y H K K T Y G G Y Q G R V	1	
104	T Y G G Y Q G R V F L K G G S	1	
112	V F L K G G S D S D A S L V I	1	
114	L K G G S D S D A S L V I T D	1	
117	G S D S D A S L V I T D L T L	1	
131	L E D Y G R Y K C E V I E G L	1	
133	D Y G R Y K C E V I E G L E D	1	
140	E V I E G L E D D T V V V A L	1	
172	L N F H E A Q Q A C L D Q D A	1	
173	N F H E A Q Q A C L D Q D A V	1	

TABLE XLIX 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
189	A S F D Q L Y D A W R G G L D	1	
192	D Q L Y D A W R G G L D W C N	1	
194	L Y D A W R G G L D W C N A G	1	
196	D A W R G G L D W C N A G W L	1	
200	G G L D W C N A G W L S D G S	1	
203	D W C N A G W L S D G S V Q Y	1	
204	W C N A G W L S D G S V Q Y P	1	
205	C N A G W L S D G S V Q Y P I	1	
209	W L S D G S V Q Y P I T K P R	1	
214	S V Q Y P I T K P R E P C G G	1	
218	P I T K P R E P C G G Q N T V	1	
223	R E P C G G Q N T V P G V R N	1	
231	T V P G V R N Y G F W D K D K	1	
233	P G V R N Y G F W D K D K S R	1	
249	D V F C F T S N F N G R F Y Y	1	
255	S N F N G R F Y Y L I H P T K	1	
256	N F N G R F Y Y L I H P T K L	1	
257	F N G R F Y Y L I H P T K L T	1	
263	Y L I H P T K L T Y D E A V Q	1	
264	L I H P T K L T Y D E A V Q A	1	
270	L T Y D E A V Q A C L N D G A	1	
274	E A V Q A C L N D G A Q I A K	1	
281	N D G A Q I A K V G Q I F A A	1	
287	A K V G Q I F A A W K I L G Y	1	
292	I F A A W K I L G Y D R C D A	1	
297	K I L G Y D R C D A G W L A D	1	
301	Y D R C D A G W L A D G S V R	1	
302	D R C D A G W L A D G S V R Y	1	
304	C D A G W L A D G S V R Y P I	1	
308	W L A D G S V R Y P I S R P R	1	
318	I S R P R R R C S P T E A A V	1	
328	T E A A V R F V G F P D K K H	1	
330	A A V R F V G F P D K K H K L	1	
338	P D K K H K L Y G V Y C F R A	1	

TABLE XLIX 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
26	G Q K M K Q D K K V D L L V P	37	
73	H W T V Y Q D E K Q R K D K V	28	
56	H V Q F V G S Y K L A Y S N D	25	
191	K A E I H Y R K N K Q L M R L	25	
43	V T G I I T Q G A K D F G H V	20	
54	F G H V Q F V G S Y K L A Y S	20	
84	K D K V L L G R K A V V V S C	20	
200	K Q L M R L Q K Q A E K N M K	20	
299	T S S S T Y D S L S P Y G P R	20	
34	K V D L L V P T K V T G I I T	19	
177	Y Q A V T A T L E E K R K E K	19	
340	K H N V L A R G K P Q R K P K	19	
359	S W Y V E N G R P A D L A G S	19	
380	W K A I E S L E E G L G G K Q	19	
14	L H I V V E S I R D H S G Q K	18	
181	T A T L E E K R K E K A E I H	18	
199	N K Q L M R L Q K Q A E K N M	18	

TABLE XLIX 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
231	G L G F I F K T I A P L A A T	18	
390	L G G K Q K D K E R K A E N G	18	
44	T G I I T Q G A K D F G H V Q	17	
64	K L A Y S N D G E H W T V Y Q	17	
91	R K A V V V S C E G I N I S G	17	
101	I N I S G S F C R N K L K Y L	17	
104	S G S F C R N K L K Y L A F L	17	
115	L A F L H K R M N T N P S R R	17	
136	P S R I F W R Q E K A D G G S	17	
170	P H E V G W K Y Q A V T A T L	17	
202	L M R L Q K Q A E K N M K K K	17	
326	G G G L K K P A R H C Q G Q K	17	
376	C G A L W K A I E S L E E G L	17	
379	L W K A I E S L E E G L G G K	17	
387	E E G L G G K Q K D K E R K A	17	
11	L R A L H I V V E S I R D H S	16	
78	Q D E K Q R K D K V L L G R K	16	
103	I S G S F C R N K L K Y L A F	16	
112	L K Y L A F L H K R M N T N P	16	
120	K R M N T N P S R R P Y H F Q	16	
137	S R I F W R Q E K A D G G S C	16	
155	G H A S E A Y K K V C L S G A	16	
185	E E K R K E K A E I H Y R K N	16	
214	K K K I D K Y T E S P G G G S	16	
229	P R G L G F I F K T I A P L A	16	
305	D S L S P Y G P R N P L P N P	16	
350	Q R K P K S E N N S W Y V E N	16	
130	P Y H F Q V P S R I F W R Q E	16	
18	V E S I R D H S G Q K M K Q D	15	
79	D E K Q R K D K V L L G R K A	14	
85	D K V L L G R K A V V V S C E	14	
92	K A V V V S C E G I N I S G S	14	
30	K Q D K K V D L L V P T K V T	14	
35	V D L L V P T K V T G I I T Q	13	
57	V Q F V G S Y K L A Y S N D G	13	
273	R A P V P A A S P A A W L P L	13	
304	Y D S L S P Y G P R N P L P N	13	
383	I E S L E E G L G G K Q K D K	13	
8	T F P L R A L H I V V E S I R	13	
13	A L H I V V E S I R D H S G Q	12	
32	D K K V D L L V P T K V T G I	12	
40	P T K V T G I I T Q G A K D F	12	
93	A V V V S C E G I N I S G S F	12	
109	R N K L K Y L A F L H K R M N	12	
141	W R Q E K A D G G S C C P Q G	12	
161	Y K K V C L S G A P H E V G W	12	
212	N M K K K I D K Y T E S P G G	12	
341	H N V L A R G K P Q R K P K S	12	
3	E H T T K T F P L R A L H I V	12	
15	H I V V E S I R D H S G Q K M	11	
17	V V E S I R D H S G Q K M K Q	11	
48	T Q G A K D F G H V Q F V G S	11	
86	K V L L G R K A V V V S C E G	11	
98	C E G I N I S G S F C R N K L	11	
100	G I N I S G S F C R N K L K Y	11	

TABLE XLIX 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
106	S F C R N K L K Y L A F L H K	11	
107	F C R N K L K Y L A F L H K R	11	
114	Y L A F L H K R M N T N P S R	11	
119	H K R M N T N P S R R P Y H F	11	
132	H F Q V P S R I F W R Q E K A	11	
163	K V C L S G A P H E V G W K Y	11	
210	E K N M K K K I D K Y T E S P	11	
232	L G F I F K T I A P L A A T R	11	
233	G F I F K T I A P L A A T R A	11	
236	F K T I A P L A A T R A T R I	11	
247	A T R I G H P G G R T P R A G	11	
267	P P A L S A R A P V P A A S P	11	
282	A A W L P L R T P W T R P S S	11	
284	W L P L R T P W T R P S S C P	11	
348	K P Q R K P K S E N N S W Y V	11	
363	E N G R P A D L A G S G Y C G	11	
367	P A D L A G S G Y C G A L W K	11	
397	K E R K A E N G P H L L V E A	11	
4	H T T K T F P L R A L H I V V	10	
27	Q K M K Q D K K V D L L V P T	10	
36	D L L V P T K V T G I I T Q G	10	
47	I T Q G A K D F G H V Q F V G	10	
62	S Y K L A Y S N D G E H W T V	10	
77	Y Q D E K Q R K D K V L L G R	10	
83	R K D K V L L G R K A V V V S	10	
179	A V T A T L E E K R K E K A E	10	
180	V T A T L E E K R K E K A E I	10	
198	K N K Q L M R L Q K Q A E K N	10	
209	A E K N M K K K I D K Y T E S	10	
223	S P G G G S P R G L G F I F K	10	
239	I A P L A A T R A T R I G H P	10	
274	A P V P A A S P A A W L P L R	10	
276	V P A A S P A A W L P L R T P	10	
293	R P S S C P T S S S T Y D S L	10	
312	P R N P L P N P R H S P S G G	10	
313	R N P L P N P R H S P S G G G	10	
318	N P R H S P S G G G G L K K P	10	
333	A R H C Q G Q K H N V L A R G	10	
358	N S W Y V E N G R P A D L A G	10	
368	A D L A G S G Y C G A L W K A	10	
375	Y C G A L W K A I E S L E E G	10	
385	S L E E G L G G K Q K D K E R	10	
6	T K T F P L R A L H I V V E S	9	
51	A K D F G H V Q F V G S Y K L	9	
61	G S Y K L A Y S N D G E H W T	9	
105	G S F C R N K L K Y L A F L H	9	
113	K Y L A F L H K R M N T N P S	9	
122	M N T N P S R R P Y H F Q V P	9	
129	R P Y H F Q V P S R I F W R Q	9	
150	S C C P Q G H A S E A Y K K V	9	
166	L S G A P H E V G W K Y Q A V	9	
173	V G W K Y Q A V T A T L E E K	9	
183	T L E E K R K E K A E I H Y R	9	
190	E K A E I H Y R K N K Q L M R	9	
193	E I H Y R K N K Q L M R L Q K	9	

TABLE XLIX 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
194	I H Y R K N K Q L M R L Q K Q	9	
203	M R L Q K Q A E K N M K K K I	9	
221	T E S P G G G S P R G L G F I	9	
225	G G G S P R G L G F I F K T I	9	
238	T I A P L A A T R A T R I G H	9	
259	R A G S S A H R P P A L S A R	9	
296	S C P T S S S T Y D S L S P Y	9	
342	N V L A R G K P Q R K P K S E	9	
344	L A R G K P Q R K P K S E N N	9	
386	L E E G L G G K Q K D K E R K	9	
391	G G K Q K D K E R K A E N G P	9	
396	D K E R K A E N G P H L L V E	9	
20	S I R D H S G Q K M K Q D K K	8	
23	D H S G Q K M K Q D K K V D L	8	
52	K D F G H V Q F V G S Y K L A	8	
66	A Y S N D G E H W T V Y Q D E	8	
74	W T V Y Q D E K Q R K D K V L	8	
96	V S C E G I N I S G S F C R N	8	
117	F L H K R M N T N P S R R P Y	8	
134	Q V P S R I F W R Q E K A D G	8	
135	V P S R I F W R Q E K A D G G	8	
151	C C P Q G H A S E A Y K K V C	8	
182	A T L E E K R K E K A E I H Y	8	
192	A E I H Y R K N K Q L M R L Q	8	
196	Y R K N K Q L M R L Q K Q A E	8	
204	R L Q K Q A E K N M K K K I D	8	
207	K Q A E K N M K K K I D K Y T	8	
208	Q A E K N M K K K I D K Y T E	8	
222	E S P G G G S P R G L G F I F	8	
248	T R I G H P G G R T P R A G S	8	
251	G H P G G R T P R A G S S A H	8	
265	H R P P A L S A R A P V P A A	8	
280	S P A A W L P L R T P W T R P	8	
285	L P L R T P W T R P S S C P T	8	
310	Y G P R N P L P N P R H S P S	8	
323	P S G G G G L K K P A R H C Q	8	
334	R H C Q G Q K H N V L A R G K	8	
349	P Q R K P K S E N N S W Y V E	8	
364	N G R P A D L A G S G Y C G A	8	
395	K D K E R K A E N G P H L L V	8	
19	E S I R D H S G Q K M K Q D K	7	
22	R D H S G Q K M K Q D K K V D	7	
41	T K V T G I I T Q G A K D F G	7	
72	E H W T V Y Q D E K Q R K D K	7	
75	T V Y Q D E K Q R K D K V L L	7	
76	V Y Q D E K Q R K D K V L L G	7	
94	V V V S C E G I N I S G S F C	7	
102	N I S G S F C R N K L K Y L A	7	
121	R M N T N P S R R P Y H F Q V	7	
126	P S R R P Y H F Q V P S R I F	7	
146	A D G G S C C P Q G H A S E A	7	
154	Q G H A S E A Y K K V C L S G	7	
164	V C L S G A P H E V G W K Y Q	7	
178	Q A V T A T L E E K R K E K A	7	
189	K E K A E I H Y R K N K Q L M	7	

TABLE XLIX 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
206	Q K Q A E K N M K K K I D K Y	7	
211	K N M K K K I D K Y T E S P G	7	
241	P L A A T R A T R I G H P G G	7	
258	P R A G S S A H R P P A L S A	7	
306	S L S P Y G P R N P L P N P R	7	
322	S P S G G G G L K K P A R H C	7	
331	K P A R H C Q G Q K H N V L A	7	
332	P A R H C Q G Q K H N V L A R	7	
338	G Q K H N V L A R G K P Q R K	7	
346	R G K P Q R K P K S E N N S W	7	
355	S E N N S W Y V E N G R P A D	7	
356	E N N S W Y V E N G R P A D L	7	
373	S G Y C G A L W K A I E S L E	7	
389	G L G G K Q K D K E R K A E N	7	
392	G K Q K D K E R K A E N G P H	7	
394	Q K D K E R K A E N G P H L L	7	
25	S G Q K M K Q D K K V D L L V	6	
50	G A K D F G H V Q F V G S Y K	6	
70	D G E H W T V Y Q D E K Q R K	6	
168	G A P H E V G W K Y Q A V T A	6	
329	L K K P A R H C Q G Q K H N V	6	
343	V L A R G K P Q R K P K S E N	6	
33	K K V D L L V P T K V T G I I	4	
108	C R N K L K Y L A F L H K R M	4	
169	A P H E V G W K Y Q A V T A T	4	
234	F I F K T I A P L A A T R A T	4	
382	A I E S L E E G L G G K Q K D	4	
393	K Q K D K E R K A E N G P H L	4	
7	K T F P L R A L H I V V E S I	3	
24	H S G Q K M K Q D K K V D L L	3	
42	K V T G I I T Q G A K D F G H	3	
60	V G S Y K L A Y S N D G E H W	3	
82	Q R K D K V L L G R K A V V V	3	
99	E G I N I S G S F C R N K L K	3	
111	K L K Y L A F L H K R M N T N	3	
125	N P S R R P Y H F Q V P S R I	3	
148	G G S C C P Q G H A S E A Y K	3	
159	E A Y K K V C L S G A P H E V	3	
160	A Y K K V C L S G A P H E V G	3	
162	K K V C L S G A P H E V G W K	3	
197	R K N K Q L M R L Q K Q A E K	3	
201	Q L M R L Q K Q A E K N M K K	3	
217	I D K Y T E S P G G G S P R G	3	
235	I F K T I A P L A A T R A T R	3	
255	G R T P R A G S S A H R P P A	3	
260	A G S S A H R P P A L S A R A	3	
262	S S A H R P P A L S A R A P V	3	
263	S A H R P P A L S A R A P V P	3	
266	R P P A L S A R A P V P A A S	3	
269	A L S A R A P V P A A S P A A	3	
270	L S A R A P V P A A S P A A W	3	
272	A R A P V P A A S P A A W L P	3	
281	P A A W L P L R T P W T R P S	3	
283	A W L P L R T P W T R P S S C	3	
289	T P W T R P S S C P T S S S T	3	

TABLE XLIX 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
295	S S C P T S S S T Y D S L S P	3	
303	T Y D S L S P Y G P R N P L P	3	
309	P Y G P R N P L P N P R H S P	3	
319	P R H S P S G G G G L K K P A	3	
320	R H S P S G G G G L K K P A R	3	
324	S G G G G L K K P A R H C Q G	3	
325	G G G G L K K P A R H C Q G Q	3	
330	K K P A R H C Q G Q K H N V L	3	
347	G K P Q R K P K S E N N S W Y	3	
362	V E N G R P A D L A G S G Y C	3	
366	R P A D L A G S G Y C G A L W	3	
377	G A L W K A I E S L E E G L G	3	
381	K A I E S L E E G L G G K Q K	3	
398	E R K A E N G P H L L V E A E	3	
400	K A E N G P H L L V E A E Q A	3	
1	M L E H T T K T F P L R A L H	2	
2	L E H T T K T F P L R A L H I	2	
5	T T K T F P L R A L H I V V E	2	
9	F P L R A L H I V V E S I R D	2	
10	P L R A L H I V V E S I R D H	2	
12	R A L H I V V E S I R D H S G	2	
28	K M K Q D K K V D L L V P T K	2	
29	M K Q D K K V D L L V P T K V	2	
31	Q D K K V D L L V P T K V T G	2	
38	L V P T K V T G I I T Q G A K	2	
55	G H V Q F V G S Y K L A Y S N	2	
67	Y S N D G E H W T V Y Q D E K	2	
71	G E H W T V Y Q D E K Q R K D	2	
80	E K Q R K D K V L L G R K A V	2	
87	V L L G R K A V V V S C E G I	2	
90	G R K A V V V S C E G I N I S	2	
97	S C E G I N I S G S F C R N K	2	
110	N K L K Y L A F L H K R M N T	2	
116	A F L H K R M N T N P S R R P	2	
131	Y H F Q V P S R I F W R Q E K	2	
138	R I F W R Q E K A D G G S C C	2	
145	K A D G G S C C P Q G H A S E	2	
152	C P Q G H A S E A Y K K V C L	2	
153	P Q G H A S E A Y K K V C L S	2	
156	H A S E A Y K K V C L S G A P	2	
165	C L S G A P H E V G W K Y Q A	2	
167	S G A P H E V G W K Y Q A V T	2	
172	E V G W K Y Q A V T A T L E E	2	
184	L E E K R K E K A E I H Y R K	2	
188	R K E K A E I H Y R K N K Q L	2	
195	H Y R K N K Q L M R L Q K Q A	2	
205	L Q K Q A E K N M K K K I D K	2	
215	K K I D K Y T E S P G G G S P	2	
218	D K Y T E S P G G G S P R G L	2	
219	K Y T E S P G G G S P R G L G	2	
224	P G G G S P R G L G F I F K T	2	
226	G G S P R G L G F I F K T I A	2	
227	G S P R G L G F I F K T I A P	2	
228	S P R G L G F I F K T I A P L	2	
230	R G L G F I F K T I A P L A A	2	

TABLE XLIX 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
237	K T I A P L A A T R A T R I G	2	
244	A T R A T R I G H P G G R T P	2	
246	R A T R I G H P G G R T P R A	2	
253	P G G R T P R A G S S A H R P	2	
254	G G R T P R A G S S A H R P P	2	
261	G S S A H R P P A L S A R A P	2	
264	A H R P P A L S A R A P V P A	2	
268	P A L S A R A P V P A A S P A	2	
275	P V P A A S P A A W L P L R T	2	
278	A A S P A A W L P L R T P W T	2	
288	R T P W T R P S S C P T S S S	2	
291	W T R P S S C P T S S S T Y D	2	
297	C P T S S S T Y D S L S P Y G	2	
301	S S T Y D S L S P Y G P R N P	2	
302	S T Y D S L S P Y G P R N P L	2	
307	L S P Y G P R N P L P N P R H	2	
308	S P Y G P R N P L P N P R H S	2	
316	L P N P R H S P S G G G G L K	2	
317	P N P R H S P S G G G G L K K	2	
321	H S P S G G G G L K K P A R H	2	
327	G G L K K P A R H C Q G Q K H	2	
335	H C Q G Q K H N V L A R G K P	2	
336	C Q G Q K H N V L A R G K P Q	2	
339	Q K H N V L A R G K P Q R K P	2	
354	K S E N N S W Y V E N G R P A	2	
360	W Y V E N G R P A D L A G S G	2	
361	Y V E N G R P A D L A G S G Y	2	
365	G R P A D L A G S G Y C G A L	2	
369	D L A G S G Y C G A L W K A I	2	
370	L A G S G Y C G A L W K A I E	2	
372	G S G Y C G A L W K A I E S L	2	
374	G Y C G A L W K A I E S L E E	2	
21	I R D H S G Q K M K Q D K K V	1	
37	L L V P T K V T G I I T Q G A	1	
39	V P T K V T G I I T Q G A K D	1	
45	G I I T Q G A K D F G H V Q F	1	
49	Q G A K D F G H V Q F V G S Y	1	
53	D F G H V Q F V G S Y K L A Y	1	
58	Q F V G S Y K L A Y S N D G E	1	
59	F V G S Y K L A Y S N D G E H	1	
63	Y K L A Y S N D G E H W T V Y	1	
65	L A Y S N D G E H W T V Y Q D	1	
69	N D G E H W T V Y Q D E K Q R	1	
81	K Q R K D K V L L G R K A V V	1	
88	L L G R K A V V V S C E G I N	1	
123	N T N P S R R P Y H F Q V P S	1	
124	T N P S R R P Y H F Q V P S R	1	
139	I F W R Q E K A D G G S C C P	1	
142	R Q E K A D G G S C C P Q G H	1	
143	Q E K A D G G S C C P Q G H A	1	
147	D G G S C C P Q G H A S E A Y	1	
157	A S E A Y K K V C L S G A P H	1	
158	S E A Y K K V C L S G A P H E	1	
171	H E V G W K Y Q A V T A T L E	1	
174	G W K Y Q A V T A T L E E K R	1	

TABLE XLIX 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0301 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
175	W K Y Q A V T A T L E E K R K	1	
176	K Y Q A V T A T L E E K R K E	1	
186	E K R K E K A E I H Y R K N K	1	
187	K R K E K A E I H Y R K N K Q	1	
213	M K K K I D K Y T E S P G G G	1	
216	K I D K Y T E S P G G G S P R	1	
220	Y T E S P G G G S P R G L G F	1	
242	L A A T R A T R I G H P G G R	1	
245	T R A T R I G H P G G R T P R	1	
250	I G H P G G R T P R A G S S A	1	
252	H P G G R T P R A G S S A H R	1	
256	R T P R A G S S A H R P P A L	1	
257	T P R A G S S A H R P P A L S	1	
277	P A A S P A A W L P L R T P W	1	
279	A S P A A W L P L R T P W T R	1	
287	L R T P W T R P S S C P T S S	1	
290	P W T R P S S C P T S S S T Y	1	
294	P S S C P T S S S T Y D S L S	1	
298	P T S S S T Y D S L S P Y G P	1	
300	S S S T Y D S L S P Y G P R N	1	
311	G P R N P L P N P R H S P S G	1	
314	N P L P N P R H S P S G G G G	1	
315	P L P N P R H S P S G G G G L	1	
328	G L K K P A R H C Q G Q K H N	1	
337	Q G Q K H N V L A R G K P Q R	1	
345	A R G K P Q R K P K S E N N S	1	
351	R K P K S E N N S W Y V E N G	1	
352	K P K S E N N S W Y V E N G R	1	
353	P K S E N N S W Y V E N G R P	1	
371	A G S G Y C G A L W K A I E S	1	
378	A L W K A I E S L E E G L G G	1	
384	E S L E E G L G G K Q K D K E	1	
388	E G L G G K Q K D K E R K A E	1	
399	R K A E N G P H L L V E A E Q	1	

TABLE L 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
78	R I K W T K L T S D Y L K E V	28	
161	F P Y F P R L G R Y N L N F H	28	
171	N L N F H E A Q Q A C L D Q D	28	
258	N G R F Y Y L I H P T K L T Y	28	
269	K L T Y D E A V Q A C L N D G	28	
38	P H L L V E A E Q A K V F S H	26	
149	T V V V A L D L Q G V V F P Y	26	
191	F D Q L Y D A W R G G L D W C	26	
247	R Y D V F C F T S N F N G R F	26	
283	G A Q I A K V G Q I F A A W K	26	
19	S D N Y T L D H D R A I H I Q	22	
60	P C K F Y R D P T A F G S G I	22	
85	T S D Y L K E V D V F V S M G	22	
134	Y G R Y K C E V I E G L E D D	22	
158	G V V F P Y F P R L G R Y N L	22	
167	L G R Y N L N F H E A Q Q A C	22	
206	N A G W L S D G S V Q Y P I T	22	

TABLE L 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
238	Y G F W D K D K S R Y D V F C	22	
245	K S R Y D V F C F T S N F N G	22	
259	G R F Y Y L I H P T K L T Y D	22	
260	R F Y Y L I H P T K L T Y D E	22	
305	D A G W L A D G S V R Y P I S	22	
1	M K S L L L L V L I S I C W A	20	
3	S L L L L V L I S I C W A D H	20	
4	L L L L V L I S I C W A D H L	20	
9	L I S I C W A D H L S D N Y T	20	
21	N Y T L D H D R A I H I Q A E	20	
29	A I H I Q A E N G P H L L V E	20	
37	G P H L L V E A E Q A K V F S	20	
71	G S G I H K I R I K W T K L T	20	
81	W T K L T S D Y L K E V D V F	20	
86	S D Y L K E V D V F V S M G Y	20	
89	L K E V D V F V S M G Y H K K	20	
93	D V F V S M G Y H K K T Y G G	20	
122	A S L V I T D L T L E D Y G R	20	
139	C E V I E G L E D D T V V V A	20	
142	I E G L E D D T V V V A L D L	20	
148	D T V V V A L D L Q G V V F P	20	
179	Q A C L D Q D A V I A S F D Q	20	
185	D A V I A S F D Q L Y D A W R	20	
229	Q N T V P G V R N Y G F W D K	20	
267	P T K L T Y D E A V Q A C L N	20	
273	D E A V Q A C L N D G A Q I A	20	
277	Q A C L N D G A Q I A K V G Q	20	
286	I A K V G Q I F A A W K I L G	20	
295	A W K I L G Y D R C D A G W L	20	
315	R Y P I S R P R R R C S P T E	20	
329	E A A V R F V G F P D K K H K	20	
18	L S D N Y T L D H D R A I H I	18	
23	T L D H D R A I H I Q A E N G	18	
57	V T L P C K F Y R D P T A F G	18	
115	K G G S D S D A S L V I T D L	18	
119	D S D A S L V I T D L T L E D	18	
141	V I E G L E D D T V V V A L D	18	
176	E A Q Q A C L D Q D A V I A S	18	
182	L D Q D A V I A S F D Q L Y D	18	
11	S I C W A D H L S D N Y T L D	16	
61	C K F Y R D P T A F G S G I H	16	
67	P T A F G S G I H K I R I K W	16	
92	V D V F V S M G Y H K K T Y G	16	
110	G R V F L K G G S D S D A S L	16	
131	L E D Y G R Y K C E V I E G L	16	
188	I A S F D Q L Y D A W R G G L	16	
195	Y D A W R G G L D W C N A G W	16	
201	G L D W C N A G W L S D G S V	16	
235	V R N Y G F W D K D K S R Y D	16	
248	Y D V F C F T S N F N G R F Y	16	
250	V F C F T S N F N G R F Y Y L	16	
293	F A A W K I L G Y D R C D A G	16	
298	I L G Y D R C D A G W L A D G	16	
331	A V R F V G F P D K K H K L Y	16	

TABLE L 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
74	I H K I R I K W T K L T S D Y	15	
2	K S L L L L V L I S I C W A D	14	
6	L L V L I S I C W A D H L S D	14	
7	L V L I S I C W A D H L S D N	14	
15	A D H L S D N Y T L D H D R A	14	
39	H L L V E A E Q A K V F S H R	14	
46	Q A K V F S H R G G N V T L P	14	
91	E V D V F V S M G Y H K K T Y	14	
111	R V F L K G G S D S D A S L V	14	
123	S L V I T D L T L E D Y G R Y	14	
126	I T D L T L E D Y G R Y K C E	14	
128	D L T L E D Y G R Y K C E V I	14	
138	K C E V I E G L E D D T V V V	14	
147	D D T V V V A L D L Q G V V F	14	
153	A L D L Q G V V F P Y F P R L	14	
156	L Q G V V F P Y F P R L G R Y	14	
169	R Y N L N F H E A Q Q A C L D	14	
199	R G G L D W C N A G W L S D G	14	
212	D G S V Q Y P I T K P R E P C	14	
232	V P G V R N Y G F W D K D K S	14	
289	V G Q I F A A W K I L G Y D R	14	
296	W K I L G Y D R C D A G W L A	14	
311	D G S V R Y P I S R P R R R C	14	
332	V R F V G F P D K K H K L Y G	14	
10	I S I C W A D H L S D N Y T L	12	
12	I C W A D H L S D N Y T L D H	12	
13	C W A D H L S D N Y T L D H D	12	
25	D H D R A I H I Q A E N G P H	12	
28	R A I H I Q A E N G P H L L V	12	
31	H I Q A E N G P H L L V E A E	12	
35	E N G P H L L V E A E Q A K V	12	
36	N G P H L L V E A E Q A K V F	12	
43	E A E Q A K V F S H R G G N V	12	
44	A E Q A K V F S H R G G N V T	12	
45	E Q A K V F S H R G G N V T L	12	
48	K V F S H R G G N V T L P C K	12	
51	S H R G G N V T L P C K F Y R	12	
63	F Y R D P T A F G S G I H K I	12	
64	Y R D P T A F G S G I H K I R	12	
68	T A F G S G I H K I R I K W T	12	
73	G I H K I R I K W T K L T S D	12	
83	K L T S D Y L K E V D V F V S	12	
87	D Y L K E V D V F V S M G Y H	12	
101	H K K T Y G G Y Q G R V F L K	12	
103	K T Y G G Y Q G R V F L K G G	12	
107	G Y Q G R V F L K G G S D S D	12	
112	V F L K G G S D S D A S L V I	12	
113	F L K G G S D S D A S L V I T	12	
116	G G S D S D A S L V I T D L T	12	
118	S D S D A S L V I T D L T L E	12	
120	S D A S L V I T D L T L E D Y	12	
127	T D L T L E D Y G R Y K C E V	12	
140	E V I E G L E D D T V V V A L	12	
145	L E D D T V V V A L D L Q G V	12	

TABLE L 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
146	E D D T V V V A L D L Q G V V	12	
166	R L G R Y N L N F H E A Q Q A	12	
168	G R Y N L N F H E A Q Q A C L	12	
170	Y N L N F H E A Q Q A C L D Q	12	
177	A Q Q A C L D Q D A V I A S F	12	
183	D Q D A V I A S F D Q L Y D A	12	
186	A V I A S F D Q L Y D A W R G	12	
196	D A W R G G L D W C N A G W L	12	
203	D W C N A G W L S D G S V Q Y	12	
204	W C N A G W L S D G S V Q Y P	12	
208	G W L S D G S V Q Y P I T K P	12	
209	W L S D G S V Q Y P I T K P R	12	
218	P I T K P R E P C G G Q N T V	12	
221	K P R E P C G G Q N T V P G V	12	
226	C G G Q N T V P G V R N Y G F	12	
234	G V R N Y G F W D K D K S R Y	12	
243	K D K S R Y D V F C F T S N F	12	
244	D K S R Y D V F C F T S N F N	12	
264	L I H P T K L T Y D E A V Q A	12	
270	L T Y D E A V Q A C L N D G A	12	
274	E A V Q A C L N D G A Q I A K	12	
276	V Q A C L N D G A Q I A K V G	12	
278	A C L N D G A Q I A K V G Q I	12	
280	L N D G A Q I A K V G Q I F A	12	
281	N D G A Q I A K V G Q I F A A	12	
287	A K V G Q I F A A W K I L G Y	12	
288	K V G Q I F A A W K I L G Y D	12	
299	L G Y D R C D A G W L A D G S	12	
303	R C D A G W L A D G S V R Y P	12	
307	G W L A D G S V R Y P I S R P	12	
308	W L A D G S V R Y P I S R P R	12	
312	G S V R Y P I S R P R R R C S	12	
320	R P R R R C S P T E A A V R F	12	
324	R C S P T E A A V R F V G F P	12	
325	C S P T E A A V R F V G F P D	12	
333	R F V G F P D K K H K L Y G V	12	
47	A K V F S H R G G N V T L P C	11	
160	V F P Y F P R L G R Y N L N F	11	
254	T S N F N G R F Y Y L I H P T	11	
334	F V G F P D K K H K L Y G V Y	11	
102	K K T Y G G Y Q G R V F L K G	10	
192	D Q L Y D A W R G G L D W C N	10	
214	S V Q Y P I T K P R E P C G G	10	
290	G Q I F A A W K I L G Y D R C	10	
313	S V R Y P I S R P R R R C S P	10	
109	Q G R V F L K G G S D S D A S	9	
5	L L L V L I S I C W A D H L S	8	
27	D R A I H I Q A E N G P H L L	8	
54	G G N V T L P C K F Y R D P T	8	
76	K I R I K W T K L T S D Y L K	8	
95	F V S M G Y H K K T Y G G Y Q	8	
121	D A S L V I T D L T L E D Y G	8	
151	V V A L D L Q G V V F P Y F P	8	
157	Q G V V F P Y F P R L G R Y N	8	

TABLE L 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
164	F P R L G R Y N L N F H E A Q	8	
184	Q D A V I A S F D Q L Y D A W	8	
207	A G W L S D G S V Q Y P I T K	8	
216	Q Y P I T K P R E P C G G Q N	8	
261	F Y Y L I H P T K L T Y D E A	8	
262	Y Y L I H P T K L T Y D E A V	8	
306	A G W L A D G S V R Y P I S R	8	
239	G F W D K D K S R Y D V F C F	7	
8	V L I S I C W A D H L S D N Y	6	
14	W A D H L S D N Y T L D H D R	6	
20	D N Y T L D H D R A I H I Q A	6	
24	L D H D R A I H I Q A E N G P	6	
26	H D R A I H I Q A E N G P H L	6	
30	I H I Q A E N G P H L L V E A	6	
33	Q A E N G P H L L V E A E Q A	6	
34	A E N G P H L L V E A E Q A K	6	
40	L L V E A E Q A K V F S H R G	6	
41	L V E A E Q A K V F S H R G G	6	
50	F S H R G G N V T L P C K F Y	6	
53	R G G N V T L P C K F Y R D P	6	
58	T L P C K F Y R D P T A F G S	6	
65	R D P T A F G S G I H K I R I	6	
66	D P T A F G S G I H K I R I K	6	
69	A F G S G I H K I R I K W T K	6	
75	H K I R I K W T K L T S D Y L	6	
79	I K W T K L T S D Y L K E V D	6	
88	Y L K E V D V F V S M G Y H K	6	
90	K E V D V F V S M G Y H K K T	6	
98	M G Y H K K T Y G G Y Q G R V	6	
104	T Y G G Y Q G R V F L K G G S	6	
106	G G Y Q G R V F L K G G S D S	6	
108	Y Q G R V F L K G G S D S D A	6	
114	L K G G S D S D A S L V I T D	6	
125	V I T D L T L E D Y G R Y K C	6	
135	G R Y K C E V I E G L E D D T	6	
136	R Y K C E V I E G L E D D T V	6	
137	Y K C E V I E G L E D D T V V	6	
143	E G L E D D T V V V A L D L Q	6	
144	G L E D D T V V V A L D L Q G	6	
150	V V V A L D L Q G V V F P Y F	6	
154	L D L Q G V V F P Y F P R L G	6	
155	D L Q G V V F P Y F P R L G R	6	
162	P Y F P R L G R Y N L N F H E	6	
165	P R L G R Y N L N F H E A Q Q	6	
173	N F H E A Q Q A C L D Q D A V	6	
174	F H E A Q Q A C L D Q D A V I	6	
175	H E A Q Q A C L D Q D A V I A	6	
178	Q Q A C L D Q D A V I A S F D	6	
180	A C L D Q D A V I A S F D Q L	6	
181	C L D Q D A V I A S F D Q L Y	6	
190	S F D Q L Y D A W R G G L D W	6	
197	A W R G G L D W C N A G W L S	6	
198	W R G G L D W C N A G W L S D	6	
200	G G L D W C N A G W L S D G S	6	

TABLE L 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
205	C N A G W L S D G S V Q Y P I	6	
210	L S D G S V Q Y P I T K P R E	6	
213	G S V Q Y P I T K P R E P C G	6	
219	I T K P R E P C G G Q N T V P	6	
220	T K P R E P C G G Q N T V P G	6	
222	P R E P C G G Q N T V P G V R	6	
223	R E P C G G Q N T V P G V R N	6	
224	E P C G G Q N T V P G V R N Y	6	
228	G Q N T V P G V R N Y G F W D	6	
236	R N Y G F W D K D K S R Y D V	6	
246	S R Y D V F C F T S N F N G R	6	
251	F C F T S N F N G R F Y Y L I	6	
252	C F T S N F N G R F Y Y L I H	6	
253	F T S N F N G R F Y Y L I H P	6	
255	S N F N G R F Y Y L I H P T K	6	
257	F N G R F Y Y L I H P T K L T	6	
265	I H P T K L T Y D E A V Q A C	6	
266	H P T K L T Y D E A V Q A C L	6	
268	T K L T Y D E A V Q A C L N D	6	
272	Y D E A V Q A C L N D G A Q I	6	
275	A V Q A C L N D G A Q I A K V	6	
284	A Q I A K V G Q I F A A W K I	6	
292	I F A A W K I L G Y D R C D A	6	
300	G Y D R C D A G W L A D G S V	6	
302	D R C D A G W L A D G S V R Y	6	
304	C D A G W L A D G S V R Y P I	6	
319	S R P R R R C S P T E A A V R	6	
321	P R R R C S P T E A A V R F V	6	
323	R R C S P T E A A V R F V G F	6	
326	S P T E A A V R F V G F P D K	6	
328	T E A A V R F V G F P D K K H	6	
330	A A V R F V G F P D K K H K L	6	
336	G F P D K K H K L Y G V Y C F	6	
338	P D K K H K L Y G V Y C F R A	6	
97	S M G Y H K K T Y G G Y Q G R	5	
105	Y G G Y Q G R V F L K G G S D	5	
237	N Y G F W D K D K S R Y D V F	5	
56	N V T L P C K F Y R D P T A F	3	
22	Y T L D H D R A I H I Q A E N	1	
70	F G S G I H K I R I K W T K L	1	
72	S G I H K I R I K W T K L T S	1	
77	I R I K W T K L T S D Y L K E	1	
96	V S M G Y H K K T Y G G Y Q G	1	
130	T L E D Y G R Y K C E V I E G	1	
163	Y F P R L G R Y N L N F H E A	1	
215	V Q Y P I T K P R E P C G G Q	1	
263	Y L I H P T K L T Y D E A V Q	1	
314	V R Y P I S R P R R R C S P T	1	
316	Y P I S R P R R R C S P T E A	1	
317	P I S R P R R R C S P T E A A	1	
318	I S R P R R R C S P T E A A V	1	
42	V E A E Q A K V F S H R G G N	-5	
59	L P C K F Y R D P T A F G S G	-5	
84	L T S D Y L K E V D V F V S M	-5	

TABLE L 151P3D4 v.1: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
132	E D Y G R Y K C E V I E G L E	-5	
193	Q L Y D A W R G G L D W C N A	-5	
217	Y P I T K P R E P C G G Q N T	-5	
230	N T V P G V R N Y G F W D K D	-5	
241	W D K D K S R Y D V F C F T S	-5	
282	D G A Q I A K V G Q I F A A W	-5	
291	Q I F A A W K I L G Y D R C D	-5	
297	K I L G Y D R C D A G W L A D	-5	
309	L A D G S V R Y P I S R P R R	-5	
327	P T E A A V R F V G F P D K K	-5	
335	V G F P D K K H K L Y G V Y C	-5	
337	F P D K K H K L Y G V Y C F R	-5	

TABLE L 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
111	K L K Y L A F L H K R M N T N	28	
281	P A A W L P L R T P W T R P S	28	
40	P T K V T G I I T Q G A K D F	26	
54	F G H V Q F V G S Y K L A Y S	26	
51	A K D F G H V Q F V G S Y K L	22	
60	V G S Y K L A Y S N D G E H W	22	
64	K L A Y S N D G E H W T V Y Q	22	
74	W T V Y Q D E K Q R K D K V L	22	
158	S E A Y K K V C L S G A P H E	22	
233	G F I F K T I A P L A A T R A	22	
288	R T P W T R P S S C P T S S S	22	
357	N N S W Y V E N G R P A D L A	22	
372	G S G Y C G A L W K A I E S L	22	
377	G A L W K A I E S L E E G L G	22	
14	L H I V V E S I R D H S G Q K	20	
26	G Q K M K Q D K K V D L L V P	20	
32	D K K V D L L V P T K V T G I	20	
73	H W T V Y Q D E K Q R K D K V	20	
93	A V V V S C E G I N I S G S F	20	
109	R N K L K Y L A F L H K R M N	20	
112	L K Y L A F L H K R M N T N P	20	
163	K V C L S G A P H E V G W K Y	20	
200	K Q L M R L Q K Q A E K N M K	20	
229	P R G L G F I F K T I A P L A	20	
236	F K T I A P L A A T R A T R I	20	
284	W L P L R T P W T R P S S C P	20	
313	R N P L P N P R H S P S G G G	20	
326	G G G L K K P A R H C Q G Q K	20	
7	K T F P L R A L H I V V E S I	18	
17	V V E S I R D H S G Q K M K Q	18	
33	K K V D L L V P T K V T G I I	18	
41	T K V T G I I T Q G A K D F G	18	
70	D G E H W T V Y Q D E K Q R K	18	
83	R K D K V L L G R K A V V V S	18	
101	I N I S G S F C R N K L K Y L	18	
134	Q V P S R I F W R Q E K A D G	18	
173	V G W K Y Q A V T A T L E E K	18	
180	V T A T L E E K R K E K A E I	18	
187	K R K E K A E I H Y R K N K Q	18	

TABLE L 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
196	Y R K N K Q L M R L Q K Q A E	18	
204	R L Q K Q A E K N M K K K I D	18	
237	K T I A P L A A T R A T R I G	18	
258	P R A G S S A H R P P A L S A	18	
263	S A H R P P A L S A R A P V P	18	
272	A R A P V P A A S P A A W L P	18	
71	G E H W T V Y Q D E K Q R K D	16	
104	S G S F C R N K L K Y L A F L	16	
128	R R P Y H F Q V P S R I F W R	16	
130	P Y H F Q V P S R I F W R Q E	16	
138	R I F W R Q E K A D G G S C C	16	
172	E V G W K Y Q A V T A T L E E	16	
174	G W K Y Q A V T A T L E E K R	16	
193	E I H Y R K N K Q L M R L Q K	16	
217	I D K Y T E S P G G G S P R G	16	
301	S S T Y D S L S P Y G P R N P	16	
358	N S W Y V E N G R P A D L A G	16	
36	D L L V P T K V T G I I T Q G	15	
170	P H E V G W K Y Q A V T A T L	15	
191	K A E I H Y R K N K Q L M R L	15	
8	T F P L R A L H I V V E S I R	14	
11	L R A L H I V V E S I R D H S	14	
13	A L H I V V E S I R D H S G Q	14	
15	H I V V E S I R D H S G Q K M	14	
18	V E S I R D H S G Q K M K Q D	14	
35	V D L L V P T K V T G I I T Q	14	
57	V Q F V G S Y K L A Y S N D G	14	
84	K D K V L L G R K A V V V S C	14	
91	R K A V V V S C E G I N I S G	14	
92	K A V V V S C E G I N I S G S	14	
98	C E G I N I S G S F C R N K L	14	
100	G I N I S G S F C R N K L K Y	14	
119	H K R M N T N P S R R P Y H F	14	
199	N K Q L M R L Q K Q A E K N M	14	
202	L M R L Q K Q A E K N M K K K	14	
232	L G F I F K T I A P L A A T R	14	
239	I A P L A A T R A T R I G H P	14	
273	R A P V P A A S P A A W L P L	14	
341	H N V L A R G K P Q R K P K S	14	
359	S W Y V E N G R P A D L A G S	14	
367	P A D L A G S G Y C G A L W K	14	
376	C G A L W K A I E S L E E G L	14	
380	W K A I E S L E E G L G G K Q	14	
383	I E S L E E G L G G K Q K D K	14	
3	E H T T K T F P L R A L H I V	12	
5	T T K T F P L R A L H I V V E	12	
10	P L R A L H I V V E S I R D H	12	
12	R A L H I V V E S I R D H S G	12	
19	E S I R D H S G Q K M K Q D K	12	
23	D H S G Q K M K Q D K K V D L	12	
30	K Q D K K V D L L V P T K V T	12	
31	Q D K K V D L L V P T K V T G	12	
37	L L V P T K V T G I I T Q G A	12	
47	I T Q G A K D F G H V Q F V G	12	
48	T Q G A K D F G H V Q F V G S	12	

TABLE L 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
53	D F G H V Q F V G S Y K L A Y	12	
65	L A Y S N D G E H W T V Y Q D	12	
67	Y S N D G E H W T V Y Q D E K	12	
81	K Q R K D K V L L G R K A V V	12	
82	Q R K D K V L L G R K A V V V	12	
89	L G R K A V V V S C E G I N I	12	
90	G R K A V V V S C E G I N I S	12	
95	V V S C E G I N I S G S F C R	12	
102	N I S G S F C R N K L K Y L A	12	
113	K Y L A F L H K R M N T N P S	12	
116	A F L H K R M N T N P S R R P	12	
124	T N P S R R P Y H F Q V P S R	12	
126	P S R R P Y H F Q V P S R I F	12	
129	R P Y H F Q V P S R I F W R Q	12	
135	V P S R I F W R Q E K A D G G	12	
146	A D G G S C C P Q G H A S E A	12	
151	C C P Q G H A S E A Y K K V C	12	
153	P Q G H A S E A Y K K V C L S	12	
167	S G A P H E V G W K Y Q A V T	12	
176	K Y Q A V T A T L E E K R K E	12	
178	Q A V T A T L E E K R K E K A	12	
188	R K E K A E I H Y R K N K Q L	12	
189	K E K A E I H Y R K N K Q L M	12	
203	M R L Q K Q A E K N M K K K I	12	
212	N M K K K I D K Y T E S P G G	12	
226	G G S P R G L G F I F K T I A	12	
228	S P R G L G F I F K T I A P L	12	
230	R G L G F I F K T I A P L A A	12	
234	F I F K T I A P L A A T R A T	12	
238	T I A P L A A T R A T R I G H	12	
241	P L A A T R A T R I G H P G G	12	
244	A T R A T R I G H P G G R T P	12	
249	R I G H P G G R T P R A G S S	12	
251	G H P G G R T P R A G S S A H	12	
254	G G R T P R A G S S A H R P P	12	
265	H R P P A L S A R A P V P A A	12	
268	P A L S A R A P V P A A S P A	12	
276	V P A A S P A A W L P L R T P	12	
285	L P L R T P W T R P S S C P T	12	
291	W T R P S S C P T S S S T Y D	12	
292	T R P S S C P T S S S T Y D S	12	
295	S S C P T S S S T Y D S L S P	12	
305	D S L S P Y G P R N P L P N P	12	
310	Y G P R N P L P N P R H S P S	12	
327	G G L K K P A R H C Q G Q K H	12	
329	L K K P A R H C Q G Q K H N V	12	
331	K P A R H C Q G Q K H N V L A	12	
333	A R H C Q G Q K H N V L A R G	12	
337	Q G Q K H N V L A R G K P Q R	12	
338	G Q K H N V L A R G K P Q R K	12	
339	Q K H N V L A R G K P Q R K P	12	
343	V L A R G K P Q R K P K S E N	12	
347	G K P Q R K P K S E N N S W Y	12	
350	Q R K P K S E N N S W Y V E N	12	
351	R K P K S E N N S W Y V E N G	12	

TABLE L 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
356	E N N S W Y V E N G R P A D L	12	
362	V E N G R P A D L A G S G Y C	12	
365	G R P A D L A G S G Y C G A L	12	
382	A I E S L E E G L G G K Q K D	12	
384	E S L E E G L G G K Q K D K E	12	
386	L E E G L G G K Q K D K E R K	12	
390	L G G K Q K D K E R K A E N G	12	
392	G K Q K D K E R K A E N G P H	12	
395	K D K E R K A E N G P H L L V	12	
396	D K E R K A E N G P H L L V E	12	
398	E R K A E N G P H L L V E A E	12	
6	T K T F P L R A L H I V V E S	11	
114	Y L A F L H K R M N T N P S R	11	
231	G L G F I F K T I A P L A A T	11	
307	L S P Y G P R N P L P N P R H	11	
56	H V Q F V G S Y K L A Y S N D	10	
137	S R I F W R Q E K A D G G S C	10	
85	D K V L L G R K A V V V S C E	9	
86	K V L L G R K A V V V S C E G	9	
115	L A F L H K R M N T N P S R R	9	
132	H F Q V P S R I F W R Q E K A	9	
181	T A T L E E K R K E K A E I H	9	
210	E K N M K K K I D K Y T E S P	9	
267	P P A L S A R A P V P A A S P	9	
34	K V D L L V P T K V T G I I T	8	
43	V T G I I T Q G A K D F G H V	8	
44	T G I I T Q G A K D F G H V Q	8	
62	S Y K L A Y S N D G E H W T V	8	
161	Y K K V C L S G A P H E V G W	8	
177	Y Q A V T A T L E E K R K E K	8	
214	K K K I D K Y T E S P G G G S	8	
247	A T R I G H P G G R T P R A G	8	
304	Y D S L S P Y G P R N P L P N	8	
16	I V V E S I R D H S G Q K M K	7	
75	T V Y Q D E K Q R K D K V L L	7	
198	K N K Q L M R L Q K Q A E K N	7	
334	R H C Q G Q K H N V L A R G K	7	
2	L E H T T K T F P L R A L H I	6	
4	H T T K T F P L R A L H I V V	6	
9	F P L R A L H I V V E S I R D	6	
20	S I R D H S G Q K M K Q D K K	6	
29	M K Q D K K V D L L V P T K V	6	
38	L V P T K V T G I I T Q G A K	6	
45	G I I T Q G A K D F G H V Q F	6	
49	Q G A K D F G H V Q F V G S Y	6	
50	G A K D F G H V Q F V G S Y K	6	
55	G H V Q F V G S Y K L A Y S N	6	
59	F V G S Y K L A Y S N D G E H	6	
61	G S Y K L A Y S N D G E H W T	6	
66	A Y S N D G E H W T V Y Q D E	6	
76	V Y Q D E K Q R K D K V L L G	6	
79	D E K Q R K D K V L L G R K A	6	
87	V L L G R K A V V V S C E G I	6	
88	L L G R K A V V V S C E G I N	6	
94	V V V S C E G I N I S G S F C	6	

TABLE L 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
96	V S C E G I N I S G S F C R N	6	
97	S C E G I N I S G S F C R N K	6	
99	E G I N I S G S F C R N K L K	6	
106	S F C R N K L K Y L A F L H K	6	
110	N K L K Y L A F L H K R M N T	6	
117	F L H K R M N T N P S R R P Y	6	
120	K R M N T N P S R R P Y H F Q	6	
121	R M N T N P S R R P Y H F Q V	6	
127	S R R P Y H F Q V P S R I F W	6	
133	F Q V P S R I F W R Q E K A D	6	
140	F W R Q E K A D G G S C C P Q	6	
141	W R Q E K A D G G S C C P Q G	6	
142	R Q E K A D G G S C C P Q G H	6	
143	Q E K A D G G S C C P Q G H A	6	
147	D G G S C C P Q G H A S E A Y	6	
148	G G S C C P Q G H A S E A Y K	6	
149	G S C C P Q G H A S E A Y K K	6	
150	S C C P Q G H A S E A Y K K V	6	
152	C P Q G H A S E A Y K K V C L	6	
154	Q G H A S E A Y K K V C L S G	6	
155	G H A S E A Y K K V C L S G A	6	
159	E A Y K K V C L S G A P H E V	6	
160	A Y K K V C L S G A P H E V G	6	
162	K K V C L S G A P H E V G W K	6	
165	C L S G A P H E V G W K Y Q A	6	
166	L S G A P H E V G W K Y Q A V	6	
168	G A P H E V G W K Y Q A V T A	6	
169	A P H E V G W K Y Q A V T A T	6	
171	H E V G W K Y Q A V T A T L E	6	
175	W K Y Q A V T A T L E E K R K	6	
179	A V T A T L E E K R K E K A E	6	
184	L E E K R K E K A E I H Y R K	6	
186	E K R K E K A E I H Y R K N K	6	
190	E K A E I H Y R K N K Q L M R	6	
195	H Y R K N K Q L M R L Q K Q A	6	
197	R K N K Q L M R L Q K Q A E K	6	
206	Q K Q A E K N M K K K I D K Y	6	
211	K N M K K K I D K Y T E S P G	6	
215	K K I D K Y T E S P G G G S P	6	
216	K I D K Y T E S P G G G S P R	6	
220	Y T E S P G G G S P R G L G F	6	
221	T E S P G G G S P R G L G F I	6	
222	E S P G G G S P R G L G F I F	6	
227	G S P R G L G F I F K T I A P	6	
246	R A T R I G H P G G R T P R A	6	
248	T R I G H P G G R T P R A G S	6	
252	H P G G R T P R A G S S A H R	6	
255	G R T P R A G S S A H R P P A	6	
257	T P R A G S S A H R P P A L S	6	
259	R A G S S A H R P P A L S A R	6	
261	G S S A H R P P A L S A R A P	6	
264	A H R P P A L S A R A P V P A	6	
266	R P P A L S A R A P V P A A S	6	
269	A L S A R A P V P A A S P A A	6	
270	L S A R A P V P A A S P A A W	6	

TABLE L 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
271	S A R A P V P A A S P A A W L	6	
274	A P V P A A S P A A W L P L R	6	
277	P A A S P A A W L P L R T P W	6	
278	A A S P A A W L P L R T P W T	6	
279	A S P A A W L P L R T P W T R	6	
280	S P A A W L P L R T P W T R P	6	
289	T P W T R P S S C P T S S S T	6	
290	P W T R P S S C P T S S S T Y	6	
293	R P S S C P T S S S T Y D S L	6	
294	P S S C P T S S S T Y D S L S	6	
296	S C P T S S S T Y D S L S P Y	6	
297	C P T S S S T Y D S L S P Y G	6	
298	P T S S S T Y D S L S P Y G P	6	
299	T S S S T Y D S L S P Y G P R	6	
300	S S S T Y D S L S P Y G P R N	6	
303	T Y D S L S P Y G P R N P L P	6	
306	S L S P Y G P R N P L P N P R	6	
311	G P R N P L P N P R H S P S G	6	
312	P R N P L P N P R H S P S G G	6	
316	L P N P R H S P S G G G G L K	6	
318	N P R H S P S G G G G L K K P	6	
319	P R H S P S G G G G L K K P A	6	
320	R H S P S G G G G L K K P A R	6	
322	S P S G G G G L K K P A R H C	6	
323	P S G G G G L K K P A R H C Q	6	
332	P A R H C Q G Q K H N V L A R	6	
344	L A R G K P Q R K P K S E N N	6	
349	P Q R K P K S E N N S W Y V E	6	
353	P K S E N N S W Y V E N G R P	6	
363	E N G R P A D L A G S G Y C G	6	
364	N G R P A D L A G S G Y C G A	6	
368	A D L A G S G Y C G A L W K A	6	
370	L A G S G Y C G A L W K A I E	6	
371	A G S G Y C G A L W K A I E S	6	
373	S G Y C G A L W K A I E S L E	6	
374	G Y C G A L W K A I E S L E E	6	
378	A L W K A I E S L E E G L G G	6	
379	L W K A I E S L E E G L G G K	6	
381	K A I E S L E E G L G G K Q K	6	
397	K E R K A E N G P H L L V E A	6	
400	K A E N G P H L L V E A E Q A	6	
136	P S R I F W R Q E K A D G G S	3	
282	A A W L P L R T P W T R P S S	3	
340	K H N V L A R G K P Q R K P K	3	
387	E E G L G G K Q K D K E R K A	3	
22	R D H S G Q K M K Q D K K V D	1	
24	H S G Q K M K Q D K K V D L L	1	
27	Q K M K Q D K K V D L L V P T	1	
28	K M K Q D K K V D L L V P T K	1	
46	I I T Q G A K D F G H V Q F V	1	
58	Q F V G S Y K L A Y S N D G E	1	
77	Y Q D E K Q R K D K V L L G R	1	
78	Q D E K Q R K D K V L L G R K	1	
105	G S F C R N K L K Y L A F L H	1	
107	F C R N K L K Y L A F L H K R	1	

TABLE L 151P3D4 v.2: HLA Peptide Scoring Results DRB1*0401 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
123	N T N P S R R P Y H F Q V P S	1	
139	I F W R Q E K A D G G S C C P	1	
156	H A S E A Y K K V C L S G A P	1	
183	T L E E K R K E K A E I H Y R	1	
192	A E I H Y R K N K Q L M R L Q	1	
194	I H Y R K N K Q L M R L Q K Q	1	
201	Q L M R L Q K Q A E K N M K K	1	
205	L Q K Q A E K N M K K K I D K	1	
208	Q A E K N M K K K I D K Y T E	1	
213	M K K K I D K Y T E S P G G G	1	
224	P G G G S P R G L G F I F K T	1	
240	A P L A A T R A T R I G H P G	1	
253	P G G R T P R A G S S A H R P	1	
260	A G S S A H R P P A L S A R A	1	
287	L R T P W T R P S S C P T S S	1	
314	N P L P N P R H S P S G G G G	1	
328	G L K K P A R H C Q G Q K H N	1	
342	N V L A R G K P Q R K P K S E	1	
346	R G K P Q R K P K S E N N S W	1	
348	K P Q R K P K S E N N S W Y V	1	
360	W Y V E N G R P A D L A G S G	1	
375	Y C G A L W K A I E S L E E G	1	
389	G L G G K Q K D K E R K A E N	1	
391	G G K Q K D K E R K A E N G P	1	
1	M L E H T T K T F P L R A L H	-5	
80	E K Q R K D K V L L G R K A V	-5	
103	I S G S F C R N K L K Y L A F	-5	
122	M N T N P S R R P Y H F Q V P	-5	
157	A S E A Y K K V C L S G A P H	-5	
182	A T L E E K R K E K A E I H Y	-5	
185	E E K R K E K A E I H Y R K N	-5	
209	A E K N M K K K I D K Y T E S	-5	
243	A A T R A T R I G H P G G R T	-5	
250	I G H P G G R T P R A G S S A	-5	
324	S G G G G L K K P A R H C Q G	-5	
325	G G G G L K K P A R H C Q G Q	-5	
345	A R G K P Q R K P K S E N N S	-5	
393	K Q K D K E R K A E N G P H L	-5	
394	Q K D K E R K A E N G P H L L	-5	

TABLE LI 151P3D4 v.1: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
235	V R N Y G F W D K D K S R Y D	25	
161	F P Y F P R L G R Y N L N F H	24	
258	N G R F Y Y L I H P T K L T Y	24	
18	L S D N Y T L D H D R A I H I	22	
289	V G Q I F A A W K I L G Y D R	22	
315	R Y P I S R P R R R C S P T E	21	
95	F V S M G Y H K K T Y G G Y Q	20	
237	N Y G F W D K D K S R Y D V F	20	
295	A W K I L G Y D R C D A G W L	20	
67	P T A F G S G I H K I R I K W	19	
86	S D Y L K E V D V F V S M G Y	19	
105	Y G G Y Q G R V F L K G G S D	19	

TABLE LI 151P3D4 v.1: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
334	F V G F P D K K H K L Y G V Y	19	
4	L L L L V L I S I C W A D H L	18	
78	R I K W T K L T S D Y L K E V	18	
158	G V V F P Y F P R L G R Y N L	18	
167	L G R Y N L N F H E A Q Q A C	18	
283	G A Q I A K V G Q I F A A W K	18	
293	F A A W K I L G Y D R C D A G	18	
92	V D V F V S M G Y H K K T Y G	17	
214	S V Q Y P I T K P R E P C G G	17	
259	G R F Y Y L I H P T K L T Y D	17	
325	C S P T E A A V R F V G F P D	17	
44	A E Q A K V F S H R G G N V T	16	
54	G G N V T L P C K F Y R D P T	16	
60	P C K F Y R D P T A F G S G I	16	
61	C K F Y R D P T A F G S G I H	16	
68	T A F G S G I H K I R I K W T	16	
188	I A S F D Q L Y D A W R G G L	16	
213	G S V Q Y P I T K P R E P C G	16	
228	G Q N T V P G V R N Y G F W D	16	
248	Y D V F C F T S N F N G R F Y	16	
312	G S V R Y P I S R P R R R C S	16	
93	D V F V S M G Y H K K T Y G G	15	
107	G Y Q G R V F L K G G S D S D	15	
128	D L T L E D Y G R Y K C E V I	15	
157	Q G V V F P Y F P R L G R Y N	15	
1	M K S L L L L V L I S I C W A	14	
9	L I S I C W A D H L S D N Y T	14	
23	T L D H D R A I H I Q A E N G	14	
40	L L V E A E Q A K V F S H R G	14	
43	E A E Q A K V F S H R G G N V	14	
75	H K I R I K W T K L T S D Y L	14	
123	S L V I T D L T L E D Y G R Y	14	
153	A L D L Q G V V F P Y F P R L	14	
191	F D Q L Y D A W R G G L D W C	14	
216	Q Y P I T K P R E P C G G Q N	14	
250	V F C F T S N F N G R F Y Y L	14	
261	F Y Y L I H P T K L T Y D E A	14	
264	L I H P T K L T Y D E A V Q A	14	
267	P T K L T Y D E A V Q A C L N	14	
280	L N D G A Q I A K V G Q I F A	14	
316	Y P I S R P R R R C S P T E A	14	
332	V R F V G F P D K K H K L Y G	14	
335	V G F P D K K H K L Y G V Y C	14	
2	K S L L L L V L I S I C W A D	13	
3	S L L L L V L I S I C W A D H	13	
19	S D N Y T L D H D R A I H I Q	13	
56	N V T L P C K F Y R D P T A F	13	
109	Q G R V F L K G G S D S D A S	13	
142	I E G L E D D T V V V A L D L	13	
147	D D T V V V A L D L Q G V V F	13	
154	L D L Q G V V F P Y F P R L G	13	
306	A G W L A D G S V R Y P I S R	13	
308	W L A D G S V R Y P I S R P R	13	
313	S V R Y P I S R P R R R C S P	13	

TABLE LI 151P3D4 v.1: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
6	L L V L I S I C W A D H L S D	12	
26	H D R A I H I Q A E N G P H L	12	
27	D R A I H I Q A E N G P H L L	12	
36	N G P H L L V E A E Q A K V F	12	
71	G S G I H K I R I K W T K L T	12	
85	T S D Y L K E V D V F V S M G	12	
88	Y L K E V D V F V S M G Y H K	12	
102	K K T Y G G Y Q G R V F L K G	12	
106	G G Y Q G R V F L K G G S D S	12	
111	R V F L K G G S D S D A S L V	12	
134	Y G R Y K C E V I E G L E D D	12	
139	C E V I E G L E D D T V V V A	12	
148	D T V V V A L D L Q G V V F P	12	
151	V V A L D L Q G V V F P Y F P	12	
160	V F P Y F P R L G R Y N L N F	12	
166	R L G R Y N L N F H E A Q Q A	12	
169	R Y N L N F H E A Q Q A C L D	12	
179	Q A C L D Q D A V I A S F D Q	12	
196	D A W R G G L D W C N A G W L	12	
207	A G W L S D G S V Q Y P I T K	12	
229	Q N T V P G V R N Y G F W D K	12	
244	D K S R Y D V F C F T S N F N	12	
269	K L T Y D E A V Q A C L N D G	12	
273	D E A V Q A C L N D G A Q I A	12	
286	I A K V G Q I F A A W K I L G	12	
296	W K I L G Y D R C D A G W L A	12	
305	D A G W L A D G S V R Y P I S	12	
329	E A A V R F V G F P D K K H K	12	
47	A K V F S H R G G N V T L P C	11	
131	L E D Y G R Y K C E V I E G L	11	
145	L E D D T V V V A L D L Q G V	11	
192	D Q L Y D A W R G G L D W C N	11	
238	Y G F W D K D K S R Y D V F C	11	
245	K S R Y D V F C F T S N F N G	11	
254	T S N F N G R F Y Y L I H P T	11	
260	R F Y Y L I H P T K L T Y D E	11	
314	V R Y P I S R P R R R C S P T	11	
331	A V R F V G F P D K K H K L Y	11	
11	S I C W A D H L S D N Y T L D	11	
97	S M G Y H K K T Y G G Y Q G R	10	
110	G R V F L K G G S D S D A S L	10	
126	I T D L T L E D Y G R Y K C E	10	
171	N L N F H E A Q Q A C L D Q D	10	
195	Y D A W R G G L D W C N A G W	10	
201	G L D W C N A G W L S D G S V	10	
206	N A G W L S D G S V Q Y P I T	10	
290	G Q I F A A W K I L G Y D R C	10	
298	I L G Y D R C D A G W L A D G	10	
307	G W L A D G S V R Y P I S R P	10	
333	R F V G F P D K K H K L Y G V	10	
20	D N Y T L D H D R A I H I Q A	9	
31	H I Q A E N G P H L L V E A E	9	
70	F G S G I H K I R I K W T K L	9	
82	T K L T S D Y L K E V D V F V	9	

TABLE LI 151P3D4 v.1: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
89	L K E V D V F V S M G Y H K K	9	
144	G L E D D T V V V A L D L Q G	9	
35	E N G P H L L V E A E Q A K V	8	
45	E Q A K V F S H R G G N V T L	8	
57	V T L P C K F Y R D P T A F G	8	
72	S G I H K I R I K W T K L T S	8	
81	W T K L T S D Y L K E V D V F	8	
91	E V D V F V S M G Y H K K T Y	8	
94	V F V S M G Y H K K T Y G G Y	8	
103	K T Y G G Y Q G R V F L K G G	8	
118	S D S D A S L V I T D L T L E	8	
130	T L E D Y G R Y K C E V I E G	8	
146	E D D T V V V A L D L Q G V V	8	
156	L Q G V V F P Y F P R L G R Y	8	
189	A S F D Q L Y D A W R G G L D	8	
215	V Q Y P I T K P R E P C G G Q	8	
226	C G G Q N T V P G V R N Y G F	8	
239	G F W D K D K S R Y D V F C F	8	
252	C F T S N F N G R F Y Y L I H	8	
310	A D G S V R Y P I S R P R R R	8	
8	V L I S I C W A D H L S D N Y	7	
37	G P H L L V E A E Q A K V F S	7	
38	P H L L V E A E Q A K V F S H	7	
39	H L L V E A E Q A K V F S H R	7	
46	Q A K V F S H R G G N V T L P	7	
49	V F S H R G G N V T L P C K F	7	
73	G I H K I R I K W T K L T S D	7	
74	I H K I R I K W T K L T S D Y	7	
119	D S D A S L V I T D L T L E D	7	
120	S D A S L V I T D L T L E D Y	7	
121	D A S L V I T D L T L E D Y G	7	
135	G R Y K C E V I E G L E D D T	7	
136	R Y K C E V I E G L E D D T V	7	
149	T V V V A L D L Q G V V F P Y	7	
150	V V V A L D L Q G V V F P Y F	7	
178	Q Q A C L D Q D A V I A S F D	7	
182	L D Q D A V I A S F D Q L Y D	7	
184	Q D A V I A S F D Q L Y D A W	7	
190	S F D Q L Y D A W R G G L D W	7	
200	G G L D W C N A G W L S D G S	7	
209	W L S D G S V Q Y P I T K P R	7	
211	S D G S V Q Y P I T K P R E P	7	
222	P R E P C G G Q N T V P G V R	7	
247	R Y D V F C F T S N F N G R F	7	
270	L T Y D E A V Q A C L N D G A	7	
276	V Q A C L N D G A Q I A K V G	7	
279	C L N D G A Q I A K V G Q I F	7	
284	A Q I A K V G Q I F A A W K I	7	
299	L G Y D R C D A G W L A D G S	7	
311	D G S V R Y P I S R P R R R C	7	
327	P T E A A V R F V G F P D K K	7	
5	L L L V L I S I C W A D H L S	6	
7	L V L I S I C W A D H L S D N	6	
12	I C W A D H L S D N Y T L D H	6	

TABLE LI 151P3D4 v.1: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
15	A D H L S D N Y T L D H D R A	6	
21	N Y T L D H D R A I H I Q A E	6	
24	L D H D R A I H I Q A E N G P	6	
29	A I H I Q A E N G P H L L V E	6	
33	Q A E N G P H L L V E A E Q A	6	
34	A E N G P H L L V E A E Q A K	6	
51	S H R G G N V T L P C K F Y R	6	
53	R G G N V T L P C K F Y R D P	6	
58	T L P C K F Y R D P T A F G S	6	
62	K F Y R D P T A F G S G I H K	6	
76	K I R I K W T K L T S D Y L K	6	
83	K L T S D Y L K E V D V F V S	6	
90	K E V D V F V S M G Y H K K T	6	
96	V S M G Y H K K T Y G G Y Q G	6	
99	G Y H K K T Y G G Y Q G R V F	6	
108	Y Q G R V F L K G G S D S D A	6	
112	V F L K G G S D S D A S L V I	6	
122	A S L V I T D L T L E D Y G R	6	
124	L V I T D L T L E D Y G R Y K	6	
125	V I T D L T L E D Y G R Y K C	6	
133	D Y G R Y K C E V I E G L E D	6	
138	K C E V I E G L E D D T V V V	6	
164	F P R L G R Y N L N F H E A Q	6	
175	H E A Q Q A C L D Q D A V I A	6	
176	E A Q Q A C L D Q D A V I A S	6	
181	C L D Q D A V I A S F D Q L Y	6	
185	D A V I A S F D Q L Y D A W R	6	
186	A V I A S F D Q L Y D A W R G	6	
197	A W R G G L D W C N A G W L S	6	
199	R G G L D W C N A G W L S D G	6	
202	L D W C N A G W L S D G S V Q	6	
203	D W C N A G W L S D G S V Q Y	6	
204	W C N A G W L S D G S V Q Y P	6	
212	D G S V Q Y P I T K P R E P C	6	
217	Y P I T K P R E P C G G Q N T	6	
223	R E P C G G Q N T V P G V R N	6	
232	V P G V R N Y G F W D K D K S	6	
256	N F N G R F Y Y L I H P T K L	6	
262	Y Y L I H P T K L T Y D E A V	6	
272	Y D E A V Q A C L N D G A Q I	6	
274	E A V Q A C L N D G A Q I A K	6	
277	Q A C L N D G A Q I A K V G Q	6	
292	I F A A W K I L G Y D R C D A	6	
301	Y D R C D A G W L A D G S V R	6	
302	D R C D A G W L A D G S V R Y	6	
303	R C D A G W L A D G S V R Y P	6	
319	S R P R R R C S P T E A A V R	6	
320	R P R R R C S P T E A A V R F	6	
326	S P T E A A V R F V G F P D K	6	
338	P D K K H K L Y G V Y C F R A	6	
227	G G Q N T V P G V R N Y G F W	4	
64	Y R D P T A F G S G I H K I R	3	
87	D Y L K E V D V F V S M G Y H	3	
225	P C G G Q N T V P G V R N Y G	3	

TABLE LI 151P3D4 v.1: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
282	D G A Q I A K V G Q I F A A W	3	
324	R C S P T E A A V R F V G F P	3	
330	A A V R F V G F P D K K H K L	3	
42	V E A E Q A K V F S H R G G N	2	
50	F S H R G G N V T L P C K F Y	2	
52	H R G G N V T L P C K F Y R D	2	
55	G N V T L P C K F Y R D P T A	2	
66	D P T A F G S G I H K I R I K	2	
69	A F G S G I H K I R I K W T K	2	
100	Y H K K T Y G G Y Q G R V F L	2	
101	H K K T Y G G Y Q G R V F L K	2	
143	E G L E D D T V V V A L D L Q	2	
152	V A L D L Q G V V F P Y F P R	2	
159	V V F P Y F P R L G R Y N L N	2	
180	A C L D Q D A V I A S F D Q L	2	
208	G W L S D G S V Q Y P I T K P	2	
243	K D K S R Y D V F C F T S N F	2	
323	R R C S P T E A A V R F V G F	2	
328	T E A A V R F V G F P D K K H	2	
340	K K H K L Y G V Y C F R A Y N	2	
14	W A D H L S D N Y T L D H D R	1	
22	Y T L D H D R A I H I Q A E N	1	
30	I H I Q A E N G P H L L V E A	1	
32	I Q A E N G P H L L V E A E Q	1	
59	L P C K F Y R D P T A F G S G	1	
79	I K W T K L T S D Y L K E V D	1	
80	K W T K L T S D Y L K E V D V	1	
84	L T S D Y L K E V D V F V S M	1	
104	T Y G G Y Q G R V F L K G G S	1	
114	L K G G S D S D A S L V I T D	1	
115	K G G S D S D A S L V I T D L	1	
116	G G S D S D A S L V I T D L T	1	
127	T D L T L E D Y G R Y K C E V	1	
132	E D Y G R Y K C E V I E G L E	1	
140	E V I E G L E D D T V V V A L	1	
141	V I E G L E D D T V V V A L D	1	
155	D L Q G V V F P Y F P R L G R	1	
162	P Y F P R L G R Y N L N F H E	1	
170	Y N L N F H E A Q Q A C L D Q	1	
172	L N F H E A Q Q A C L D Q D A	1	
177	A Q Q A C L D Q D A V I A S F	1	
187	V I A S F D Q L Y D A W R G G	1	
205	C N A G W L S D G S V Q Y P I	1	
210	L S D G S V Q Y P I T K P R E	1	
230	N T V P G V R N Y G F W D K D	1	
233	P G V R N Y G F W D K D K S R	1	
236	R N Y G F W D K D K S R Y D V	1	
240	F W D K D K S R Y D V F C F T	1	
249	D V F C F T S N F N G R F Y Y	1	
251	F C F T S N F N G R F Y Y L I	1	
253	F T S N F N G R F Y Y L I H P	1	
255	S N F N G R F Y Y L I H P T K	1	
257	F N G R F Y Y L I H P T K L T	1	
266	H P T K L T Y D E A V Q A C L	1	

TABLE LI 151P3D4 v.1: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
271	T Y D E A V Q A C L N D G A Q	1	
278	A C L N D G A Q I A K V G Q I	1	
287	A K V G Q I F A A W K I L G Y	1	
288	K V G Q I F A A W K I L G Y D	1	
294	A A W K I L G Y D R C D A G W	1	
304	C D A G W L A D G S V R Y P I	1	
309	L A D G S V R Y P I S R P R R	1	
322	R R R C S P T E A A V R F V G	1	
337	F P D K K H K L Y G V Y C F R	1	

TABLE LI 151P3D4 v.2: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
229	P R G L G F I F K T I A P L A	27	
137	S R I F W R Q E K A D G G S C	24	
44	T G I I T Q G A K D F G H V Q	22	
51	A K D F G H V Q F V G S Y K L	22	
158	S E A Y K K V C L S G A P H E	22	
233	G F I F K T I A P L A A T R A	22	
244	A T R A T R I G H P G G R T P	22	
301	S S T Y D S L S P Y G P R N P	22	
338	G Q K H N V L A R G K P Q R K	22	
34	K V D L L V P T K V T G I I T	21	
112	L K Y L A F L H K R M N T N P	21	
163	K V C L S G A P H E V G W K Y	21	
181	T A T L E E K R K E K A E I H	21	
14	L H I V V E S I R D H S G Q K	20	
40	P T K V T G I I T Q G A K D F	20	
111	K L K Y L A F L H K R M N T N	20	
199	N K Q L M R L Q K Q A E K N M	20	
236	F K T I A P L A A T R A T R I	20	
313	R N P L P N P R H S P S G G G	20	
130	P Y H F Q V P S R I F W R Q E	19	
380	W K A I E S L E E G L G G K Q	19	
15	H I V V E S I R D H S G Q K M	18	
56	H V Q F V G S Y K L A Y S N D	18	
217	I D K Y T E S P G G G S P R G	18	
357	N N S W Y V E N G R P A D L A	18	
358	N S W Y V E N G R P A D L A G	18	
174	G W K Y Q A V T A T L E E K R	17	
60	V G S Y K L A Y S N D G E H W	16	
73	H W T V Y Q D E K Q R K D K V	16	
138	R I F W R Q E K A D G G S C C	16	
281	P A A W L P L R T P W T R P S	16	
285	L P L R T P W T R P S S C P T	16	
377	G A L W K A I E S L E E G L G	16	
11	L R A L H I V V E S I R D H S	15	
32	D K K V D L L V P T K V T G I	15	
82	Q R K D K V L L G R K A V V V	15	
84	K D K V L L G R K A V V V S C	15	
89	L G R K A V V V S C E G I N I	15	
105	G S F C R N K L K Y L A F L H	15	
119	H K R M N T N P S R R P Y H F	15	
168	G A P H E V G W K Y Q A V T A	15	
207	K Q A E K N M K K K I D K Y T	15	

TABLE LI 151P3D4 v.2: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
222	E S P G G G S P R G L G F I F	15	
257	T P R A G S S A H R P P A L S	15	
344	L A R G K P Q R K P K S E N N	15	
373	S G Y C G A L W K A I E S L E	15	
387	E E G L G G K Q K D K E R K A	15	
26	G Q K M K Q D K K V D L L V P	14	
71	G E H W T V Y Q D E K Q R K D	14	
83	R K D K V L L G R K A V V V S	14	
128	R R P Y H F Q V P S R I F W R	14	
196	Y R K N K Q L M R L Q K Q A E	14	
211	K N M K K K I D K Y T E S P G	14	
232	L G F I F K T I A P L A A T R	14	
251	G H P G G R T P R A G S S A H	14	
258	P R A G S S A H R P P A L S A	14	
312	P R N P L P N P R H S P S G G	14	
322	S P S G G G G L K K P A R H C	14	
323	P S G G G G L K K P A R H C Q	14	
326	G G G L K K P A R H C Q G Q K	14	
327	G G L K K P A R H C Q G Q K H	14	
340	K H N V L A R G K P Q R K P K	14	
356	E N N S W Y V E N G R P A D L	14	
8	T F P L R A L H I V V E S I R	13	
29	M K Q D K K V D L L V P T K V	13	
54	F G H V Q F V G S Y K L A Y S	13	
86	K V L L G R K A V V V S C E G	13	
93	A V V V S C E G I N I S G S F	13	
247	A T R I G H P G G R T P R A G	13	
264	A H R P P A L S A R A P V P A	13	
279	A S P A A W L P L R T P W T R	13	
284	W L P L R T P W T R P S S C P	13	
304	Y D S L S P Y G P R N P L P N	13	
57	V Q F V G S Y K L A Y S N D G	12	
74	W T V Y Q D E K Q R K D K V L	12	
95	V V S C E G I N I S G S F C R	12	
109	R N K L K Y L A F L H K R M N	12	
115	L A F L H K R M N T N P S R R	12	
116	A F L H K R M N T N P S R R P	12	
179	A V T A T L E E K R K E K A E	12	
214	K K K I D K Y T E S P G G G S	12	
267	P P A L S A R A P V P A A S P	12	
270	L S A R A P V P A A S P A A W	12	
288	R T P W T R P S S C P T S S S	12	
367	P A D L A G S G Y C G A L W K	12	
4	H T T K T F P L R A L H I V V	11	
6	T K T F P L R A L H I V V E S	11	
120	K R M N T N P S R R P Y H F Q	11	
2	L E H T T K T F P L R A L H I	10	
50	G A K D F G H V Q F V G S Y K	10	
64	K L A Y S N D G E H W T V Y Q	10	
103	I S G S F C R N K L K Y L A F	10	
104	S G S F C R N K L K Y L A F L	10	
114	Y L A F L H K R M N T N P S R	10	
172	E V G W K Y Q A V T A T L E E	10	
187	K R K E K A E I H Y R K N K Q	10	
193	E I H Y R K N K Q L M R L Q K	10	

TABLE LI 151P3D4 v.2: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
231	G L G F I F K T I A P L A A T	10	
241	P L A A T R A T R I G H P G G	10	
307	L S P Y G P R N P L P N P R H	10	
336	C Q G Q K H N V L A R G K P Q	10	
372	G S G Y C G A L W K A I E S L	10	
389	G L G G K Q K D K E R K A E N	10	
7	K T F P L R A L H I V V E S I	9	
12	R A L H I V V E S I R D H S G	9	
20	S I R D H S G Q K M K Q D K K	9	
25	S G Q K M K Q D K K V D L L V	9	
36	D L L V P T K V T G I I T Q G	9	
37	L L V P T K V T G I I T Q G A	9	
55	G H V Q F V G S Y K L A Y S N	9	
76	V Y Q D E K Q R K D K V L L G	9	
78	Q D E K Q R K D K V L L G R K	9	
101	I N I S G S F C R N K L K Y L	9	
113	K Y L A F L H K R M N T N P S	9	
129	R P Y H F Q V P S R I F W R Q	9	
154	Q G H A S E A Y K K V C L S G	9	
177	Y Q A V T A T L E E K R K E K	9	
190	E K A E I H Y R K N K Q L M R	9	
192	A E I H Y R K N K Q L M R L Q	9	
206	Q K Q A E K N M K K K I D K Y	9	
333	A R H C Q G Q K H N V L A R G	9	
385	S L E E G L G G K Q K D K E R	9	
398	E R K A E N G P H L L V E A E	9	
10	P L R A L H I V V E S I R D H	8	
13	A L H I V V E S I R D H S G Q	8	
16	I V V E S I R D H S G Q K M K	8	
22	R D H S G Q K M K Q D K K V D	8	
48	T Q G A K D F G H V Q F V G S	8	
65	L A Y S N D G E H W T V Y Q D	8	
75	T V Y Q D E K Q R K D K V L L	8	
81	K Q R K D K V L L G R K A V V	8	
88	L L G R K A V V V S C E G I N	8	
91	R K A V V V S C E G I N I S G	8	
121	R M N T N P S R R P Y H F Q V	8	
124	T N P S R R P Y H F Q V P S R	8	
132	H F Q V P S R I F W R Q E K A	8	
134	Q V P S R I F W R Q E K A D G	8	
148	G G S C C P Q G H A S E A Y K	8	
155	G H A S E A Y K K V C L S G A	8	
157	A S E A Y K K V C L S G A P H	8	
178	Q A V T A T L E E K R K E K A	8	
180	V T A T L E E K R K E K A E I	8	
183	T L E E K R K E K A E I H Y R	8	
188	R K E K A E I H Y R K N K Q L	8	
189	K E K A E I H Y R K N K Q L M	8	
203	M R L Q K Q A E K N M K K K I	8	
208	Q A E K N M K K K I D K Y T E	8	
220	Y T E S P G G G S P R G L G F	8	
238	T I A P L A A T R A T R I G H	8	
239	I A P L A A T R A T R I G H P	8	
240	A P L A A T R A T R I G H P G	8	
248	T R I G H P G G R T P R A G S	8	

TABLE LI 151P3D4 v.2: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
249	R I G H P G G R T P R A G S S	8	
253	P G G R T P R A G S S A H R P	8	
256	R T P R A G S S A H R P P A L	8	
263	S A H R P P A L S A R A P V P	8	
265	H R P P A L S A R A P V P A A	8	
269	A L S A R A P V P A A S P A A	8	
280	S P A A W L P L R T P W T R P	8	
283	A W L P L R T P W T R P S S C	8	
295	S S C P T S S S T Y D S L S P	8	
305	D S L S P Y G P R N P L P N P	8	
310	Y G P R N P L P N P R H S P S	8	
332	P A R H C Q G Q K H N V L A R	8	
341	H N V L A R G K P Q R K P K S	8	
342	N V L A R G K P Q R K P K S E	8	
343	V L A R G K P Q R K P K S E N	8	
346	R G K P Q R K P K S E N N S W	8	
390	L G G K Q K D K E R K A E N G	8	
391	G G K Q K D K E R K A E N G P	8	
392	G K Q K D K E R K A E N G P H	8	
5	T T K T F P L R A L H I V V E	7	
18	V E S I R D H S G Q K M K Q D	7	
23	D H S G Q K M K Q D K K V D L	7	
33	K K V D L L V P T K V T G I I	7	
79	D E K Q R K D K V L L G R K A	7	
85	D K V L L G R K A V V V S C E	7	
90	G R K A V V V S C E G I N I S	7	
100	G I N I S G S F C R N K L K Y	7	
125	N P S R R P Y H F Q V P S R I	7	
133	F Q V P S R I F W R Q E K A D	7	
135	V P S R I F W R Q E K A D G G	7	
136	P S R I F W R Q E K A D G G S	7	
156	H A S E A Y K K V C L S G A P	7	
159	E A Y K K V C L S G A P H E V	7	
170	P H E V G W K Y Q A V T A T L	7	
197	R K N K Q L M R L Q K Q A E K	7	
230	R G L G F I F K T I A P L A A	7	
250	I G H P G G R T P R A G S S A	7	
260	A G S S A H R P P A L S A R A	7	
266	R P P A L S A R A P V P A A S	7	
271	S A R A P V P A A S P A A W L	7	
275	P V P A A S P A A W L P L R T	7	
297	C P T S S S T Y D S L S P Y G	7	
306	S L S P Y G P R N P L P N P R	7	
311	G P R N P L P N P R H S P S G	7	
321	H S P S G G G G L K K P A R H	7	
334	R H C Q G Q K H N V L A R G K	7	
337	Q G Q K H N V L A R G K P Q R	7	
360	W Y V E N G R P A D L A G S G	7	
371	A G S G Y C G A L W K A I E S	7	
376	C G A L W K A I E S L E E G L	7	
383	I E S L E E G L G G K Q K D K	7	
9	F P L R A L H I V V E S I R D	6	
31	Q D K K V D L L V P T K V T G	6	
35	V D L L V P T K V T G I I T Q	6	
39	V P T K V T G I I T Q G A K D	6	

TABLE LI 151P3D4 v.2: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
41	T K V T G I I T Q G A K D F G	6	
43	V T G I I T Q G A K D F G H V	6	
59	F V G S Y K L A Y S N D G E H	6	
62	S Y K L A Y S N D G E H W T V	6	
70	D G E H W T V Y Q D E K Q R K	6	
92	K A V V V S C E G I N I S G S	6	
94	V V V S C E G I N I S G S F C	6	
97	S C E G I N I S G S F C R N K	6	
98	C E G I N I S G S F C R N K L	6	
106	S F C R N K L K Y L A F L H K	6	
126	P S R R P Y H F Q V P S R I F	6	
139	I F W R Q E K A D G G S C C P	6	
142	R Q E K A D G G S C C P Q G H	6	
144	E K A D G G S C C P Q G H A S	6	
146	A D G G S C C P Q G H A S E A	6	
147	D G G S C C P Q G H A S E A Y	6	
149	G S C C P Q G H A S E A Y K K	6	
160	A Y K K V C L S G A P H E V G	6	
161	Y K K V C L S G A P H E V G W	6	
167	S G A P H E V G W K Y Q A V T	6	
171	H E V G W K Y Q A V T A T L E	6	
191	K A E I H Y R K N K Q L M R L	6	
198	K N K Q L M R L Q K Q A E K N	6	
200	K Q L M R L Q K Q A E K N M K	6	
202	L M R L Q K Q A E K N M K K K	6	
210	E K N M K K K I D K Y T E S P	6	
212	N M K K K I D K Y T E S P G G	6	
213	M K K K I D K Y T E S P G G G	6	
215	K K I D K Y T E S P G G G S P	6	
216	K I D K Y T E S P G G G S P R	6	
218	D K Y T E S P G G G S P R G L	6	
226	G G S P R G L G F I F K T I A	6	
242	L A A T R A T R I G H P G G R	6	
243	A A T R A T R I G H P G G R T	6	
252	H P G G R T P R A G S S A H R	6	
261	G S S A H R P P A L S A R A P	6	
268	P A L S A R A P V P A A S P A	6	
272	A R A P V P A A S P A A W L P	6	
273	R A P V P A A S P A A W L P L	6	
282	A A W L P L R T P W T R P S S	6	
287	L R T P W T R P S S C P T S S	6	
289	T P W T R P S S C P T S S S T	6	
290	P W T R P S S C P T S S S T Y	6	
291	W T R P S S C P T S S S T Y D	6	
298	P T S S S T Y D S L S P Y G P	6	
300	S S S T Y D S L S P Y G P R N	6	
308	S P Y G P R N P L P N P R H S	6	
314	N P L P N P R H S P S G G G G	6	
315	P L P N P R H S P S G G G G L	6	
316	L P N P R H S P S G G G G L K	6	
317	P N P R H S P S G G G G L K K	6	
348	K P Q R K P K S E N N S W Y V	6	
354	K S E N N S W Y V E N G R P A	6	
359	S W Y V E N G R P A D L A G S	6	
361	Y V E N G R P A D L A G S G Y	6	

TABLE LI 151P3D4 v.2: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
362	V E N G R P A D L A G S G Y C	6	
363	E N G R P A D L A G S G Y C G	6	
364	N G R P A D L A G S G Y C G A	6	
366	R P A D L A G S G Y C G A L W	6	
374	G Y C G A L W K A I E S L E E	6	
378	A L W K A I E S L E E G L G G	6	
381	K A I E S L E E G L G G K Q K	6	
384	E S L E E G L G G K Q K D K E	6	
393	K Q K D K E R K A E N G P H L	6	
394	Q K D K E R K A E N G P H L L	6	
400	K A E N G P H L L V E A E Q A	6	
1	M L E H T T K T F P L R A L H	3	
28	K M K Q D K K V D L L V P T K	3	
166	L S G A P H E V G W K Y Q A V	3	
53	D F G H V Q F V G S Y K L A Y	2	
69	N D G E H W T V Y Q D E K Q R	2	
80	E K Q R K D K V L L G R K A V	2	
87	V L L G R K A V V V S C E G I	2	
99	E G I N I S G S F C R N K L K	2	
118	L H K R M N T N P S R R P Y H	2	
173	V G W K Y Q A V T A T L E E K	2	
194	I H Y R K N K Q L M R L Q K Q	2	
195	H Y R K N K Q L M R L Q K Q A	2	
234	F I F K T I A P L A A T R A T	2	
246	R A T R I G H P G G R T P R A	2	
278	A A S P A A W L P L R T P W T	2	
299	T S S S T Y D S L S P Y G P R	2	
303	T Y D S L S P Y G P R N P L P	2	
324	S G G G G L K K P A R H C Q G	2	
355	S E N N S W Y V E N G R P A D	2	
3	E H T T K T F P L R A L H I V	1	
24	H S G Q K M K Q D K K V D L L	1	
27	Q K M K Q D K K V D L L V P T	1	
30	K Q D K K V D L L V P T K V T	1	
38	L V P T K V T G I I T Q G A K	1	
42	K V T G I I T Q G A K D F G H	1	
47	I T Q G A K D F G H V Q F V G	1	
52	K D F G H V Q F V G S Y K L A	1	
66	A Y S N D G E H W T V Y Q D E	1	
77	Y Q D E K Q R K D K V L L G R	1	
102	N I S G S F C R N K L K Y L A	1	
108	C R N K L K Y L A F L H K R M	1	
110	N K L K Y L A F L H K R M N T	1	
152	C P Q G H A S E A Y K K V C L	1	
153	P Q G H A S E A Y K K V C L S	1	
175	W K Y Q A V T A T L E E K R K	1	
184	L E E K R K E K A E I H Y R K	1	
201	Q L M R L Q K Q A E K N M K K	1	
204	R L Q K Q A E K N M K K K I D	1	
205	L Q K Q A E K N M K K K I D K	1	
209	A E K N M K K K I D K Y T E S	1	
221	T E S P G G G S P R G L G F I	1	
225	G G G S P R G L G F I F K T I	1	
227	G S P R G L G F I F K T I A P	1	
237	K T I A P L A A T R A T R I G	1	

TABLE LI 151P3D4 v.2: HLA Peptide Scoring Results DRB1*1101 15 - mers SYFPEITHI			
Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score	SEQ. ID NO.
277	P A A S P A A W L P L R T P W	1	
319	P R H S P S G G G G L K K P A	1	
320	R H S P S G G G G L K K P A R	1	
325	G G G G L K K P A R H C Q G Q	1	
330	K K P A R H C Q G Q K H N V L	1	
352	K P K S E N N S W Y V E N G R	1	
369	D L A G S G Y C G A L W K A I	1	
397	K E R K A E N G P H L L V E A	1	
399	R K A E N G P H L L V E A E Q	1	

Table LII (A). Exon compositions of 151P3D4 v.1

Exon Number	Start	End
Exon 1	1	289
Exon 2	290	415
Exon 3	416	787
Exon 4	788	1090
Exon 5	1091	1957

Table LII (B). Exon compositions of 151P3D4 v.2

Exon Number	Start	End
Exon 1	1	102
Exon 2	103	258
Exon 3	259	425
Exon 4	426	667
Exon 5	668	863
Exon 6	864	999
Exon 7	1000	1201
Exon 8	1202	1573
Exon 9	1574	1876
Exon 10	1877	2166

Table LIII. Nucleotide sequence of transcript variant 151P3D4 v.2

```
atgttggagc atactactaa gacattcccc ttaagagcac tgcacatagt tgtggaaagc     60
attagggacc acagtggcca aaaaatgaag caggataaga aggtggatct tcttgttcca    120
accaaagtga ctggcatcat tacacaagga gctaaagatt ttggtcatgt acagtttgtt    180
ggctcctaca aactggctta cagcaatgat ggagaacact ggactgtata ccaggatgaa    240
aagcaaagaa aagataaggt actgctgggc cggaaggcgg tggtcgtaag ctgcgaaggc    300
atcaacattt ctggcagttt ctgcagaaac aagttgaagt acctggcttt cctccacaag    360
cggatgaaca ccaacccttc tcgacgcccc taccacttcc aggtccccag ccgcatcttc    420
tggcgacaag aaaaagcaga tggtggttcc tgctgccctc aaggtcatgc gtctgaagcc    480
tacaagaaag tttgcctatc tggggcgcct cacgaggttg gctggaagta ccaggcagtg    540
acagccaccc tggaggaaaa gaggaaagag aaagccgaga tccactaccg gaagaataaa    600
cagctcatga ggctacagaa acaggccgag aagaacatga agaagaaaat tgacaaatac    660
acagagagtc caggaggagg cagtccccgt ggcttaggct ttatctttaa gacaatagcg    720
ccgctcgccg ccacccgcgc gactcggatc gggcatcccg gcggccgcac cccgcgcgct    780
ggctcatctg cacaccggcc acctgcattg tcggccagag cccccgtccc ggcggcttcc    840
ccagcagctt ggctgcccct caggacgccc tggacccgcc catcctcctg ccccactagc    900
tcatcgactt acgactccct cagtccctac ggcccacgga accctctccc caacccgcgc    960
cacagcccga gcggcggcgg cggccttaag aagcccgcaa gacactgtca aggtcaaaag   1020
cacaatgtgc tagccagggg gaaaccccag agaaagccaa aatctgaaaa taacagctgg   1080
tatgtagaaa acggcagacc tgctgacttg gcaggctcag gatattgtgg tgctctttgg   1140
aaggcaatag agtccttgga ggaaggactt ggaggaaaac aaaaggacaa ggaaaggaaa   1200
gcagaaaatg gcccccatct acttgtggaa gcagagcaag ccaaggtgtt ttcacacaga   1260
ggtggcaatg ttacactgcc atgtaaattt tatcgagacc ctacagcatt tggctcagga   1320
atccataaaa tccgaattaa gtggaccaag ctaacttcgg attacctcaa ggaagtggat   1380
gtttttgttt ccatgggata ccacaaaaaa acctatggag gctaccaggg tagagtgttt   1440
ctgaagggag gcagtgatag tgatgcttct ctggtcatca cagacctcac tctggaagat   1500
tatgggagat ataagtgtga ggtgattgaa ggattagaag atgatactgt tgtggtagca   1560
ctggacttac aaggtgtggt attcccttac tttccacgac tggggcgcta caatctcaat   1620
tttcacgagg cgcagcaggc gtgtctggac caggatgctg tgatcgcctc cttcgaccag   1680
ctgtacgacg cctggcgggg cgggctggac tggtgcaatg ccggctggct cagtgatggc   1740
tctgtgcaat atcccatcac aaagcccaga gagccctgtg gggggcagaa cacagtgccc   1800
ggagtcagga actacggatt ttgggataaa gataaaagca gatatgatgt ttctgtttt    1860
acatccaatt tcaatggccg tttttactat ctgatccacc ccaccaaact gacctatgat   1920
gaagcggtgc aagcttgtct caatgatggt gctcagattg caaaagtggg ccagatattt   1980
gctgcctgga aaattctcgg atatgaccgc tgtgatgcgg gctggttggc ggatggcagc   2040
gtccgctacc ccatctctag gccaagaagg cgctgcagtc ctactgaggc tgcagtgcgc   2100
ttcgtgggtt tcccagataa aaagcataag ctgtatggtg tctactgctt cagagcatac   2160
aactga                                                              2166
```

Table LIV. Nucleotide sequence alignment of 121P1F1 v.1 and 151P3D4 v.2

```
151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        ATGTTGGAGCATACTACTAAGACATTCCCCTTAAGAGCACTGCACATAGTTGTGGAAAGC 60

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        ATTAGGGACCACAGTGGCCAAAAAATGAAGCAGGATAAGAAGGTGGATCTTCTTGTTCCA 120

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        ACCAAAGTGACTGGCATCATTACACAAGGAGCTAAAGATTTTGGTCATGTACAGTTTGTT 180

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        GGCTCCTACAAACTGGCTTACAGCAATGATGGAGAACACTGGACTGTATACCAGGATGAA 240

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        AAGCAAAGAAAAGATAAGGTACTGCTGGGCCGGAAGGCGGTGGTCGTAAGCTGCGAAGGC 300

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        ATCAACATTTCTGGCAGTTTCTGCAGAAACAAGTTGAAGTACCTGGCTTTCCTCCACAAG 360

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        CGGATGAACACCAACCCTTCTCGACGCCCCTACCACTTCCAGGTCCCCAGCCGCATCTTC 420

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        TGGCGACAAGAAAAAGCAGATGGTGGTTCCTGCTGCCCTCAAGGTCATGCGTCTGAAGCC 480

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        TACAAGAAAGTTTGCCTATCTGGGGCGCCTCACGAGGTTGGCTGGAAGTACCAGGCAGTG 540

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        ACAGCCACCCTGGAGGAAAAGAGGAAAGAGAAAGCCGAGATCCACTACCGGAAGAATAAA 600

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        CAGCTCATGAGGCTACAGAAACAGGCCGAGAAGAACATGAAGAAGAAAATTGACAAATAC 660

151P3D4v.1        ------------------------------------------------------------
151P3D4v.2        ACAGAGAGTCCAGGAGGAGGCAGTCCCCGTGGCTTAGGCTTTATCTTTAAGACAATAGCG 720

151P3D4v.1        ----------------------------------------------TTAGGCTGTA-ATT 13
151P3D4v.2        CCGCTCGCCGCCACCCGCGCGACTCGGATCGGGCATCCCGGCGGCCGCACCCCGCGCGCT 780
                                                                  *  * *     *

151P3D4v.1        AGGGGATTTGGGAGGAGA--ACTTTCCTGGTGACGCTTTGCTTTTCTTCTGCT--CTTGG 69
151P3D4v.2        GGCTCATCTGCACACCGGCCACCTGCATTGTCGGCCAGAGCCCCCGTCCCGGCGGCTTCC 840
                   *   ** **      *   ** * * * **    *   **     * * *    ***

151P3D4v.1        TGAGAAAGT-GCCTCCTTCTTCCCAGGATCAGGACCT--CTGCCATCCAGCGCCACAA-- 124
151P3D4v.2        CCAGCAGCTTGGCTGCCCCTCAGGACGCCCTGGACCCGCCCATCCTCCTGCCCCACTAGC 900
                    ** *  * * ** *  **    * *  * *****   *   * *** ** **** *

151P3D4v.1        --AGAGACATTCTGCACACACACTCACACACACACACACACACACTCTCACACTCGC- 181
151P3D4v.2        TCATCGACTTACGACTCCCTCAGTCCCTACGGCCCACGGA-ACCCTCTCCCCAACCCGCG 959
                    *  *** * *  * * * ** ** *     * ***  * ** * *** *  ** ***

151P3D4v.1        CCAGAGACAAACTTAAGGTGAGG-----AGAAAGAGCGCTA--CGTTCACTTGATCTCCA 234
151P3D4v.2        CCACAGCCCGAGCGGCGGCGGCGGCCTTAAGAAGCCCGCAAGACACTGTCAAGGTCAAAA 1019
                  *** ** *  *     ** *  *     *  ***  *** *  *  *  *  * **   *

151P3D4v.1        GC------TTCCAACTTAAGCAGAACTTGAGAGCATCCGAACTCCTGGATTTCAGGACAA 288
151P3D4v.2        GCACAATGTGCTAGCCAGGGGGAAACCCCAGAGAAAGCCAAAATCTGAAAATAACAGCTG 1079
                  **      * * * *    *   ***   **** *  * **   *** *  * *   *
```

```
151P3D4v.1   GTGAAGAAGATTCTTTGGGC-TATAAAGATGA-AGAGTCTACTTCTTCTGGTGCTGATTT 346
151P3D4v.2   GTATGTAGAAAACGGCAGACCTGCTGACTTGGCAGGCTCAGGATATTGTGGTGCTCTTTG 1139
             **    *  *  *    * * *    *  **  **  **    * ** *******  **

151P3D4v.1   CAATCTGCTGGGCTGATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTC 406
151P3D4v.2   GAAGGCAATAGA------GTCCTTGGAGGAAGGACTTGGAGGAAAACAAAAGGACAAGGA 1193
              **     * *        ** **     **  *      ***  *  * **  * *

151P3D4v.1   ACATCCAAGCAGAAAATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTT 466
151P3D4v.2   A-AGGAAAGCAGAAAATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTT 1252
             * *   ******************************************************

151P3D4v.1   CACACAGAGGTGGCAATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTG 526
151P3D4v.2   CACACAGAGGTGGCAATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTG 1312
             ************************************************************

151P3D4v.1   GCTCAGGAATCCATAAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGG 586
151P3D4v.2   GCTCAGGAATCCATAAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGG 1372
             ************************************************************

151P3D4v.1   AAGTGGATGTTTTTGTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTA 646
151P3D4v.2   AAGTGGATGTTTTTGTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTA 1432
             ************************************************************

151P3D4v.1   GAGTGTTTCTGAAGGGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTC 706
151P3D4v.2   GAGTGTTTCTGAAGGGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTC 1492
             ************************************************************

151P3D4v.1   TGGAAGATTATGGGAGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTG 766
151P3D4v.2   TGGAAGATTATGGGAGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTG 1552
             ************************************************************

151P3D4v.1   TGGTAGCACTGGACTTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACA 826
151P3D4v.2   TGGTAGCACTGGACTTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACA 1612
             ************************************************************

151P3D4v.1   ATCTCAATTTTCACGAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCT 886
151P3D4v.2   ATCTCAATTTTCACGAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCT 1672
             ************************************************************

151P3D4v.1   TCGACCAGCTGTACGACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCA 946
151P3D4v.2   TCGACCAGCTGTACGACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCA 1732
             ************************************************************

151P3D4v.1   GTGATGGCTCTGTGCAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACA 1006
151P3D4v.2   GTGATGGCTCTGTGCAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGGCAGAACA 1792
             **************************************************** *******

151P3D4v.1   CAGTGCCCGGAGTCAGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTT 1066
151P3D4v.2   CAGTGCCCGGAGTCAGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTT 1852
             ************************************************************

151P3D4v.1   TCTGTTTTACATCCAATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGA 1126
151P3D4v.2   TCTGTTTTACATCCAATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGA 1912
             ************************************************************

151P3D4v.1   CCTATGATGAAGCGGTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCC 1186
151P3D4v.2   CCTATGATGAAGCGGTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCC 1972
             ************************************************************

151P3D4v.1   AGATATTTGCTGCCTGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGG 1246
151P3D4v.2   AGATATTTGCTGCCTGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGG 2032
             ************************************************************

151P3D4v.1   ATGGCAGCGTCCGCTACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTG 1306
151P3D4v.2   ATGGCAGCGTCCGCTACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTG 2092
             ************************************************************

151P3D4v.1   CAGTGCGCTTCGTGGGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCA 1366
151P3D4v.2   CAGTGCGCTTCGTGGGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCA 2152
             ************************************************************
```

```
151P3D4v.1      GAGCATACAACTGAATGTGCCCTTAGAGCGCATCAGTTTTAAAGTCATTAAGAACATGTG 1426
151P3D4v.2      GAGCATACAACTGA---------------------------------------------- 2166
                **************

151P3D4v.1      AAAGGTGTTTTTTTTTCCAATATGAACTCATGCAAGTTACCAAAACTGTGATAACCCTT 1486
151P3D4v.2      ------------------------------------------------------------

151P3D4v.1      TTTTACTTACTGTAAAGAGTCATTTTCATAAGATCAATTCATTGATTTGTTTTTTGTAAA 1546
151P3D4v.2      ------------------------------------------------------------

151P3D4v.1      GCTATCATTCAATATATATTATAAATTAATATAAATTTAAGGGAAGCTCTATGTAAGGAG 1606
151P3D4v.2      ------------------------------------------------------------

151P3D4v.1      ACTTAGAGCCAAACTGTTTAAGCTGTATCATCCCAACAAAGTATCCTTTCATGAACGGGG 1666
151P3D4v.2      ------------------------------------------------------------

151P3D4v.1      CATGCAATAGCTTAAGAATTGCTAGGATTAAATTAAGGAAAGTAAAGCTACTCAGAGCAA 1726
151P3D4v.2      ------------------------------------------------------------

151P3D4v.1      CAGGTTCCACAAGCACAAACTTTACACATTTGTACAATTTTGAAATGCACTACAATAAAC 1786
151P3D4v.2      ------------------------------------------------------------

151P3D4v.1      AAATTAGAGCAACACATTTGAAATACAGGCTTCTTTACATAAACTGAGAGGTTATACAAA 1846
151P3D4v.2      ------------------------------------------------------------

151P3D4v.1      ACTCAGTTTCACAAGGGAACAATCTATACCTTTCTAAAAGTTAATATTTCAAGTCTCTAA 1906
151P3D4v.2      ------------------------------------------------------------

151P3D4v.1      TAGGCAGAATATTTTACTCTTTAAAATCCTGCCTTTCTGACCAAAAAAAAA 1957
151P3D4v.2      ---------------------------------------------------
```

Table LV. Amino acid sequence alignment of 121P1F1 v.1 and 151P3D4 v.2

```
151P3D4v.1      ------------------------------------------------------------
151P3D4v.2      MLEHTTKTFPLRALHIVVESIRDHSGQKMKQDKKVDLLVPTKVTGIITQGAKDFGHVQFV 60

151P3D4v.1      ------------------------------------------------------------
151P3D4v.2      GSYKLAYSNDGEHWTVYQDEKQRKDKVLLGRKAVVVSCEGINISGSFCRNKLKYLAFLHK 120

151P3D4v.1      -------MKSLLLLVLISICWADHLSDN-------------------------------- 21
151P3D4v.2      RMNTNPSRRPYHFQVPSRIFWRQEKADGGSCCPQGHASEAYKKVCLSGAPHEVGWKYQAV 180
                        :.  : *   * * :. :*.

151P3D4v.1      ---------------------------------------YT------------------- 23
151P3D4v.2      TATLEEKRKEKAEIHYRKNKQLMRLQKQAEKNMKKKIDKYTESPGGGSPRGLGFIFKTIA 240
                                                       **

151P3D4v.1      -LDHDRAIHI-------------------------------------------------- 32
151P3D4v.2      PLAATRATRIGHPGGRTPRAGSSAHRPPALSARAPVPAASPAAWLPLRTPWTRPSSCPTS 300
                 *   ** :*

151P3D4v.1      ------------------------------------------------------------
151P3D4v.2      SSTYDSLSPYGPRNPLPNPRHSPSGGGGLKKPARHCQGQKHNVLARGKPQRKPKSENNSW 360

151P3D4v.1      ---------------------------------------QAENGPHLLVEAEQAKVFSHR 53
151P3D4v.2      YVENGRPADLAGSGYCGALWKAIESLEEGLGGKQKDKERKAENGPHLLVEAEQAKVFSHR 420
                                                       :********************

151P3D4v.1      GGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVF 113
151P3D4v.2      GGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVF 480
                ************************************************************

151P3D4v.1      LKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLN 173
151P3D4v.2      LKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLN 540
                ************************************************************

151P3D4v.1      FHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVP 233
151P3D4v.2      FHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVP 600
                ************************************************************

151P3D4v.1      GVRNYGFWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIF 293
151P3D4v.2      GVRNYGFWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIF 660
                ************************************************************

151P3D4v.1      AAWKILGYDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAY 353
151P3D4v.2      AAWKILGYDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAY 720
                ************************************************************

151P3D4v.1      N 354
151P3D4v.2      N 721
                *
```

CLAIMS:

1. A composition comprising:

a substance that a) modulates the status of a protein of Figure 2 (SEQ ID NOS: ___), or b) a molecule that is modulated by a protein of Figure 2, whereby the status of a cell that expresses a protein of Figure 2 is modulated.

2. A composition of claim 1, further comprising a physiologically acceptable carrier.

3. A pharmaceutical composition that comprises the composition of claim 1 in a human unit dose form.

4. A composition of claim 1 wherein the substance comprises an antibody or fragment thereof that specifically binds to a protein that is related to a protein of Figure 2.

5. An antibody or fragment thereof of claim 4, which is monoclonal.

6. An antibody of claim 4, which is a human antibody, a humanized antibody or a chimeric antibody.

7. A non-human transgenic animal that produces an antibody of claim 4.

8. A hybridoma that produces an antibody of claim 5.

9. A method of delivering a cytotoxic agent or a diagnostic agent to a cell that expresses a protein of Figure 2 (SEQ ID NOS: ___), said method comprising:

providing the cytotoxic agent or the diagnostic agent conjugated to an antibody or fragment thereof of claim 4; and,

exposing the cell to the antibody-agent or fragment-agent conjugate.

10. A composition of claim 1 wherein the substance comprises a polynucleotide that encodes an antibody or fragment thereof, either of which immunospecifically bind to a protein of Figure 2.

11. A composition of claim 1 wherein the substance comprises a protein related to a protein of Figure 2.

12. A protein of claim 11 that is at least 90% homologous to an entire amino acid sequence shown in Figure 2 (SEQ ID NOS: ___).

13. A composition of claim 1 wherein the substance comprises:

a) a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of Figure 2;

b) a peptide of Tables V to XVIII (SEQ ID NOS: ____);

c) a peptide of Tables XXII to XLVII (SEQ ID NOS: ____); or,

d) a peptide of Tables XLVIII to LI (SEQ ID NOS: ____).

14. A composition of claim 1 wherein the substance comprises a CTL polypeptide or an analog thereof, from the amino acid sequence of a protein of Figure 2 (SEQ ID NOS: ____).

15. A composition of claim 14 further limited by a *proviso* that the epitope is not an entire amino acid sequence of Figure 2 (SEQ ID NOS:).

16. A composition of claim 14 wherein the substance comprises a CTL polypeptide set forth in Tables V to XVIII (SEQ ID NOS: ____).

17. A composition of claim 16 further limited by a *proviso* that the polypeptide is not an entire amino acid sequence of a protein of Figure 2 (SEQ ID NOS: ____).

18. A composition of claim 1 wherein the substance comprises an antibody polypeptide epitope from an amino acid sequence of Figure 2 (SEQ ID NOS: ____).

19. A composition of claim 18 further limited by a *proviso* that the epitope is not an entire amino acid sequence of Figure 2 (SEQ ID NOS: ____).

20. A composition of claim 18 wherein the antibody epitope comprises a peptide region of at least 5 amino acids of Figure 2 (SEQ ID NOS: ____) in any whole number increment up to the end of said peptide, wherein the epitope comprises an amino acid position selected from:

a) an amino acid position having a value greater than 0.5 in the Hydrophilicity profile of Figure 5,

b) an amino acid position having a value less than 0.5 in the Hydropathicity profile of Figure 6;

c) an amino acid position having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

d) an amino acid position having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

e) an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figure 9;

f) a combination of at least two of a) through e);

g) a combination of at least three of a) through e);

h) a combination of at least four of a) through e); or

i) a combination of five of a) through e).

21. A composition of claim 20 further limited by a *proviso* that the epitope is not an entire amino acid sequence of Figure 2 (SEQ ID NOS: ____).

22. A polynucleotide that encodes a protein of claim 11.

23. A polynucleotide of claim 22 that comprises a nucleic acid molecule set forth in Figure 2.

24. A polynucleotide of claim 22 further limited by a *proviso* that the encoded protein is not an entire amino acid sequence of Figure 2 (SEQ ID NOS: ____).

25. A polynucleotide of claim 22 wherein T is substituted with U.

26. A composition of claim 1 wherein the substance comprises a polynucleotide that comprises a coding sequence of a nucleic acid sequence of Figure 2 (SEQ ID NOS: ____).

27. A polynucleotide of claim 22 that further comprises an additional nucleotide sequence that encodes an additional protein of claim 11.

28. A composition comprising a polynucleotide that is fully complementary to a polynucleotide of claim 22.

29. A composition comprising a polynucleotide that is fully complementary to a polynucleotide of claim 25.

30. A composition comprising a polynucleotide that is fully complementary to a polynucleotide of claim 27.

31. A composition of claim 1 wherein the substance comprises a) a ribozyme that cleaves a polynucleotide having a 151P3D4 coding sequence, or b) a nucleic acid molecule that encodes the ribozyme; and, a physiologically acceptable carrier.

32. A composition of claim 1 wherein the substance comprises human T cells, wherein said T cells specifically recognize a 151P3D4 peptide subsequence in the context of a particular HLA molecule.

33. A method of inhibiting growth of cancer cells that express a protein of Figure 2, the method comprising:

administering to the cells the composition of claim 1.

34. A method of claim 33 of inhibiting growth of cancer cells that express a protein of Figure 2, the method comprising steps of:

administering to said cells an antibody or fragment thereof, either of which specifically bind to a 151P3D4-related protein.

35. A method of claim 33 of inhibiting growth of cancer cells that express a protein of Figure 2, the method comprising steps of:

administering to said cells a 151P3D4-related protein.

36. A method of claim 33 of inhibiting growth of cancer cells that express a protein of Figure 2, the method comprising steps of:

administering to said cells a polynucleotide comprising a coding sequence for a 151P3D4-related protein or comprising a polynucleotide complementary to a coding sequence for a 151P3D4-related protein.

37. A method of claim 33 of inhibiting growth of cancer cells that express a protein of Figure 2, the method comprising steps of:

administering to said cells a ribozyme that cleaves a polynucleotide that encodes a protein of Figure 2.

38. A method of claim 33 of inhibiting growth of cancer cells that express a protein of Figure 2 and a particular HLA molecule, the method comprising steps of:

administering human T cells to said cancer cells, wherein said T cells specifically recognize a peptide subsequence of a protein of Figure 2 while the subsequence is in the context of the particular HLA molecule.

39. A method of claim 33, the method comprising steps of:

administering a vector that delivers a nucleotide that encodes a single chain monoclonal antibody, whereby the encoded single chain antibody is expressed intracellularly within cancer cells that express a protein of Figure 2.

40. A method of generating a mammalian immune response directed to a protein of Figure 2, the method comprising:

exposing cells of the mammal's immune system to a portion of

a) a 151P3D4-related protein and/or

b) a nucleotide sequence that encodes said protein,

whereby an immune response is generated to said protein.

41. A method of generating an immune response of claim 40, said method comprising:

providing a 151P3D4-related protein that comprises at least one T cell or at least one B cell epitope; and,

contacting the epitope with a mammalian immune system T cell or B cell respectively, whereby the T cell or B cell is activated.

42. A method of claim 41 wherein the immune system cell is a B cell, whereby the induced B cell generates antibodies that specifically bind to the 151P3D4-related protein.

43. A method of claim 41 wherein the immune system cell is a T cell that is a cytotoxic T cell (CTL), whereby the activated CTL kills an autologous cell that expresses the 151P3D4-related protein.

44. A method of claim 41 wherein the immune system cell is a T cell that is a helper T cell (HTL), whereby the activated HTL secretes cytokines that facilitate the cytotoxic activity of a cytotoxic T cell (CTL) or the antibody-producing activity of a B cell.

45. A method for detecting, in a sample, the presence of a 151P3D4-related protein or a 151P3D4-related polynucleotide, comprising steps of:

contacting the sample with a substance of claim 1 that specifically binds to the 151P3D4-related protein or to the 151P3D4-related polynucleotide, respectively; and,

determining that there is a complex of the substance with the 151P3D4-related protein or the substance with the 151P3D4-related polynucleotide, respectively.

46. A method of claim 45 for detecting the presence of a 151P3D4-related protein in a sample comprising steps of:

contacting the sample with an antibody or fragment thereof either of which specifically bind to the 151P3D4-related protein; and,

determining that there is a complex of the antibody or fragment thereof and the 151P3D4-related protein.

47. A method of claim 45 further comprising a step of:
taking the sample from a patient who has or who is suspected of having cancer.

48. A method of claim 45 for detecting the presence of a protein of Figure 2 mRNA in a sample comprising:

producing cDNA from the sample by reverse transcription using at least one primer;

amplifying the cDNA so produced using 151P3D4 polynucleotides as sense and antisense primers, wherein the 151P3D4 polynucleotides used as the sense and antisense primers serve to amplify a 151P3D4 cDNA; and,

detecting the presence of the amplified 151P3D4 cDNA.

49. A method of claim 45 for monitoring one or more 151P3D4 gene products in a biological sample from a patient who has or who is suspected of having cancer, the method comprising:

determining the status of one or more 151P3D4 gene products expressed by cells in a tissue sample from an individual;

comparing the status so determined to the status of one or more 151P3D4 gene products in a corresponding normal sample; and,

identifying the presence of one or more aberrant gene products of 151P3D4 in the sample relative to the normal sample.

50. The method of claim 49 further comprising a step of determining if there are one or more elevated gene products of a 151P3D4 mRNA or a 151P3D4 protein, whereby the presence of one or more elevated gene products in the test sample relative to the normal tissue sample indicates the presence or status of a cancer.

51. A method of claim 50 wherein the cancer occurs in a tissue set forth in Table I.

<u>Figure 1.</u> **151P3D4 SSH sequence of 417 nucleotides.**

```
  1 GATCCACCCC ACCAAACTGA CCTATGATGA AGCGGTGCAA GCTTGTCTCA ATGATGGTGC
 61 TCAGATTGCA AAAGTGGGCC AGATATTTGC TGCCTGGAAA ATTCTCGGAT ATGACCGCTG
121 TGATGCGGGC TGGTTGGCGG ATGGCAGCGT CCGCTACCCC ATCTCTAGGC CAAGAAGGCG
181 CTGCAGTCCT ACTGAGGCTG CAGTGCGCTT CGTGGGTTTC CCAGATAAAA AGCATAAGCT
241 GTATGGTGTC TACTGCTTCA GAGCATACAA CTGAATGTGC CCTTAGAGCG CATCAGTTTT
301 AAAGTCATTA AGAACATGTG AAAGGTGTTT TTTTTTTCCA ATATGAACTC ATGCAAGTTA
361 CCAAAACTGT GATAACCCTT TTTTACTTAC TGNAAAGAAG TCATTTTCAT AAAGATC
```

Figure 2A. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.1 clone 1-placenta. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A  C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC
316 Y P I S R P R R R C S P T E A A V R F V
1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG
336 G F P D K K H K L Y G V Y C F R A Y N *
1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA
1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgttttttt
1441 tttccaatatgaactcatgcaagttaccaaaactgtgataaccctttttttacttactgta
1501 aagagtcattttcataagatcaattcattgatttgtttttgtaaagctatcattcaata
1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac
1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta
1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc
1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca
1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa
1861 gggaacaatctatacctttctaaaagttaatatttcaagtctctaataggcagaatattt
1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-2166 including the stop codon.

```
   1 M  L  E  H  T  T  K  T  F  P  L  R  A  L  H  I  V  V  E  S
   1 ATGTTGGAGCATACTACTAAGACATTCCCCTTAAGAGCACTGCACATAGTTGTGGAAAGC
  21 I  R  D  H  S  G  Q  K  M  K  Q  D  K  K  V  D  L  L  V  P
  61 ATTAGGGACCACAGTGGCCAAAAAATGAAGCAGGATAAGAAGGTGGATCTTCTTGTTCCA
  41 T  K  V  T  G  I  I  T  Q  G  A  K  D  F  G  H  V  Q  F  V
 121 ACCAAAGTGACTGGCATCATTACACAAGGAGCTAAAGATTTTGGTCATGTACAGTTTGTT
  61 G  S  Y  K  L  A  Y  S  N  D  G  E  H  W  T  V  Y  Q  D  E
 181 GGCTCCTACAAACTGGCTTACAGCAATGATGGAGAACACTGGACTGTATACCAGGATGAA
  81 K  Q  R  K  D  K  V  L  L  G  R  K  A  V  V  V  S  C  E  G
 241 AAGCAAAGAAAAGATAAGGTACTGCTGGGCCGGAAGGCGGTGGTCGTAAGCTGCGAAGGC
 101 I  N  I  S  G  S  F  C  R  N  K  L  K  Y  L  A  F  L  H  K
 301 ATCAACATTTCTGGCAGTTTCTGCAGAAACAAGTTGAAGTACCTGGCTTTCCTCCACAAG
 121 R  M  N  T  N  P  S  R  R  P  Y  H  F  Q  V  P  S  R  I  F
 361 CGGATGAACACCAACCCTTCTCGACGCCCCTACCACTTCCAGGTCCCCAGCCGCATCTTC
 141 W  R  Q  E  K  A  D  G  G  S  C  C  P  Q  G  H  A  S  E  A
 421 TGGCGACAAGAAAAAGCAGATGGTGGTTCCTGCTGCCCTCAAGGTCATGCGTCTGAAGCC
 161 Y  K  K  V  C  L  S  G  A  P  H  E  V  G  W  K  Y  Q  A  V
 481 TACAAGAAAGTTTGCCTATCTGGGGCGCCTCACGAGGTTGGCTGGAAGTACCAGGCAGTG
 181 T  A  T  L  E  E  K  R  K  E  K  A  E  I  H  Y  R  K  N  K
 541 ACAGCCACCCTGGAGGAAAAGAGGAAAGAGAAAGCCGAGATCCACTACCGGAAGAATAAA
 201 Q  L  M  R  L  Q  K  Q  A  E  K  N  M  K  K  K  I  D  K  Y
 601 CAGCTCATGAGGCTACAGAAACAGGCCGAGAAGAACATGAAGAAGAAAATTGACAAATAC
 221 T  E  S  P  G  G  G  S  P  R  G  L  G  F  I  F  K  T  I  A
 661 ACAGAGAGTCCAGGAGGAGGCAGTCCCCGTGGCTTAGGCTTTATCTTTAAGACAATAGCG
 241 P  L  A  A  T  R  A  T  R  I  G  H  P  G  G  R  T  P  R  A
 721 CCGCTCGCCGCCACCCGCGCGACTCGGATCGGGCATCCCGGCGGCCGCACCCCGCGCGCT
 261 G  S  S  A  H  R  P  P  A  L  S  A  R  A  P  V  P  A  A  S
 781 GGCTCATCTGCACACCGGCCACCTGCATTGTCGGCCAGAGCCCCCGTCCCGGCGGCTTCC
 281 P  A  A  W  L  P  L  R  T  P  W  T  R  P  S  S  C  P  T  S
 841 CCAGCAGCTTGGCTGCCCCTCAGGACGCCCTGGACCCGCCCATCCTCCTGCCCCACTAGC
 301 S  S  T  Y  D  S  L  S  P  Y  G  P  R  N  P  L  P  N  P  R
 901 TCATCGACTTACGACTCCCTCAGTCCCTACGGCCCACGGAACCCTCTCCCCAACCCGCGC
 321 H  S  P  S  G  G  G  G  L  K  K  P  A  R  H  C  Q  G  Q  K
 961 CACAGCCCGAGCGGCGGCGGCGGCCTTAAGAAGCCCGCAAGACACTGTCAAGGTCAAAAG
 341 H  N  V  L  A  R  G  K  P  Q  R  K  P  K  S  E  N  N  S  W
1021 CACAATGTGCTAGCCAGGGGGAAACCCCAGAGAAAGCCAAAATCTGAAAATAACAGCTGG
```

361 Y V E N G R P A D L A G S G Y C G A L W
1081 TATGTAGAAAACGGCAGACCTGCTGACTTGGCAGGCTCAGGATATTGTGGTGCTCTTTGG
381 K A I E S L E E G L G G K Q K D K E R K
1141 AAGGCAATAGAGTCCTTGGAGGAAGGACTTGGAGGAAAACAAAAGGACAAGGAAAGGAAA
401 A E N G P H L L V E A E Q A K V F S H R
1201 GCAGAAAATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGA
421 G G N V T L P C K F Y R D P T A F G S G
1261 GGTGGCAATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGA
441 I H K I R I K W T K L T S D Y L K E V D
1321 ATCCATAAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGAT
461 V F V S M G Y H K K T Y G G Y Q G R V F
1381 GTTTTTGTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTT
481 L K G G S D S D A S L V I T D L T L E D
1441 CTGAAGGGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGAT
501 Y G R Y K C E V I E G L E D D T V V V A
1501 TATGGGAGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCA
521 L D L Q G V V F P Y F P R L G R Y N L N
1561 CTGGACTTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAAT
541 F H E A Q Q A C L D Q D A V I A S F D Q
1621 TTTCACGAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAG
561 L Y D A W R G G L D W C N A G W L S D G
1681 CTGTACGACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGC
581 S V Q Y P I T K P R E P C G G Q N T V P
1741 TCTGTGCAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGGCAGAACACAGTGCCC
601 G V R N Y G F W D K D K S R Y D V F C F
1801 GGAGTCAGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTT
621 T S N F N G R F Y Y L I H P T K L T Y D
1861 ACATCCAATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGAT
641 E A V Q A C L N D G A Q I A K V G Q I F
1921 GAAGCGGTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTT
661 A A W K I L G Y D R C D A G W L A D G S
1981 GCTGCCTGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGC
681 V R Y P I S R P R R R C S P T E A A V R
2041 GTCCGCTACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGC
701 F V G F P D K K H K L Y G V Y C F R A Y
2101 TTCGTGGGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATAC
721 N *
2161 AACTGA

Figure 2C. The cDNA (SEQ ID. NO.:____) and amino acid sequence (SEQ ID. NO.:____) of 151P3D4 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacacactcacacacgcacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A .C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC
316 Y P I S R P R R R C S P T E A A V R F V
1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG
336 G F P D K K H K L Y G V Y C F R A Y N *
1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA
1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgtttttt
1441 tttccaatatgaactcatgcaagttaccaaaactgtgataaccctttttacttactgta
1501 aagagtcattttcataagatcaattcattgatttgtttttgtaaagctatcattcaata
1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac
1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta
1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc
1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca
1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa
1861 gggaacaatctataccttctaaaagttaatatttcaagtctctaataggcagaatattt
1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa

Figure 2D. The cDNA (SEQ ID. NO.:____) and amino acid sequence (SEQ ID. NO.:____) of 151P3D4 v.4. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctaggttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A  C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

```
1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGCTGGTTGGCGGATGGCAGCGTCCGC
 316 Y  P  I  S  R  P  R  R  R  C  S  P  T  E  A  A  V  R  F  V
1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG
 336 G  F  P  D  K  K  H  K  L  Y  G  V  Y  C  F  R  A  Y  N  *
1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA
1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgttttttt
1441 tttccaatatgaactcatgcaagttaccaaaactgtgataaccctttttacttactgta
1501 aagagtcattttcataagatcaattcattgatttgtttttgtaaagctatcattcaata
1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac
1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta
1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc
1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca
1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa
1861 gggaacaatctatacctttctaaaagttaatatttcaagtctctaataggcagaatattt
1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa
```

Figure 2E. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.5. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacactcacacacacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctaccttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A  C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC

316 Y P I S R P R R R C S P T E A A V R F V

1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG

336 G F P D K K H K L Y G V Y C F R A Y N *

1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA

1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgttttttt

1441 tttccaatatgaactcatgcaagttaccaaaactgtgataacccttttttacttactgta

1501 aagagtcattttcataagatcaattcattgatttgtttttgtaaagctatcattcaata

1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac

1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta

1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc

1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca

1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa

1861 gggaacaatctatacctttctaaaagttaatatttcaagtctctaataggcagaatattt

1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa

Figure 2F. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.6. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacacactcacacacacacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGGCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A  C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC
316 Y P I S R P R R R C S P T E A A V R F V
1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG
336 G F P D K K H K L Y G V Y C F R A Y N *
1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA
1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgttttttt
1441 tttccaatatgaactcatgcaagttaccaaaactgtgataaccctttttttacttactgta
1501 aagagtcattttcataagatcaattcattgatttgtttttttgtaaagctatcattcaata
1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac
1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta
1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc
1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca
1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa
1861 gggaacaatctataccttttctaaaagttaatatttcaagtctctaataggcagaatattt
1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa

Figure 2G. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.7. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgctttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A  C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC
316 Y P I S R P R R R C S P T E A A V R F V
1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG
336 G F P D K K H K L Y G V Y C F R A Y N *
1321 GGTTTTCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA
1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgttttttt
1441 tttccaatatgaactcatgcaagttaccaaaactgtgataaccctttttacttactgta
1501 aagagtcattttcataagatcaattcattgatttgtttttgtaaagctatcattcaata
1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac
1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta
1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc
1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca
1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa
1861 gggaacaatctatacctttctaaaagttaatatttcaagtctctaataggcagaatattt
1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa

Figure 2H. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.8. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc

61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc

121 acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg

181 cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc

241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt

1 M K S L L L L V L I S I C W A

301 ctttgggctataaag<u>ATG</u>AAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT

16 D H L S D N Y T L D H D R A I H I Q A E

361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA

36 N G P H L L V E A E Q A K V F S H R G G

421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC

56 N V T L P C K F Y R D P T A F G S G I H

481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT

76 K I R I K W T K L T S D Y L K E V D V F

541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT

96 V S M G Y H K K T Y G G Y Q G R V F L K

601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG

116 G G S D S D A S L V I T D L T L E D Y G

661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG

136 R Y K C E V I E G L E D D T V V V A L D

721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC

156 L Q G V V F P Y F P R L G R Y N L N F H

781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC

176 E A Q Q A C L D Q D A V I A S F D Q L Y

841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC

196 D A W R G G L D W C N A G W L S D G S V

901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG

216 Q Y P I T K P R E P C G G Q N T V P G V

961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC

236 R N Y G F W D K D K S R Y D V F C F T S

1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC

256 N F N G R F Y Y L I H P T K L T Y D E A

1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG

276 V Q A C L N D G A Q I A K V G Q I F A A

1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC

296 W K I L G Y D R C D A G W L A D G S V R

1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC

316 Y P I S R P R R R C S P T E A A V R F V

1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG

336 G F P D K K H K L Y G V Y C F R A Y N *

1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA

1381 atgtgcccttagagcgcaccagttttaaagtcattaagaacatgtgaaaggtgttttttt

1441 tttccaatatgaactcatgcaagttaccaaaactgtgataacccttttttacttactgta

1501 aagagtcattttcataagatcaattcattgatttgtttttttgtaaagctatcattcaata

1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac

1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta

1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc

1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca

1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa

1861 gggaacaatctatacctttctaaaagttaatatttcaagtctctaataggcagaatattt

1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa

Figure 2I. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.9. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A  C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC

316 Y P I S R P R R R C S P T E A A V R F V

1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG

336 G F P D K K H K L Y G V Y C F R A Y N *

1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA

1381 atgtgcccttagagcgcattagttttaaagtcattaagaacatgtgaaaggtgttttttt

1441 tttccaatatgaactcatgcaagttaccaaaactgtgataacccttttttacttactgta

1501 aagagtcattttcataagatcaattcattgatttgtttttttgtaaagctatcattcaata

1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac

1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta

1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc

1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca

1801, catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa

1861 gggaacaatctatacctttctaaaagttaatatttcaagtctctaataggcagaatattt

1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa

Figure 2J. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.10. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A  C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC
316 Y P I S R P R R R C S P T E A A V R F V
1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG
336 G F P D K K H K L Y G V Y C F R A Y N *
1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA
1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgttttttt
1441 tttccaatatgaactcatgcaagttaccaaaactgtgataaccctttttacttactgta
1501 aagagtcattttcataagatcaattcattgatttgtttttgtaaagctatcattcaata
1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac
1621 tgtttaagctgtatcatcccaacaaagtatcccttcatgaacggggcatgcaatagctta
1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcaacaggttccacaagc
1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca
1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa
1861 gggaacaatctatacctttctaaaagttaatatttcaagtctctaataggcagaatattt
1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa

Figure 2K. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 151P3D4 v.11. The start methionine is underlined. The open reading frame extends from nucleic acid 316-1380 including the stop codon.

```
   1 ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc
  61 tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc
 121 acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg
 181 cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc
 241 aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt
   1                M  K  S  L  L  L  L  V  L  I  S  I  C  W  A
 301 ctttgggctataaagATGAAGAGTCTACTTCTTCTGGTGCTGATTTCAATCTGCTGGGCT
  16 D  H  L  S  D  N  Y  T  L  D  H  D  R  A  I  H  I  Q  A  E
 361 GATCATCTTTCAGACAACTATACTCTGGATCATGACAGAGCTATTCACATCCAAGCAGAA
  36 N  G  P  H  L  L  V  E  A  E  Q  A  K  V  F  S  H  R  G  G
 421 AATGGCCCCCATCTACTTGTGGAAGCAGAGCAAGCCAAGGTGTTTTCACACAGAGGTGGC
  56 N  V  T  L  P  C  K  F  Y  R  D  P  T  A  F  G  S  G  I  H
 481 AATGTTACACTGCCATGTAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAT
  76 K  I  R  I  K  W  T  K  L  T  S  D  Y  L  K  E  V  D  V  F
 541 AAAATCCGAATTAAGTGGACCAAGCTAACTTCGGATTACCTCAAGGAAGTGGATGTTTTT
  96 V  S  M  G  Y  H  K  K  T  Y  G  G  Y  Q  G  R  V  F  L  K
 601 GTTTCCATGGGATACCACAAAAAAACCTATGGAGGCTACCAGGGTAGAGTGTTTCTGAAG
 116 G  G  S  D  S  D  A  S  L  V  I  T  D  L  T  L  E  D  Y  G
 661 GGAGGCAGTGATAGTGATGCTTCTCTGGTCATCACAGACCTCACTCTGGAAGATTATGGG
 136 R  Y  K  C  E  V  I  E  G  L  E  D  D  T  V  V  V  A  L  D
 721 AGATATAAGTGTGAGGTGATTGAAGGATTAGAAGATGATACTGTTGTGGTAGCACTGGAC
 156 L  Q  G  V  V  F  P  Y  F  P  R  L  G  R  Y  N  L  N  F  H
 781 TTACAAGGTGTGGTATTCCCTTACTTTCCACGACTGGGGCGCTACAATCTCAATTTTCAC
 176 E  A  Q  Q  A  C  L  D  Q  D  A  V  I  A  S  F  D  Q  L  Y
 841 GAGGCGCAGCAGGCGTGTCTGGACCAGGATGCTGTGATCGCCTCCTTCGACCAGCTGTAC
 196 D  A  W  R  G  G  L  D  W  C  N  A  G  W  L  S  D  G  S  V
 901 GACGCCTGGCGGGGCGGGCTGGACTGGTGCAATGCCGGCTGGCTCAGTGATGGCTCTGTG
 216 Q  Y  P  I  T  K  P  R  E  P  C  G  G  Q  N  T  V  P  G  V
 961 CAATATCCCATCACAAAGCCCAGAGAGCCCTGTGGGGGCCAGAACACAGTGCCCGGAGTC
 236 R  N  Y  G  F  W  D  K  D  K  S  R  Y  D  V  F  C  F  T  S
1021 AGGAACTACGGATTTTGGGATAAAGATAAAAGCAGATATGATGTTTTCTGTTTTACATCC
 256 N  F  N  G  R  F  Y  Y  L  I  H  P  T  K  L  T  Y  D  E  A
1081 AATTTCAATGGCCGTTTTTACTATCTGATCCACCCCACCAAACTGACCTATGATGAAGCG
 276 V  Q  A  C  L  N  D  G  A  Q  I  A  K  V  G  Q  I  F  A  A
1141 GTGCAAGCTTGTCTCAATGATGGTGCTCAGATTGCAAAAGTGGGCCAGATATTTGCTGCC
 296 W  K  I  L  G  Y  D  R  C  D  A  G  W  L  A  D  G  S  V  R
```

```
1201 TGGAAAATTCTCGGATATGACCGCTGTGATGCGGGCTGGTTGGCGGATGGCAGCGTCCGC
 316 Y  P  I  S  R  P  R  R  R  C  S  P  T  E  A  A  V  R  F  V
1261 TACCCCATCTCTAGGCCAAGAAGGCGCTGCAGTCCTACTGAGGCTGCAGTGCGCTTCGTG
 336 G  F  P  D  K  K  H  K  L  Y  G  V  Y  C  F  R  A  Y  N  *
1321 GGTTTCCCAGATAAAAAGCATAAGCTGTATGGTGTCTACTGCTTCAGAGCATACAACTGA
1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgttttttt
1441 tttccaatatgaactcatgcaagttaccaaaactgtgataaccctttttacttactgta
1501 aagagtcattttcataagatcaattcattgatttgtttttgtaaagctatcattcaata
1561 tatattataaattaatataaatttaagggaagctctatgtaaggagacttagagccaaac
1621 tgtttaagctgtatcatcccaacaaagtatcctttcatgaacggggcatgcaatagctta
1681 agaattgctaggattaaattaaggaaagtaaagctactcagagcagcaggttccacaagc
1741 acaaactttacacatttgtacaattttgaaatgcactacaataaacaaattagagcaaca
1801 catttgaaatacaggcttctttacataaactgagaggttatacaaaactcagtttcacaa
1861 gggaacaatctatacctttctaaaagttaatatttcaagtctctaataggcagaatattt
1921 tactctttaaaatcctgcctttctgaccaaaaaaaaa
```

Figure 3A. Amino acid sequence of 151P3D4 v.1 clone 151P3D4 clone 1-placenta (SEQ ID. NO. :____). The 151P3D4 v.1 protein has 354 amino acids.

```
  1 MKSLLLLVLI SICWADHLSD NYTLDHDRAI HIQAENGPHL LVEAEQAKVF SHRGGNVTLP
 61 CKFYRDPTAF GSGIHKIRIK WTKLTSDYLK EVDVFVSMGY HKKTYGGYQG RVFLKGGSDS
121 DASLVITDLT LEDYGRYKCE VIEGLEDDTV VVALDLQGVV FPYFPRLGRY NLNFHEAQQA
181 CLDQDAVIAS FDQLYDAWRG GLDWCNAGWL SDGSVQYPIT KPREPCGGQN TVPGVRNYGF
241 WDKDKSRYDV FCFTSNFNGR FYYLIHPTKL TYDEAVQACL NDGAQIAKVG QIFAAWKILG
301 YDRCDAGWLA DGSVRYPISR PRRRCSPTEA AVRFVGFPDK KHKLYGVYCF RAYN
```

Figure 3B. Amino acid sequence of 151P3D4 v.2 (SEQ ID. NO. :____). The 151P3D4 v.2 protein has 721 amino acids.

```
  1 MLEHTTKTFP LRALHIVVES IRDHSGQKMK QDKKVDLLVP TKVTGIITQG AKDFGHVQFV
 61 GSYKLAYSND GEHWTVYQDE KQRKDKVLLG RKAVVVSCEG INISGSFCRN KLKYLAFLHK
121 RMNTNPSRRP YHFQVPSRIF WRQEKADGGS CCPQGHASEA YKKVCLSGAP HEVGWKYQAV
181 TATLEEKRKE KAEIHYRKNK QLMRLQKQAE KNMKKKIDKY TESPGGGSPR GLGFIFKTIA
241 PLAATRATRI GHPGGRTPRA GSSAHRPPAL SARAPVPAAS PAAWLPLRTP WTRPSSCPTS
301 SSTYDSLSPY GPRNPLPNPR HSPSGGGGLK KPARHCQGQK HNVLARGKPQ RKPKSENNSW
361 YVENGRPADL AGSGYCGALW KAIESLEEGL GGKQKDKERK AENGPHLLVE AEQAKVFSHR
421 GGNVTLPCKF YRDPTAFGSG IHKIRIKWTK LTSDYLKEVD VFVSMGYHKK TYGGYQGRVF
481 LKGGSDSDAS LVITDLTLED YGRYKCEVIE GLEDDTVVVA LDLQGVVFPY FPRLGRYNLN
541 FHEAQQACLD QDAVIASFDQ LYDAWRGGLD WCNAGWLSDG SVQYPITKPR EPCGGQNTVP
601 GVRNYGFWDK DKSRYDVFCF TSNFNGRFYY LIHPTKLTYD EAVQACLNDG AQIAKVGQIF
661 AAWKILGYDR CDAGWLADGS VRYPISRPRR RCSPTEAAVR FVGFPDKKHK LYGVYCFRAY
721 N
```

Figure 4A. **Nucleic acid alignment of 151P3D4 v.1 with the mRNA for human cartilage link protein.**

```
>gi|463246|emb|X17405.1|HSLINKC Human mRNA for cartilage link protein
          Length = 1492

 Score = 2918 bits (1472), Expect = 0.0
 Identities = 1487/1492 (99%)
 Strand = Plus / Plus


Query: 1     ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1     ttaggctgtaattaggggatttgggaggagaactttcctggtgacgctttgcttttcttc 60


Query: 61    tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61    tgctcttggtgagaaagtgcctccttcttcccaggatcaggacctctgccatccagcgcc 120


Query: 121   acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   acaaagagacattctgcacacacactcacacacacacacacacacactctcacactcg 180


Query: 181   cccagagacaaacttaaggtgaggagaaagagcgctacgttcacttgatctccagcttcc 240
             |||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Sbjct: 181   cccagagacaaacttaaggtgaggagaaagagcgctagcttcacttgatctccagcttcc 240


Query: 241   aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241   aacttaagcagaacttgagagcatccgaactcctggatttcaggacaagtgaagaagatt 300


Query: 301   ctttgggctataaagatgaagagtctacttcttctggtgctgatttcaatctgctgggct 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   ctttgggctataaagatgaagagtctacttcttctggtgctgatttcaatctgctgggct 360


Query: 361   gatcatctttcagacaactatactctggatcatgacagagctattcacatccaagcagaa 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361   gatcatctttcagacaactatactctggatcatgacagagctattcacatccaagcagaa 420


Query: 421   aatggcccccatctacttgtggaagcagagcaagccaaggtgttttcacacagaggtggc 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421   aatggcccccatctacttgtggaagcagagcaagccaaggtgttttcacacagaggtggc 480


Query: 481   aatgttacactgccatgtaaattttatcgagaccctacagcatttggctcaggaatccat 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481   aatgttacactgccatgtaaattttatcgagaccctacagcatttggctcaggaatccat 540


Query: 541   aaaatccgaattaagtggaccaagctaacttcggattacctcaaggaagtggatgttttt 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 541  aaaatccgaattaagtggaccaagctaacttcggattacctcaaggaagtggatgttttt 600

Query: 601  gtttccatgggataccacaaaaaaacctatggaggctaccagggtagagtgtttctgaag 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  gtttccatgggataccacaaaaaaacctatggaggctaccagggtagagtgtttctgaag 660

Query: 661  ggaggcagtgatagtgatgcttctctggtcatcacagacctcactctggaagattatggg 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  ggaggcagtgatagtgatgcttctctggtcatcacagacctcactctggaagattatggg 720

Query: 721  agatataagtgtgaggtgattgaaggattagaagatgatactgttgtggtagcactggac 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  agatataagtgtgaggtgattgaaggattagaagatgatactgttgtggtagcactggac 780

Query: 781  ttacaaggtgtggtattcccttactttccacgactggggcgctacaatctcaattttcac 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  ttacaaggtgtggtattcccttactttccacgactggggcgctacaatctcaattttcac 840

Query: 841  gaggcgcagcaggcgtgtctggaccaggatgctgtgatcgcctccttcgaccagctgtac 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841  gaggcgcagcaggcgtgtctggaccaggatgctgtgatcgcctccttcgaccagctgtac 900

Query: 901  gacgcctggcggggcgggctggactggtgcaatgccggctggctcagtgatggctctgtg 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901  gacgcctggcggggcgggctggactggtgcaatgccggctggctcagtgatggctctgtg 960

Query: 961  caatatcccatcacaaagcccagagagccctgtgggggccagaacacagtgcccggagtc 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961  caatatcccatcacaaagcccagagagccctgtgggggccagaacacagtgcccggagtc 1020

Query: 1021 aggaactacggattttgggataaagataaaagcagatatgatgttttctgttttacatcc 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021 aggaactacggattttgggataaagataaaagcagatatgatgttttctgttttacatcc 1080

Query: 1081 aatttcaatggccgttttttactatctgatccaccccaccaaactgacctatgatgaagcg 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081 aatttcaatggccgttttttactatctgatccaccccaccaaactgacctatgatgaagcg 1140

Query: 1141 gtgcaagcttgtctcaatgatggtgctcagattgcaaaagtgggccagatatttgctgcc 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141 gtgcaagcttgtctcaatgatggtgctcagattgcaaaagtgggccagatatttgctgcc 1200

Query: 1201 tggaaaattctcggatatgaccgctgtgatgcgggctggttggcggatggcagcgtccgc 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201 tggaaaattctcggatatgaccgctgtgatgcgggctggttggcggatggcagcgtccgc 1260

Query: 1261 taccccatctctaggccaagaaggcgctgcagtcctactgaggctgcagtgcgcttcgtg 1320
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261 taccccatctctaggccaagaaggcgctgcagtcctactgaggctgcagtgcgcttcgtg 1320

Query: 1321 ggtttcccagataaaaagcataagctgtatggtgtctactgcttcagagcatacaactga 1380
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321 ggttttccagataaaaagcataagctgtatggtgtctactgcttcagagcatacaactga 1380

Query: 1381 atgtgcccttagagcgcatcagttttaaagtcattaagaacatgtgaaaggtgttttttt 1440
            ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381 atgtgcccttagagcgcactagttttaaagtcattaagaacatgtgaaaggtgttttttt 1440

Query: 1441 tttccaatatgaactcatgcaagttaccaaaactgtgataacccttttttac 1492
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441 tttccaatatgaactcatgcaagttaccaaaactgtgataacccttttttac 1492
```

Figure 4B. **Amino acid alignment of 151P3D4 v.1 with human cartilage link protein.**

```
Score =  751 bits (1938), Expect = 0.0
Identities = 354/354 (100%), Positives = 354/354 (100%)

Query: 1   MKSLLLLVLISICWADHLSDNYTLDHDRAIHIQAENGPHLLVEAEQAKVFSHRGGNVTLP 60
            MKSLLLLVLISICWADHLSDNYTLDHDRAIHIQAENGPHLLVEAEQAKVFSHRGGNVTLP
Sbjct: 1   MKSLLLLVLISICWADHLSDNYTLDHDRAIHIQAENGPHLLVEAEQAKVFSHRGGNVTLP 60

Query: 61  CKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVFLKGGSDS 120
            CKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVFLKGGSDS
Sbjct: 61  CKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVFLKGGSDS 120

Query: 121 DASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLNFHEAQQA 180
            DASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLNFHEAQQA
Sbjct: 121 DASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLNFHEAQQA 180

Query: 181 CLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF 240
            CLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF
Sbjct: 181 CLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF 240

Query: 241 WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKILG 300
            WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKILG
Sbjct: 241 WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKILG 300

Query: 301 YDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN 354
            YDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN
Sbjct: 301 YDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN 354
```

Figure 4C. **Amino acid alignment of 151P3D4 v.1 with mouse cartilage link protein.**

```
>gi|4218976|gb|AAD12253.1| (AF098460) link protein [Mus musculus]
          Length = 355

 Score =  703 bits (1815), Expect = 0.0
 Identities = 341/355 (96%), Positives = 349/355 (98%), Gaps = 1/355 (0%)

Query: 1   MKSLLLLVLISICWADHLSDNYT-LDHDRAIHIQAENGPHLLVEAEQAKVFSHRGGNVTL 59
            M+SLLLLVLIS+CWADHLSD+YT  D DR IHIQAENGP LLVEAEQAKVFSHRGGNVTL
Sbjct: 1   MRSLLLLVLISVCWADHLSDSYTPPDQDRVIHIQAENGPRLLVEAEQAKVFSHRGGNVTL 60

Query: 60  PCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVFLKGGSD 119
            PCKFYRDPTAFGSGIHKIRIKWTKLTSDYL+EVDVFVSMGYHKKTYGGYQGRVFLKGGSD
Sbjct: 61  PCKFYRDPTAFGSGIHKIRIKWTKLTSDYLREVDVFVSMGYHKKTYGGYQGRVFLKGGSD 120

Query: 120 SDASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLNFHEAQQ 179
            +DASLVITDLTLEDYGRYKCEVIEGLEDDT VVAL+LQGVVFPYFPRLGRYNLNFHEA+Q
Sbjct: 121 NDASLVITDLTLEDYGRYKCEVIEGLEDDTAVVALELQGVVFPYFPRLGRYNLNFHEARQ 180

Query: 180 ACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYG 239
            ACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYG
Sbjct: 181 ACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYG 240

Query: 240 FWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKIL 299
            FWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWK+L
Sbjct: 241 FWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKLL 300

Query: 300 GYDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN 354
            GYDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN
Sbjct: 301 GYDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN 355
```

Figure 4D. **Amino acid alignment of 151P3D4 v.1 with 151P3D4 v.2.**

```
Score =  684 bits (1765), Expect = 0.0
Identities = 321/322 (99%), Positives = 322/322 (99%)

v.1: 33  QAENGPHLLVEAEQAKVFSHRGGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEV 92
         +AENGPHLLVEAEQAKVFSHRGGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEV
v.2: 400 KAENGPHLLVEAEQAKVFSHRGGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEV 459

v.1: 93  DVFVSMGYHKKTYGGYQGRVFLKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVV 152
         DVFVSMGYHKKTYGGYQGRVFLKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVV
v.2: 460 DVFVSMGYHKKTYGGYQGRVFLKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVV 519

v.1: 153 ALDLQGVVFPYFPRLGRYNLNFHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSD 212
         ALDLQGVVFPYFPRLGRYNLNFHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSD
v.2: 520 ALDLQGVVFPYFPRLGRYNLNFHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSD 579

v.1: 213 GSVQYPITKPREPCGGQNTVPGVRNYGFWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTY 272
         GSVQYPITKPREPCGGQNTVPGVRNYGFWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTY
v.2: 580 GSVQYPITKPREPCGGQNTVPGVRNYGFWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTY 639

v.1: 273 DEAVQACLNDGAQIAKVGQIFAAWKILGYDRCDAGWLADGSVRYPISRPRRRCSPTEAAV 332
         DEAVQACLNDGAQIAKVGQIFAAWKILGYDRCDAGWLADGSVRYPISRPRRRCSPTEAAV
v.2: 640 DEAVQACLNDGAQIAKVGQIFAAWKILGYDRCDAGWLADGSVRYPISRPRRRCSPTEAAV 699

v.1: 333 RFVGFPDKKHKLYGVYCFRAYN 354
         RFVGFPDKKHKLYGVYCFRAYN
v.2: 700 RFVGFPDKKHKLYGVYCFRAYN 721
```

Figure 4E. Amino acid alignment of 151P3D4 v.2 with hypothetical protein XP_094318.

```
>gi|18560342|ref|XP_094318.1| (XM_094318) hypothetical protein XP_094318
[Homo sapiens]
          Length = 187

 Score =  312 bits (799), Expect = 8e-84
 Identities = 167/168 (99%), Positives = 168/168 (99%)

Query: 122 MNTNPSRRPYHFQVPSRIFWRQEKADGGSCCPQGHASEAYKKVCLSGAPHEVGWKYQAVT 181
           MNTNPSRRPYHFQVPSRIFWRQEKADGGSCCPQGHASEAYKKVCLSGAPHEVGWKYQAVT
Sbjct: 1   MNTNPSRRPYHFQVPSRIFWRQEKADGGSCCPQGHASEAYKKVCLSGAPHEVGWKYQAVT 60

Query: 182 ATLEEKRKEKAEIHYRKNKQLMRLQKQAEKNMKKKIDKYTESPGGGSPRGLGFIFKTIAP 241
           ATLEEKRKEKAEIHYRKNKQLMRLQKQAEKNMKKKIDKYTESPGGGSPRGLGFIFKTIAP
Sbjct: 61  ATLEEKRKEKAEIHYRKNKQLMRLQKQAEKNMKKKIDKYTESPGGGSPRGLGFIFKTIAP 120

Query: 242 LAATRATRIGHPGGRTPRAGSSAHRPPALSARAPVPAASPAAWLPLRT 289
           LAATRATRIGHPGGRTPRAGSSAHRPPALSARAPVPAASPAAWLPLR+
Sbjct: 121 LAATRATRIGHPGGRTPRAGSSAHRPPALSARAPVPAASPAAWLPLRS 168
```

Figure 4F. **Alignment with Bovine Cartilage Link Protein**

```
Score =  717 bits (1850), Expect = 0.0
 Identities = 341/354 (96%), Positives = 345/354 (97%)

Query: 1   MKSLLLLVLISICWADHLSDNYTLDHDRAIHIQAENGPHLLVEAEQAKVFSHRGGNVTLP 60
           MKSLLLLVLIS CWADH SDNYT+DHDR IHIQAENGP LLVEAEQAKVFS RGGNVTLP
Sbjct: 1   MKSLLLLVLISFCWADHHSDNYTVDHDRVIHIQAENGPRLLVEAEQAKVFSRRGGNVTLP 60

Query: 61  CKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVFLKGGSDS 120
           CKFYRDPTAFGSG HKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGY GRVFLKGGSD+
Sbjct: 61  CKFYRDPTAFGSGTHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYHGRVFLKGGSDN 120

Query: 121 DASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLNFHEAQQA 180
           DASLVITDLTLEDYGRYKCEVIEGLEDDT VVALDLQGVVFPYFPRLGRYNLNFHEAQQA
Sbjct: 121 DASLVITDLTLEDYGRYKCEVIEGLEDDTAVVALDLQGVVFPYFPRLGRYNLNFHEAQQA 180

Query: 181 CLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF 240
           CLDQDAVIASFDQLYDAWR GLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF
Sbjct: 181 CLDQDAVIASFDQLYDAWRSGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF 240

Query: 241 WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKILG 300
           WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWK+LG
Sbjct: 241 WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKLLG 300

Query: 301 YDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN 354
           YDRCDAGWLADGSVRYPISRPRRRCSP+EAAVRFVGFPDKKHKLYGVYCFRAYN
Sbjct: 301 YDRCDAGWLADGSVRYPISRPRRRCSPSEAAVRFVGFPDKKHKLYGVYCFRAYN 354
```

Figure 4G. Alignment with Rat Cartilage Link Protein

```
Score =  715 bits (1846), Expect = 0.0
 Identities = 338/354 (95%), Positives = 347/354 (97%)

Query: 1   MKSLLLLVLISICWADHLSDNYTLDHDRAIHIQAENGPHLLVEAEQAKVFSHRGGNVTLP 60
           M+SLL LVLIS+C ADHLSD+YT D DR IHIQAENGP LLVEAEQAKVFSHRGGNVTLP
Sbjct: 1   MRSLLFLVLISVCRADHLSDSYTPDQDRVIHIQAENGPRLLVEAEQAKVFSHRGGNVTLP 60

Query: 61  CKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVFLKGGSDS 120
           CKFYRDPTAFGSGIHKIRIKWTKLTSDYL+EVDVFVSMGYHKKTYGGYQGRVFLKGGSD+
Sbjct: 61  CKFYRDPTAFGSGIHKIRIKWTKLTSDYLREVDVFVSMGYHKKTYGGYQGRVFLKGGSDN 120

Query: 121 DASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLNFHEAQQA 180
           DASL+ITDLTLEDYGRYKCEVIEGLEDDT VVAL+LQGVVFPYFPRLGRYNLNFHEA+QA
Sbjct: 121 DASLIITDLTLEDYGRYKCEVIEGLEDDTAVVALELQGVVFPYFPRLGRYNLNFHEARQA 180

Query: 181 CLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF 240
           CLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF
Sbjct: 181 CLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGF 240

Query: 241 WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKILG 300
           WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWK+LG
Sbjct: 241 WDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKLLG 300

Query: 301 YDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN 354
           YDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN
Sbjct: 301 YDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAYN 354
```

Figure 4H. Alignment with human Cartilage Link Protein

```
Score =  435 bits (1118), Expect = e-121
 Identities = 200/201 (99%), Positives = 201/201 (99%)

Query: 400 KAENGPHLLVEAEQAKVFSHRGGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEV 459
           +AENGPHLLVEAEQAKVFSHRGGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEV
Sbjct: 33  QAENGPHLLVEAEQAKVFSHRGGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEV 92

Query: 460 DVFVSMGYHKKTYGGYQGRVFLKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVV 519
           DVFVSMGYHKKTYGGYQGRVFLKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVV
Sbjct: 93  DVFVSMGYHKKTYGGYQGRVFLKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVV 152

Query: 520 ALDLQGVVFPYFPRLGRYNLNFHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSD 579
           ALDLQGVVFPYFPRLGRYNLNFHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSD
Sbjct: 153 ALDLQGVVFPYFPRLGRYNLNFHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSD 212

Query: 580 GSVQYPITKPREPCGGQNTVP 600
           GSVQYPITKPREPCGGQNTVP
Sbjct: 213 GSVQYPITKPREPCGGQNTVP 233
```

Figure 4I. **CLUSTAL W Alignment of 151P3D4-v.1 and v.2**

```
v.1             ------------------------------------------------------------
v.2             MLEHTTKTFPLRALHIVVESIRDHSGQKMKQDKKVDLLVPTKVTGIITQGAKDFGHVQFV

v.1             ------------------------------------------------------------
v.2             GSYKLAYSNDGEHWTVYQDEKQRKDKVLLGRKAVVVSCEGINISGSFCRNKLKYLAFLHK

v.1             ------------------------------------------------------------
v.2             RMNTNPSRRPYHFQVPSRIFWRQEKADGGSCCPQGHASEAYKKVCLSGAPHEVGWKYQAV

v.1             ------------------------------------------------------------
v.2             TATLEEKRKEKAEIHYRKNKQLMRLQKQAEKNMKKKIDKYTESPGGGSPRGLGFIFKTIA

v.1             ------------------------------------------------------------
v.2             PLAATRATRIGHPGGRTPRAGSSAHRPPALSARAPVPAASPAAWLPLRTPWTRPSSCPTS

v.1             ------------------------------------------------------------
v.2             SSTYDSLSPYGPRNPLPNPRHSPSGGGGLKKPARHCQGQKHNVLARGKPQRKPKSENNSW

v.1             ---MKSLLLLVLISIC---WADHLSDNYTLDHDR-AIHIQAENGPHLLVEAEQAKVFSHR
v.2             YVENGRPADLAGSGYCGALWKAIESLEEGLGGKQKDKERKAENGPHLLVEAEQAKVFSHR
                         *.  . *   *    * :  *. .:   . :********************

v.1             GGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVF
v.2             GGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVF
                ************************************************************

v.1             LKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLN
v.2             LKGGSDSDASLVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLN
                ************************************************************

v.1             FHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVP
v.2             FHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVP
                ************************************************************

v.1             GVRNYGFWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACLNDGAQIAKVGQIF
v.2             ------------------------------------------------------------

v.1             AAWKILGYDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCFRAY
v.2             ------------------------------------------------------------

v.1             N
v.2             -
```

Figure 5A

151P3D4 variant 1 Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

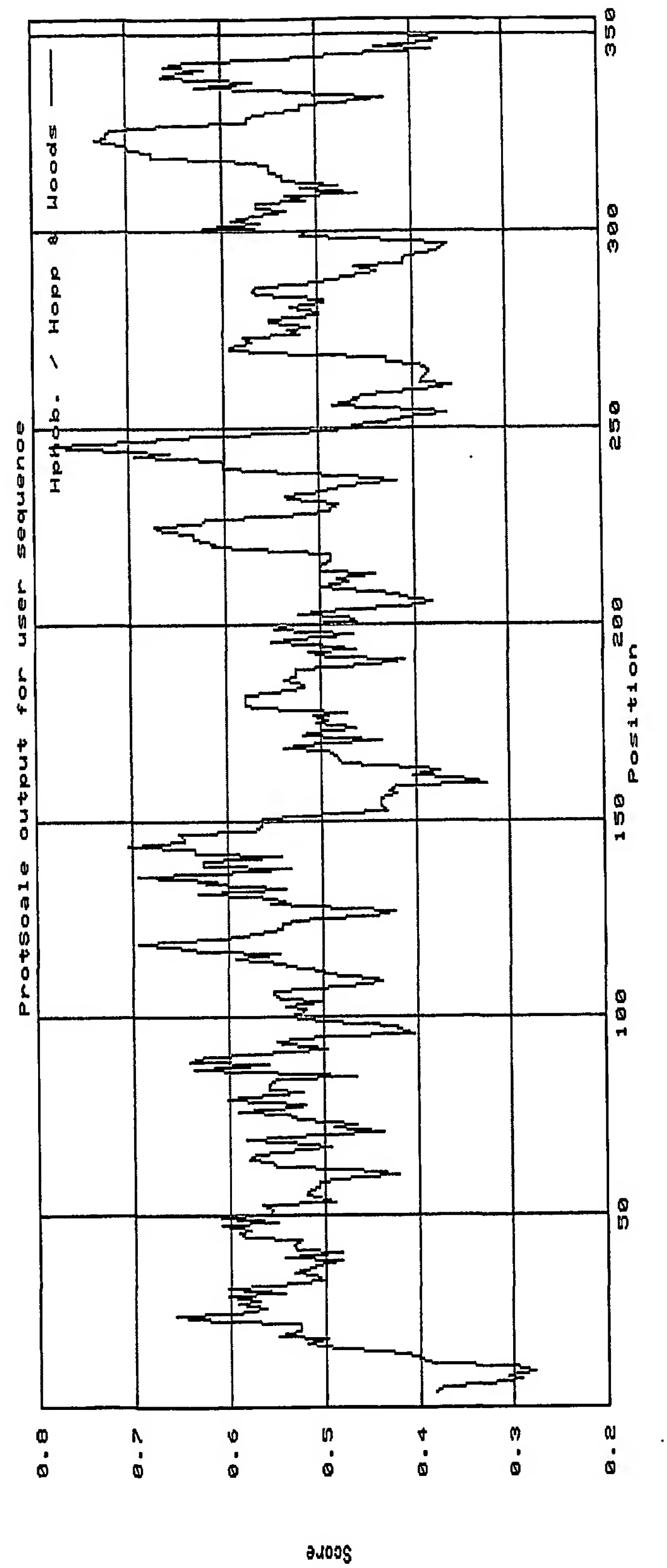


Figure 5B

151P3D4 variant 2 Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

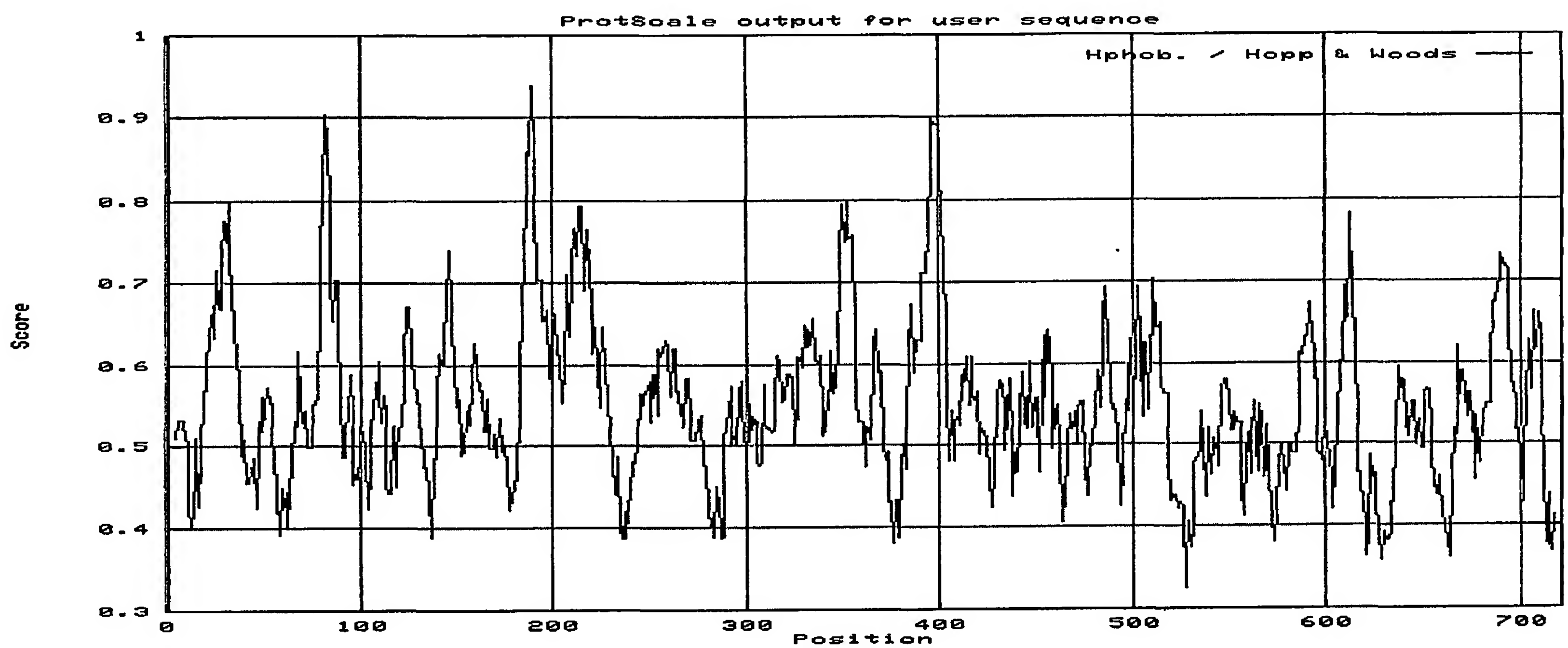


Figure 6A
151P3D4 variant 1 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

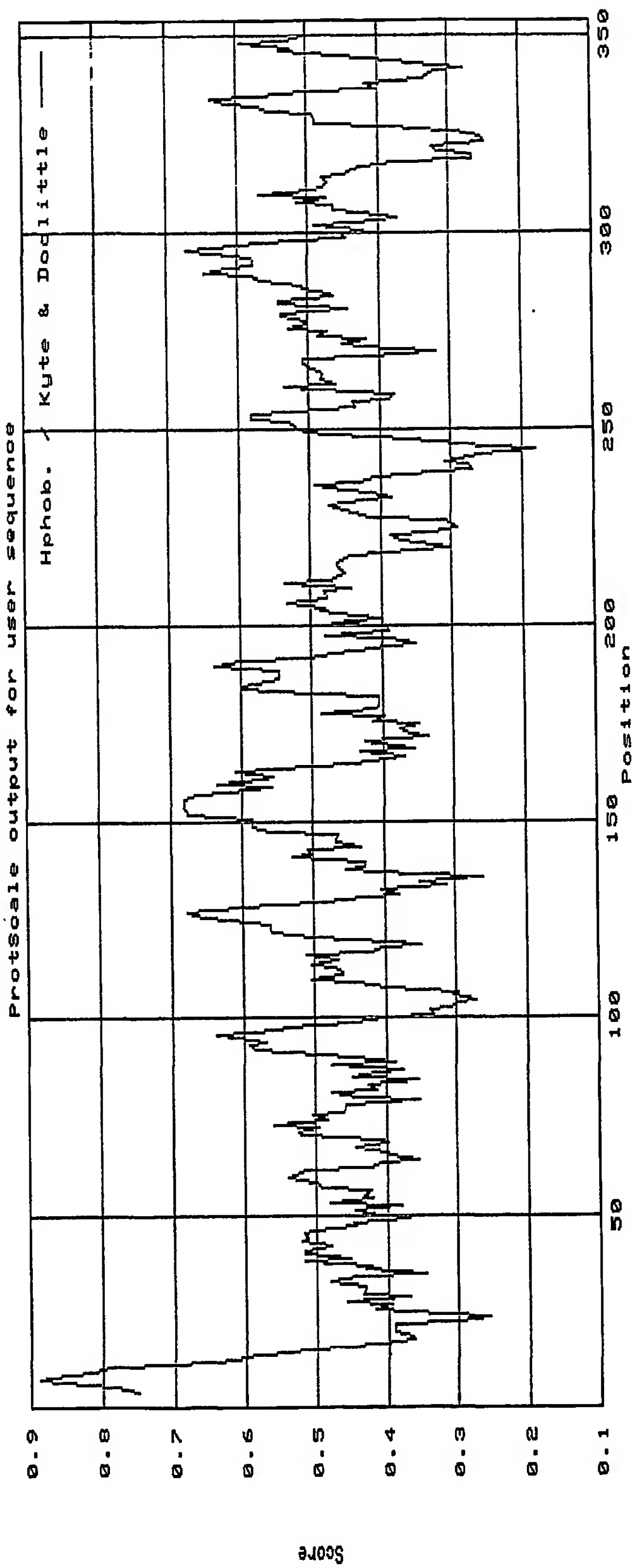


Figure 6B

151P3D4 variant 2 Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

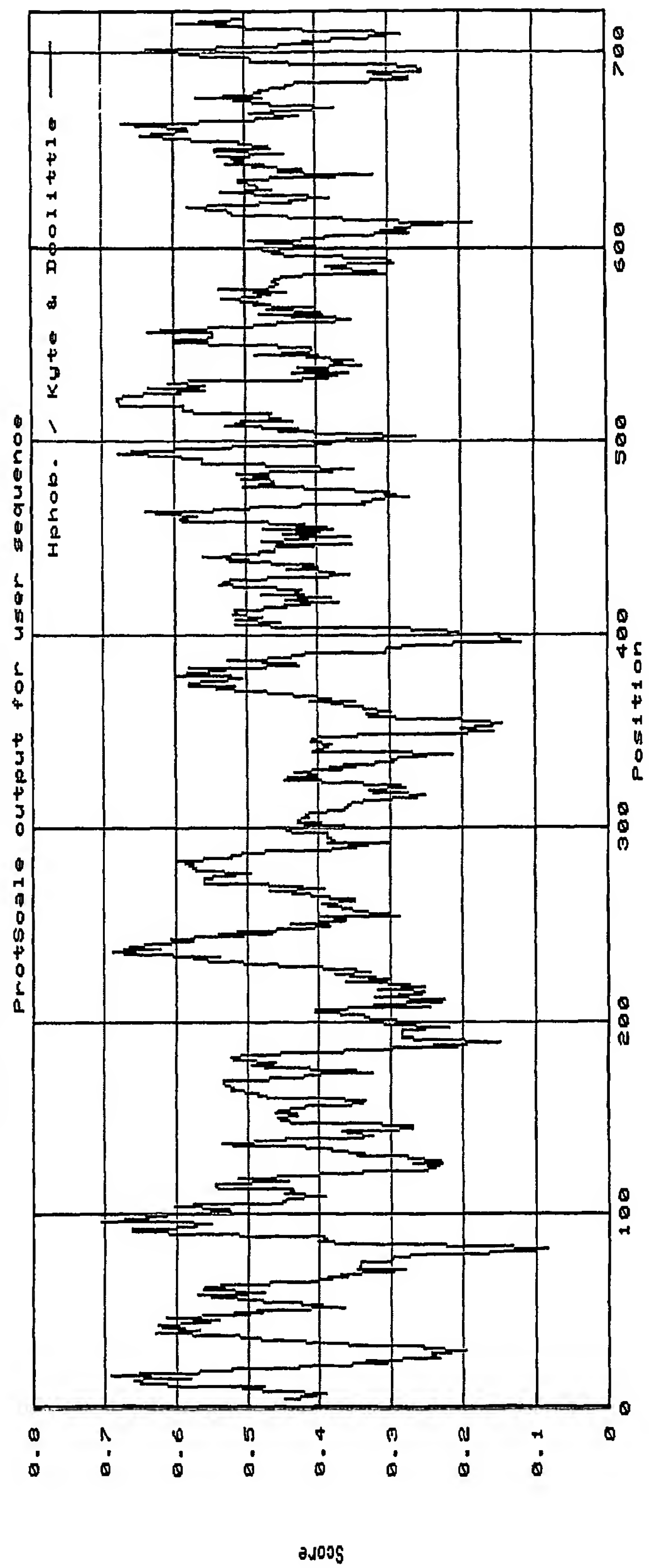


Figure 7A

151P3D4 variant 1 % Accessible Residues Profile

(Janin J., 1979. Nature 277:491-492)

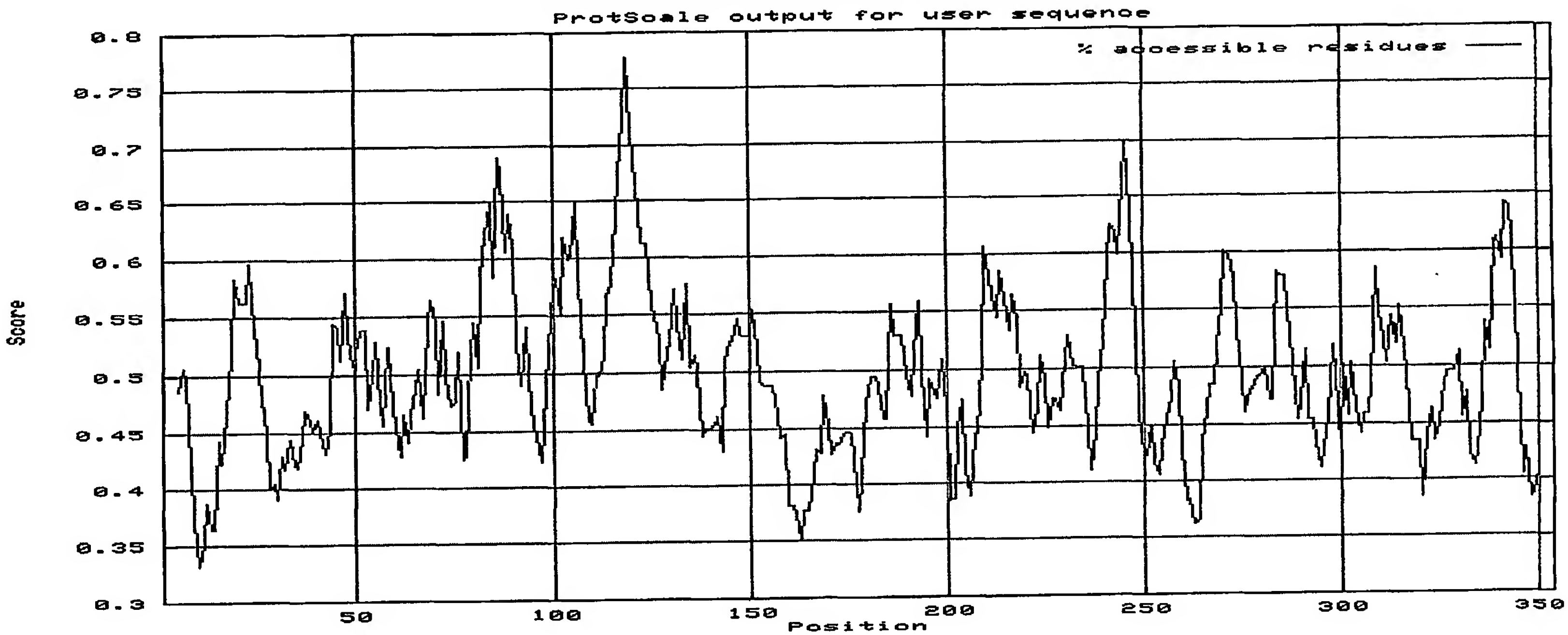


Figure 7B

151P3D4 variant 2 % Accessible Residues Profile

(Janin J., 1979. Nature 277:491-492)

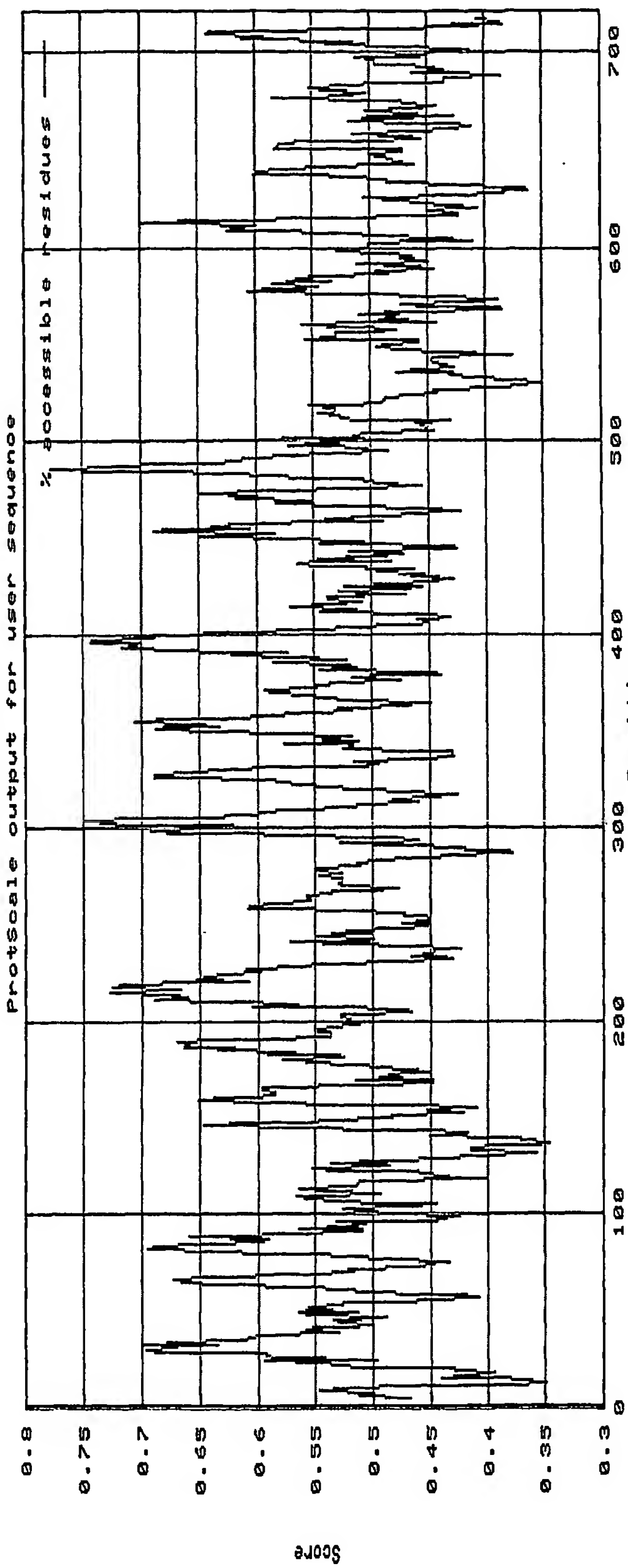


Figure 8A

151P3D4 variant 1 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

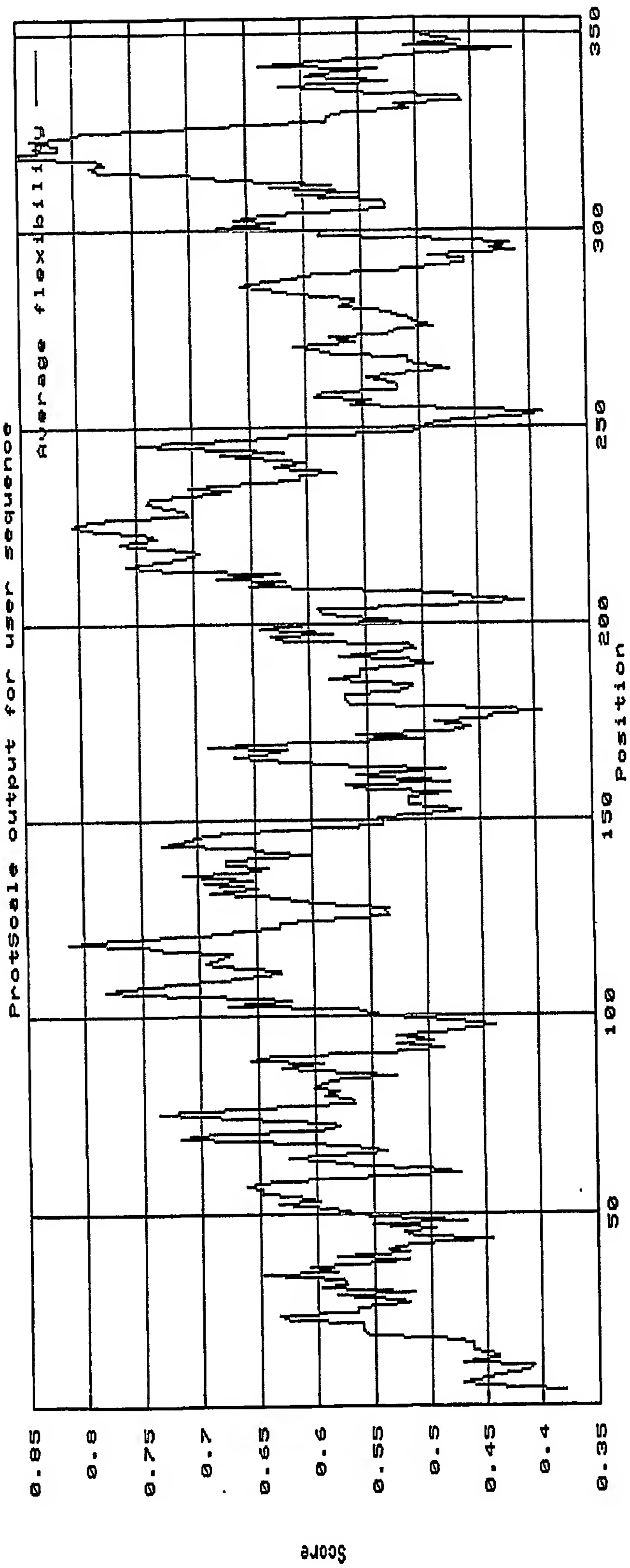


Figure 8B

151P3D4 variant 2 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

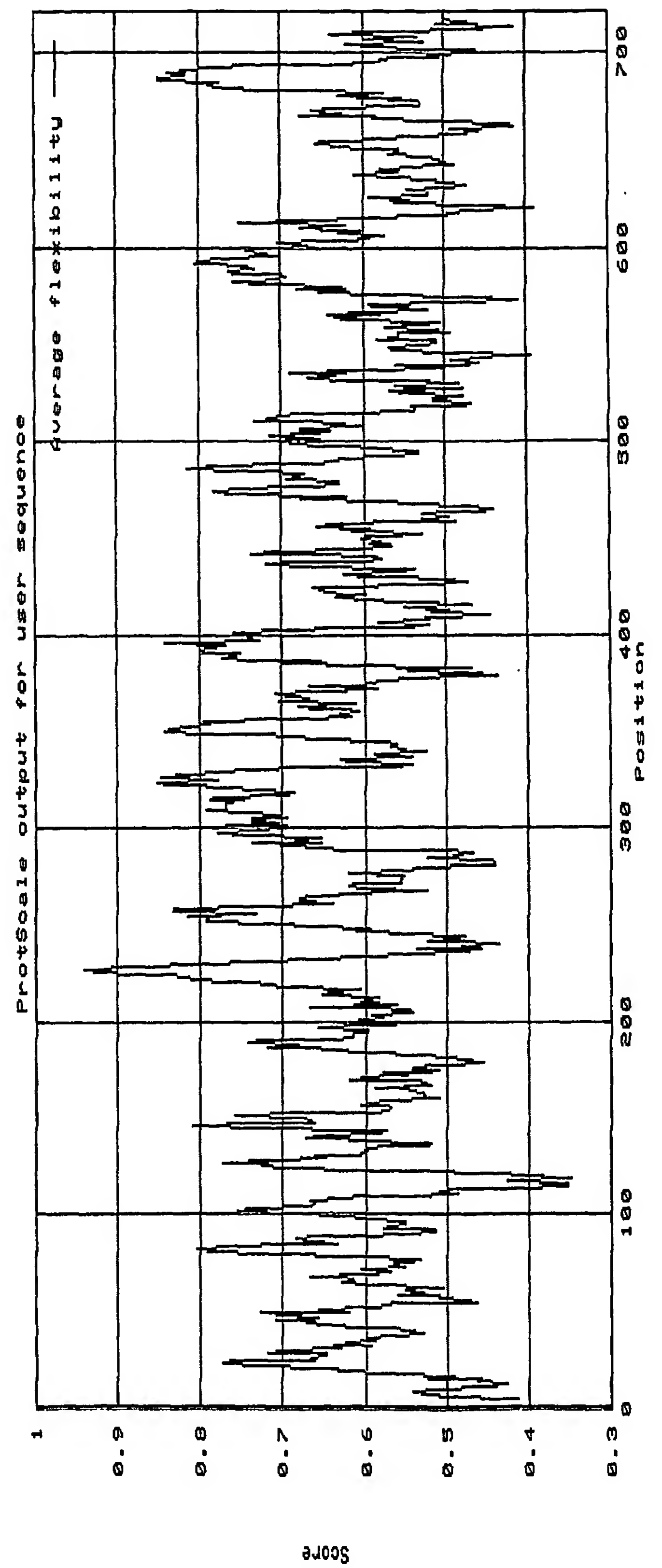


Figure 9A

151P3D4 variant 1 Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

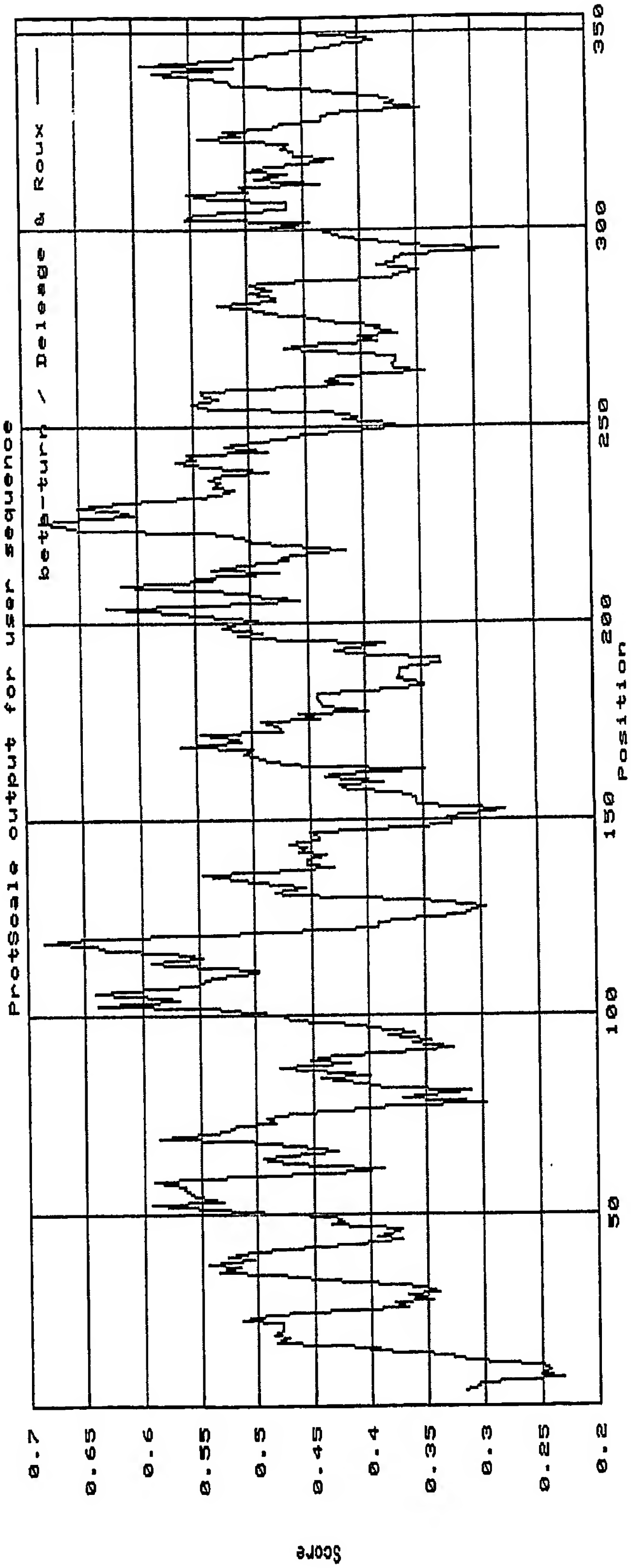


Figure 9B

151P3D4 variant 2 Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

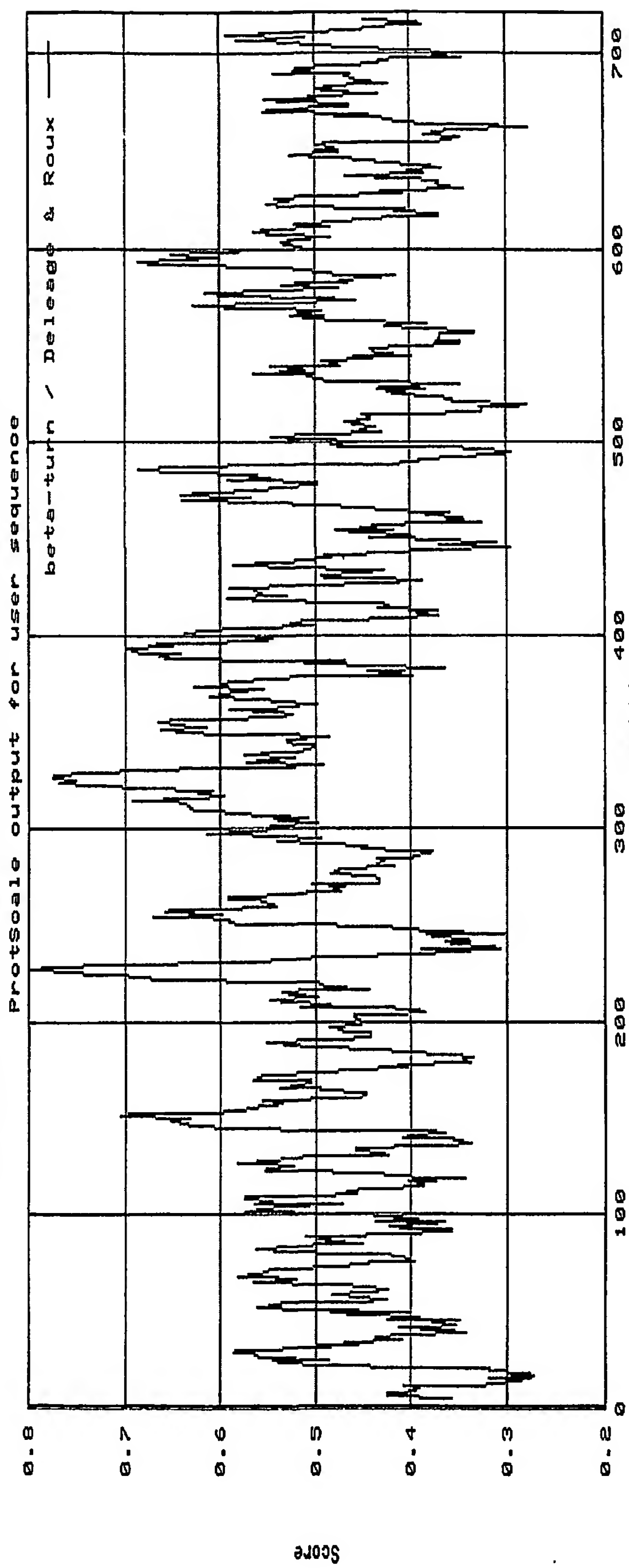


Figure 10

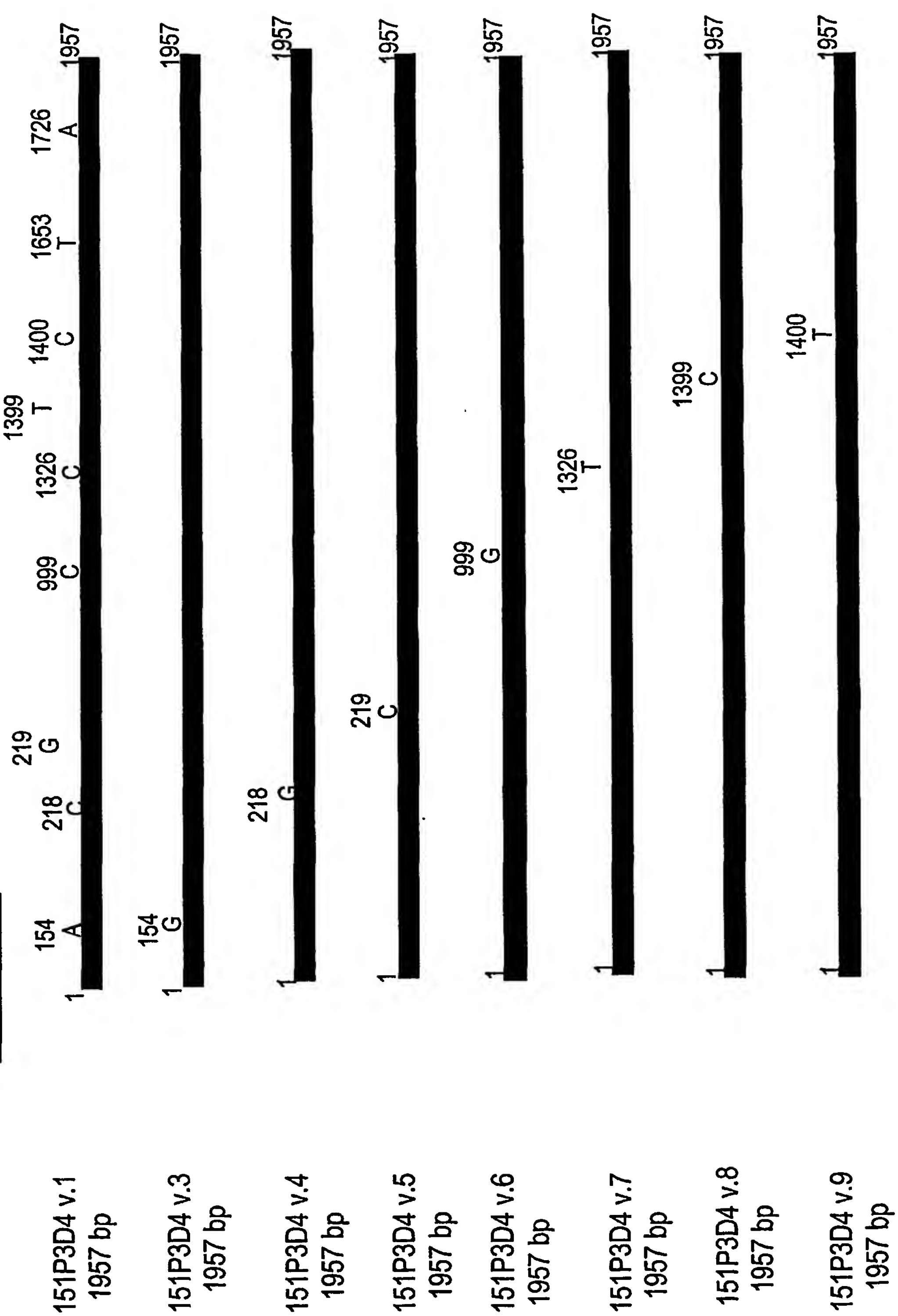

151P3D4 v.1
1957 bp
1
154
A
218
C
219
G
999
C
1326
C
1399
T
1400
C
1653
T
1726
A
1957
151P3D4 v.3
1957 bp
154
G
151P3D4 v.4
1957 bp
218
G
151P3D4 v.5
1957 bp
219
C
151P3D4 v.6
1957 bp
999
G
151P3D4 v.7
1957 bp
1326
T
151P3D4 v.8
1957 bp
1399
C
151P3D4 v.9
1957 bp
1400
T

Figure 10 (continued)

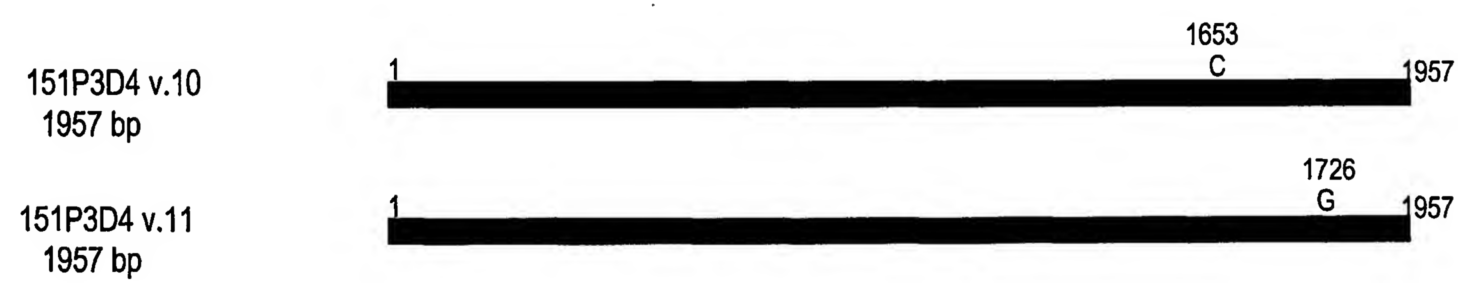


Figure 11

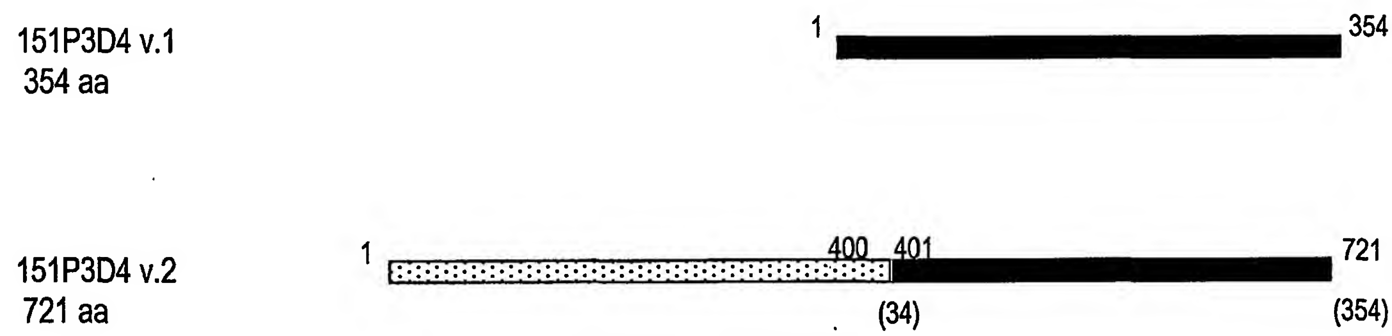


Figure 12

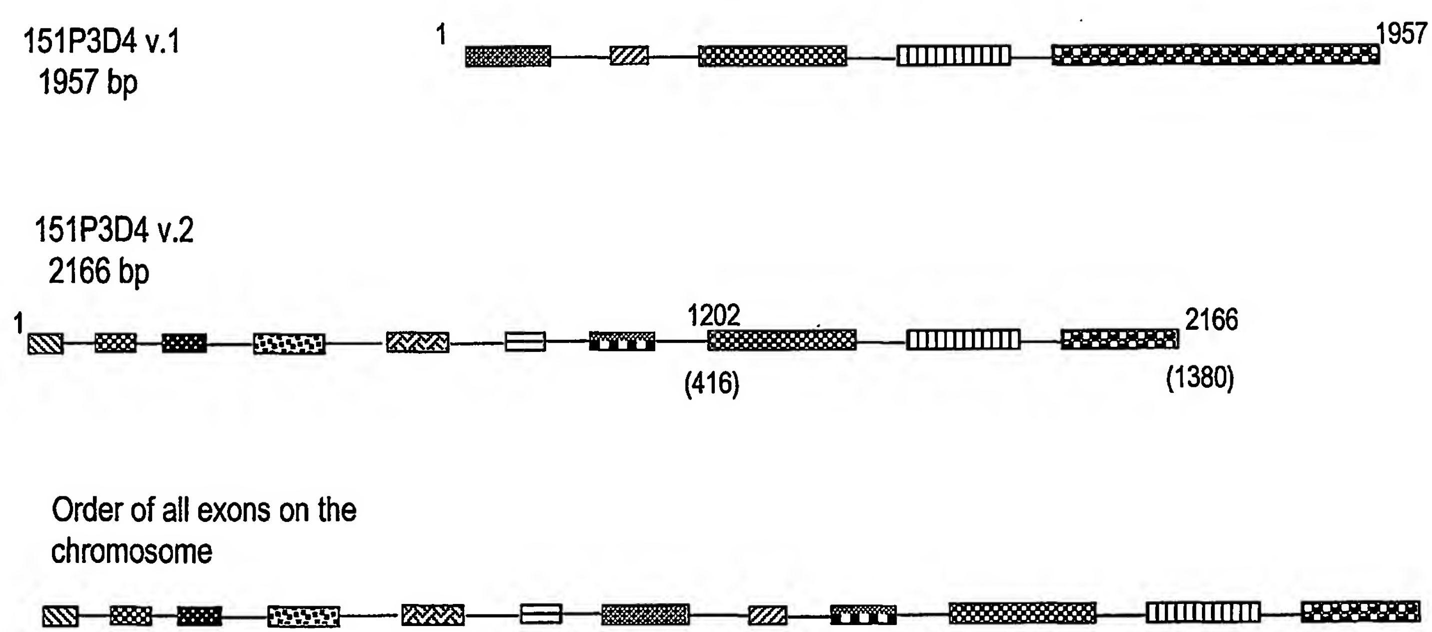

151P3D4 v.1
1957 bp
1
1957
151P3D4 v.2
2166 bp
1
1202
(416)
2166
(1380)
Order of all exons on the chromosome

Figure 13A Secondary structure prediction of 151P3D4 variant 1

```
          10        20        30        40        50        60        70
           |         |         |         |         |         |         |
MKSLLLLVLISICWADHLSDNYTLDHDRAIHIQAENGPHLLVEAEQAKVFSHRGGNVTLPCKFYRDPTAF
cchhhhhheeeeehhhcccccccchhhheeehcccccceeeehhhhhhhccccccceecccccccccc
GSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVFLKGGSDSDASLVITDLTLEDYGRYKCE
cchhheeeeehccccchhhhhhhhheeeccccccccccceeeeeecccccccceeeeeeeehcccccccehe
VIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLNFHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWL
eeecccchhheeeeehhccchecccccchhcccccchhhhhhhcccchhhhhhhhhhhhhcccccccccc
SDGSVQYPITKPREPCGGQNTVPGVRNYGFWDKDKSRYDVFCFTSNFNGRFYYLIHPTKLTYDEAVQACL
cccccccccccccccccccccccccccccccccccceeeeeeecccccceeeeeeeccccccchhhhhhhh
NDGAQIAKVGQIFAAWKILGYDRCDAGWLADGSVRYPISRPRRRCSPTEAAVRFVGFPDKKHKLYGVYCF
hcchhhhhhhhhhhhhheeccccccccccccccccccccccccccccceeeeecccccccceeeeeeee
RAYN
Eecc
```

```
Alpha helix       (h):   25.71%
Extended strand   (e):   21.47%
Random coil       (c):   52.82%
```

Figure 13B Secondary structure prediction of 151P3D4 variant 2

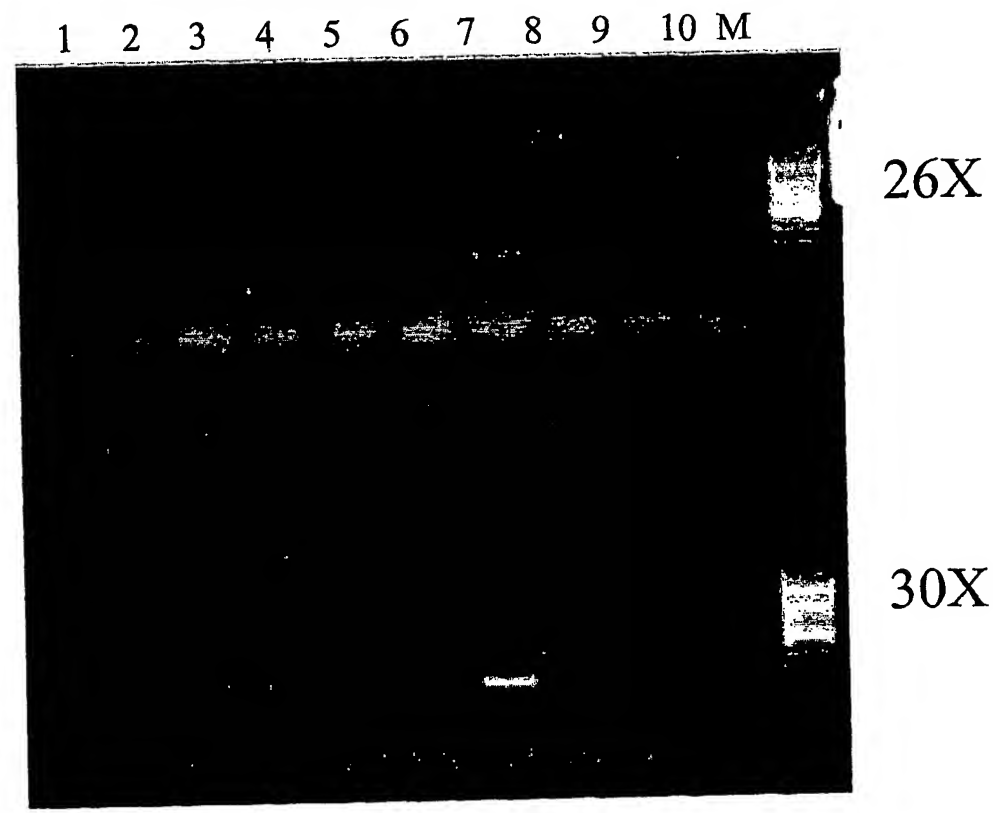
```
        10        20        30        40        50        60        70
         |         |         |         |         |         |         |
MLEHTTKTFPLRALHIVVESIRDHSGQKMKQDKKVDLLVPTKVTGIITQGAKDFGHVQFVGSYKLAYSND
cccccccccchhhheehhhhccccccccccceeeeeccceeeeeeecccccccceeeeeecceeeeeeccc
GEHWTVYQDEKQRKDKVLLGRKAVVVSCEGINISGSFCRNKLKYLAFLHKRMNTNPSRRPYHFQVPSRIF
ccceeeeccccccccceeeccceeeeeeecccccchhhhhhhhhhhhhhhhccccccccccccccchhee
WRQEKADGGSCCPQGHASEAYKKVCLSGAPHEVGWKYQAVTATLEEKRKEKAEIHYRKNKQLMRLQKQAE
eehcccccccchhchhheeeeccccccccccccchhhhhhcchhhhhhhhhhhhhhhhhhhhhhhhhhh
KNMKKKIDKYTESPGGGSPRGLGFIFKTIAPLAATRATRIGHPGGRTPRAGSSAHRPPALSARAPVPAAS
hhhhhhcccccccccccccchhhhehhhhhhhhhhhhhhccccccccccccccccccccccccccccccc
PAAWLPLRTPWTRPSSCPTSSSTYDSLSPYGPRNPLPNPRHSPSGGGGLKKPARHCQGQKHNVLARGKPQ
ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccceeeeccccc
RKPKSENNSWYVENGRPADLAGSGYCGALWKAIESLEEGLGGKQKDKERKAENGPHLLVEAEQAKVFSHR
ccccccccceeecccccccccccchhhhhhhhhhhhhhcccccchhhhhhccccceeeehhhhhhhhhcc
GGNVTLPCKFYRDPTAFGSGIHKIRIKWTKLTSDYLKEVDVFVSMGYHKKTYGGYQGRVFLKGGSDSDAS
cccceeccccccccccccchhheeeeehcccchhhhhhhhheeeccccccccccceeeeeeecccccccce
LVITDLTLEDYGRYKCEVIEGLEDDTVVVALDLQGVVFPYFPRLGRYNLNFHEAQQACLDQDAVIASFDQ
eeeeeeehcccccceheeeecchhheeeehhccchecccccchhccccchhhhhhhhcccchhhhhhhhh
LYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCGGQNTVPGVRNYGFWDKDKSRYDVFCFTSNFNGRFYY
hhhhhcccccccccccccccccccccccccccccccccccccccccccccccceeeeeeecccccceeee
LIHPTKLTYDEAVQACLNDGAQIAKVGQIFAAWKILGYDRCDAGWLADGSVRYPISRPRRRCSPTEAAVR
eecccccchhhhhhhhhhhcchhhhhhhhhhhhhheeccccccccccccccccccccccccccccccceee
FVGFPDKKHKLYGVYCFRAYN
eecccccceeeeeeeeeeecc
```

Alpha helix (h):
25.80%

Extended strand(e):
16.64%

Random coil (c):
57.56%

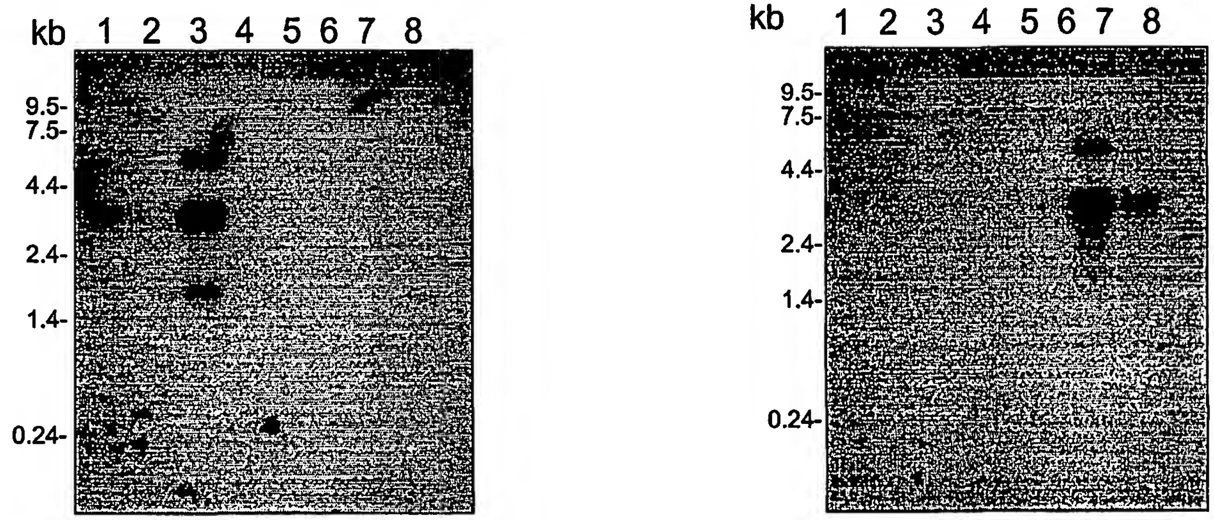
Figure 14 **Expression of 151P3D4 by RT-PCR**



1) Vital Pool 1
2) Vital Pool 2
3) Bladder Cancer Pool
4) Kidney cancer Pool
5) Colon Cancer Pool
6) Lung Cancer Pool
7) Ovary Cancer Pool
8) Breast Cancer Pool
9) Metastasis Cancer Pool
10) H2O
M = Marker

BEST AVAILABLE COPY

Figure 15 Expression of 151P3D4 in Normal Tissues by Northern Blot

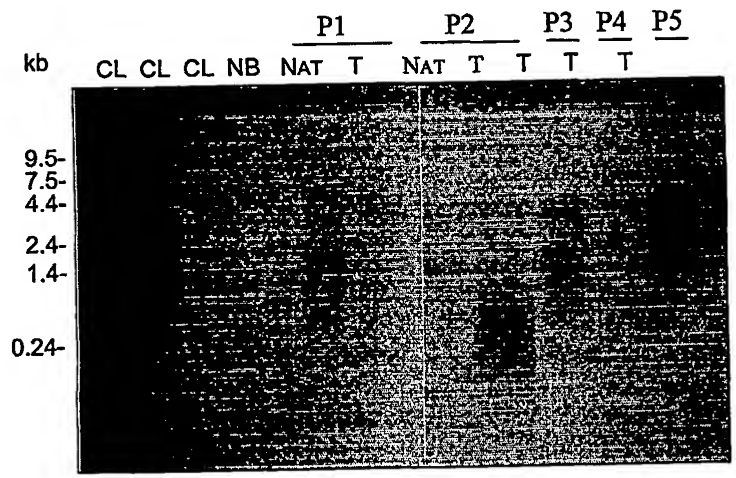


1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

BEST AVAILABLE COPY

Figure 16 Expression of 151P3D4 in Bladder Cancer Patient Specimens

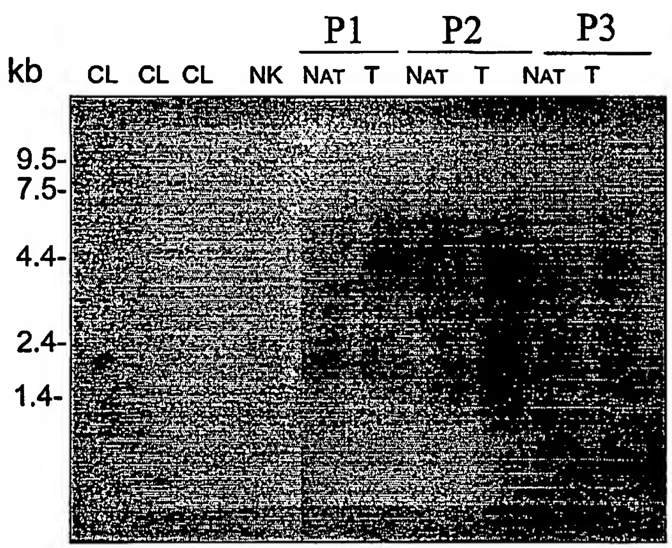


P1 - Transitional, grade 4
P2 - Transitional, invasive, grade 3
P3 - Papillary, non-invasive, grade 1/3
P4 - Papillary, invasive, grade 3/3
P5 - Transitional, grade 3/2

Cl = cell lines listed in order: UM-UC-3, J82, SCABER
P = Patient
NB = Normal Bladder
NAT = Normal adjacent tissue
T = Tumor

BEST AV...

Figure 17 Expression of 151P3D4 in Kidney Cancer Patient Specimens

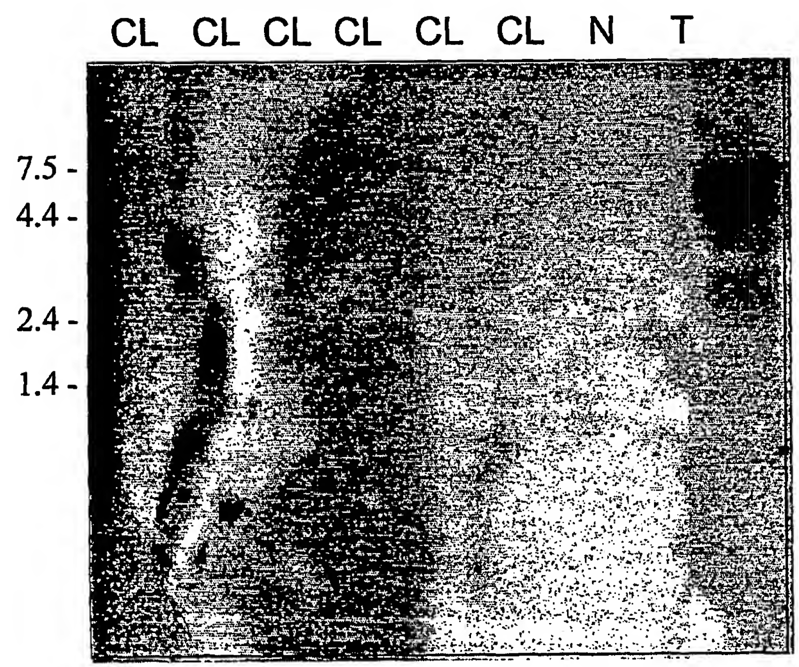


P1 - clear cell, grade 2/4
P2 - clear cell, grade 3/4
P3 - clear cell, grade 3/4

CL = cell lines listed in order: 769-P, A498, SW839
NK = Normal kidney
NAT = Normal adjacent tumor
T = Tumor

BEST AVAILABLE COPY

Figure 18 **Expression of 151P3D4 in Ovary Cancer Patient Specimens**

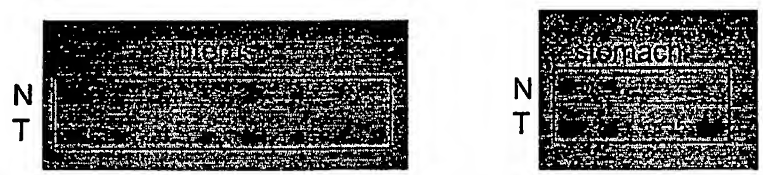


N = Normal ovary
CL = Cancer Cell lines (listed in order)
Cervical: A431, Hela
Ovarian: OV-1063, PA-1, SW-626, CaOv-3

T – Ovary cancer; granulosa tumor, low grade, stage Ia1

BEST AVAILABLE COPY

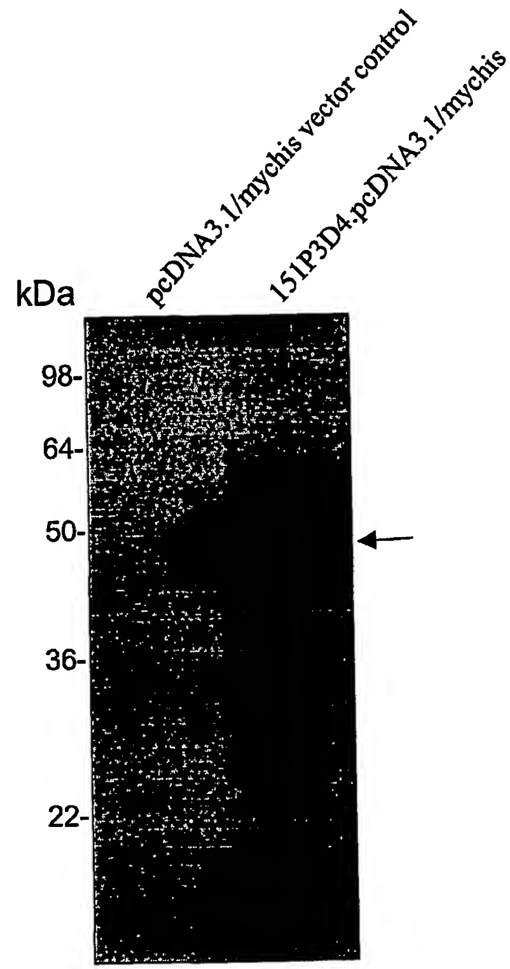
<u>Figure 19</u> Expression of 151P3D4 in stomach and uterus human cancer specimens



N = normal adjacent tissue RNA
T = tumor RNA

BEST AVAILABLE COPY

Figure 20 **151P3D4 Expression in 293T Cells Following Transfection**



BEST AVAILABLE COPY

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☑ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: ____________________

IMAGES ARE BEST AVAILABLE COPY.
As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)